

## SEARCH REQUEST FORM

Requestor's  
Name: \_\_\_\_\_Serial  
Number: \_\_\_\_\_

Date: \_\_\_\_\_

Phone: \_\_\_\_\_

Art Unit: \_\_\_\_\_

**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

**STAFF USE ONLY**Date completed: 01-21-03Searcher: Beverly C 4994Terminal time: 20

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: 30

Number of Searches: \_\_\_\_\_

Number of Databases: 1**Search Site**

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

**Type of Search**

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

**Vendors**

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

\_\_\_\_\_ ☒ Other CGN



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:20 ; Search time 5.58 Seconds  
(without alignments)  
66.897 Million cell updates/sec

Title: US-10-007-790-10  
Perfect score: 58  
Sequence: 1 QHHYGTPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	82.8	108	1	KVSD_MOUSE	P01636 mus musculus
2	40	69.0	808	1	DHG_GLUOX	P27175 gluconobact
3	38	65.5	393	1	Y732_METJA	Q58142 methanococc
4	37	63.8	288	1	ALF_MYCPN	P75089 mycoplasma
5	36	62.1	416	1	HMTI_DROME	P22711 drosophila
6	36	62.1	731	1	YB88_YEAST	P38330 saccharomyc
7	36	62.1	1687	1	Z142_HUMAN	P52746 homo sapien
8	36	62.1	2842	1	APC_RAT	P70478 rattus norv
9	36	62.1	2843	1	APC_HUMAN	P25054 homo sapien
10	36	62.1	2845	1	APC_MOUSE	O61315 mus musculu
11	35	60.3	145	1	HB22_XENBO	P07433 xenopus bor
12	35	60.3	206	1	KGUA_THETN	Q8r9s6 thermoanaer
13	35	60.3	294	1	CC2A_ARATH	P24100 arabidopsis
14	35	60.3	301	1	META_CLOAB	Q97129 clostridium
15	35	60.3	396	1	HRG_BOVIN	P33433 bos taurus
16	35	60.3	422	1	ENO_DEIRA	Q9rr60 deinococcus
17	35	60.3	480	1	YAAQ_BACSU	P37536 bacillus su
18	35	60.3	646	1	PIXB_HUMAN	Q14155 homo sapien
19	35	60.3	703	1	PIXB_RAT	O55043 rattus norv
20	35	60.3	703	1	UL17_HSV11	P10201 herpes simp
21	35	60.3	705	1	PIXB_MOUSE	Q9es28 mus musculu
22	35	60.3	965	1	AMPN_RABIT	P15541 oryctolagus
23	34	58.6	93	1	VAPD_BACNO	Q46565 bacteroides
24	34	58.6	95	1	VAPD_ACTAC	O52243 actinobacil
25	34	58.6	114	1	KV4A_HUMAN	P01625 homo sapien
26	34	58.6	140	1	TYRT_STRLN	P55048 streptomyce
27	34	58.6	149	1	KV5A_MOUSE	P01633 mus musculu
28	34	58.6	239	1	KGUA_DEIRA	Q9ra38 deinococcus
29	34	58.6	269	1	HXA9_MORSA	Q9pww5 morone saxa
30	34	58.6	270	1	COX3_CVACA	P48873 cyanidium c
31	34	58.6	313	1	SPEB_STRCL	P37819 streptomyce
32	34	58.6	315	1	GBF1_ARATH	P42774 arabidopsis
33	34	58.6	321	1	HMDL_BRAFL	P53772 branchiosto

34	34	58.6	361	1	KITH_HSVSM	P04408 herpesvirus
35	34	58.6	399	1	LGI_MAIZE	O04003 zea mays (m
36	34	58.6	475	1	PAAH_ECOLI	P76083 escherichia
37	34	58.6	475	1	VP40_HSVSA	Q01002 herpesvirus
38	34	58.6	482	1	YSR2_CAEEL	O09950 caenorhabdi
39	34	58.6	647	1	KMIL_CHICK	P05825 gallus gall
40	34	58.6	648	1	KRAF_HUMAN	P04049 homo sapien
41	34	58.6	648	1	KRAF_RAT	P11345 rattus norv
42	34	58.6	835	1	AXN1_BRARE	P57094 brachydanio
43	34	58.6	880	1	BRC4_DROME	Q24206 drosophila
44	34	58.6	1115	1	TBC2_CHLRE	O8vxp3 chlamydomon
45	34	58.6	1132	1	TERT_HUMAN	O14746 homo sapien

ALIGNMENTS

RESULT 1  
KVSD\_MOUSE STANDARD; PRT; 108 AA.  
AC P01636;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region MOPC 149.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE.  
RC STRAIN=BALB/c;  
RX MEDLINE=82057806; PubMed=6795447;  
RA Appella E., Alvarez V.L.;  
RT "Amino acid sequence of the variable region of M149 mouse myeloma  
light chain: comparison with the nucleotide sequence of K2 and K3  
clones."  
RL Mol. Immunol. 17:1507-1513(1980).  
CC -!- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR HSP; P01607; 1REI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
KW SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 12030 MW; 0B5244D2B410D84C CRC64;

Query Match 82.8%; Score 48; DB 1; Length 108;  
Best Local Similarity 77.8%; Pred. No. 0.042;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 89 QHHYGTPT 97

RESULT 2  
DHG\_GLUOX STANDARD; PRT; 808 AA.  
ID DHG\_GLUOX  
AC P27175;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glucose dehydrogenase [pyrroloquinoline-quinone] precursor  
DE (EC 1.1.1.99.17).  
GN GH.  
OS Gluconobacter oxydans (Gluconobacter suboxydans).  
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;  
OC Gluconobacter.  
OX NCBI\_TaxID=442;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=92017653; PubMed=1833618;  
RA Cleton-Jansen A.-M., Dekker S., van de Putte P., Goosen N.;  
RA "A single amino acid substitution changes the substrate specificity  
RT of quinoprotein glucose dehydrogenase in Gluconobacter oxydans.";  
RL Mol. Gen. Genet. 229:206-212(1991).  
RN [2]  
RN REVISION TO 213.  
RA Goosen N.;  
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: D-glucose + acceptor = D-glucono-1,5-lactone +  
CC reduced acceptor.  
CC -1- COFACTOR: PQ.  
CC -1- SUBCELLULAR LOCATION: OUTSIDE OF THE PERIPLASMIC MEMBRANE.  
CC -1- MISCELLANEOUS: THE P1 FORM CAN OXIDIZE ONLY D-GLUCOSE, WHILE THE  
CC P2 FORM CAN ALSO OXIDIZE MALTOSE. THE SEQUENCE OF P1 FORM IS SHOWN  
CC HERE.  
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQO DEHYDROGENASE FAMILY.  
CC  
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CC  
CC EMBL; X62710; CAA44594.1; ALT\_SEQ.  
DR PIR; S17716; OPKEX.  
DR InterPro; IPR001479; Bac\_PQO.  
DR InterPro; IPR002372; Bac\_PQO\_repeat.  
DR Pfam; PF01011; Bacterial\_PQO; 7.  
DR PROSITE; PS00363; BACTERIAL\_PQO\_1; 1.  
DR PROSITE; PS00364; BACTERIAL\_PQO\_2; 1.  
KW Oxidoreductase; PQO; Transmembrane; Periplasmic; Signal.  
FT SIGNAL 1 33 POTENTIAL.  
FT CHAIN 34 808 GLUCOSE DEHYDROGENASE [PYRROLOQUINOLINE-  
FT QUINONE)].  
FT TRANSMEM 35 54 POTENTIAL.  
FT TRANSMEM 59 76 POTENTIAL.  
FT TRANSMEM 94 108 POTENTIAL.  
FT TRANSMEM 123 138 POTENTIAL.  
FT ACT\_SITE 470 470 BASE (POTENTIAL).  
FT VARIANT 788 788 H -> N (IN P2 FORM).  
SQ SEQUENCE 808 AA; 87567 MW; 0F4160DA78652445 CRC64;  
Query Match 69.0%; Score 40; DB 1; Length 808;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 QHNYGTPY 8  
Db 647 QHNYGIPY 654  
RESULT 3  
ID Y732\_METJA STANDARD; PRT; 393 AA.  
AC Q58142;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein MJ0732.  
GN MJ0732.  
OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanocaldococcaceae; Methanocaldococcus.  
OX NCBI\_TaxID=2190;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
RX MEDLINE=96337999; PubMed=8688087;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  
RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
RT jannaschii.";  
RL Science 273:1058-1073(1996).  
CC -1- SIMILARITY: STRONG, TO M.JANNASCHII MJ0748, AND LOW, TO  
CC M.JANNASCHII MJ0534.  
CC  
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CC  
CC EMBL; U67519; AAB98728.1; -.  
DR HSSP; Q9F0J6; 1E5D.  
DR TIGR; MJ0732; -.  
DR InterPro; IPR001279; Blactmase-like.  
DR InterPro; IPR001226; Flavodoxin.  
DR Pfam; PF00258; flavodoxin; 1.  
DR Pfam; PF00753; lactamase B; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 393 AA; 45554 MW; CF01B59793BBA20F CRC64;  
Query Match 65.5%; Score 38; DB 1; Length 393;  
Best Local Similarity 85.7%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 HHYGTPT 8  
Db 26 HGXGTPY 32  
RESULT 4  
ID ALF\_MYCPN STANDARD; PRT; 288 AA.  
AC P75089;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Fructose-bisphosphate aldolase (EC 4.1.2.13).  
GN FBA OR TSR OR MPN025 OR MP129.  
OS Mycoplasma pneumoniae.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2104;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=ATCC 29342 / M129;  
RX MEDLINE=97105885; PubMed=8948633;  
RA Himmelreich R., Hilbert H., Plogens H., Pirkel E., Li B.-C.,  
RA Herrmann R.;  
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
RT pneumoniae";  
RL Nucleic Acids Res. 24:4420-4449(1996).  
CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyceraldehyde  
CC phosphate + D-glyceraldehyde 3-phosphate.  
CC -1- COFACTOR: ZINC (BY SIMILARITY).  
CC -1- PATHWAY: Glycolysis; sixth step.

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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE
CC FAMILY.
CC
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CC -----
CC EMBL; A8000015; AAB95777.1; -
CC HSSP; P11604; IBS7.
CC InterPro; IPR000771; F bp aldolase.
CC Pfam; PF01116; F bp aldolase; 1.
CC ProDom; PD002376; F bp aldolase; 1.
CC TIGRFAMs; TIGR00167; cbaa; 1.
CC PROSITE; PS00602; ALDOLASE_CLASS_II_1; FALSE_NEG.
CC PROSITE; PS00806; ALDOLASE_CLASS_II_2; 1.
CC Lyase; Glycolysis; Zinc; Complete proteome.
CC METAL 82 ZINC (BY SIMILARITY).
CC METAL 85 ZINC (BY SIMILARITY).
CC SEQUENCE 288 AA; 31069 MW; 17487F2E4E215FD8 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 288;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
DB 14 QHHYAVPH 21

RESULT 5
HMTI_DROME STANDARD; PRT; 416 AA.
AC P22711;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Muscle-specific homeobox protein timman (Msh-2) (NK-4).
GN TIN OR MSH2.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91209226; PubMed=1982429;
RA Bodmer R.; Jan L.Y.; Jan Y.N.;
RT "A new homeobox-containing gene, msh-2, is transiently expressed
RT early during mesoderm formation of Drosophila.";
RL Development 110:661-669(1990).
RN [2]
RP SEQUENCE OF 267-416 FROM N.A.
RX MEDLINE=90046666; PubMed=2573059;
RA Kim Y.; Nirenberg M.;
RT "Drosophila NK-homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7716-7720(1989).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=94357069; PubMed=7915669;
RA Bodmer R.;
RT "The gene timman is required for specification of the heart and
RT visceral muscles in Drosophila.";
RL Development 118:719-729(1993).
CC -1- FUNCTION: REQUIRED FOR THE DEVELOPMENT OF VISCERAL MUSCLE; FOR THE
CC FORMATION OF SOMATIC MUSCLES. HAS A CRUCIAL FUNCTION IN THE EARLY
CC MESODERMAL SUBDIVISIONS. LOSS OF ACTIVITY RESULTS IN ABSENCE OF
CC CARDIAC AND MIDGUT VISCERAL MUSCLE, AND DEFECTS IN A SUBSET OF
CC DORSAL BODY WALL MUSCLES.
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CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: IS INITIALLY EXPRESSED THROUGHOUT THE
CC PRESUMPTIVE MESODERM AND BECOMES RESTRICTED TO CARDIAC AND
CC VISCERAL MUSCLE.
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CC -----
CC EMBL; X55192; CAA38978.1; -
CC EMBL; M27292; AAA28619.1; -
CC Pfam; D33976; D33976.
CC PIR; A43561; A43561.
CC HSSP; P23441; 1FTT.
CC TRANSFAC; T03612; -.
CC FlyBase; FBgn0004110; tin.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT DOMAIN 119 122 POLY-PRO.
FT DNA_BIND 301 360 HOMEBOX.
FT DOMAIN 398 405 POLY-GLN.
FT DOMAIN 409 414 POLY-GLN.
FT SEQUENCE 416 AA; 46124 MW; 77A6AEGF1EAA4FD7 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 416;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
DB 140 QHHGHGPH 147

RESULT 6
YB88 YEAST STANDARD; PRT; 731 AA.
AC P38330;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 83.7 kDa protein in PRP5-THI2 intergenic region.
GN YBR238C OR YBR1608.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Aljinovic G.; Pohl F.M.; Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YGL107C.
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CC -----
CC EMBL; Z36107; CAA85201.1; -
CC PIR; S46115; S46115.
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DR SGD: S0000442; YBR238C.
KW Hypothetical protein.
SQ SEQUENCE 731 AA; 83761 MW; 4A6800D8475F3DE2 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 731;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 OHHYGTPYT 9
Db 44 EHNYAIPYT 52

RESULT 7
Z142_HUMAN STANDARD; PRT; 1687 AA.
AC P52746; Q92510;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 142 (HA4654).
GN ZNF142 OR KIAA0236.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN [2]
RP SEQUENCE OF 460-632 FROM N.A.
RC TISSUE=Insulinoma;
RX MEDLINE=96044430; PubMed=7557990;
RA Tommerup N., Vissing H.;
RT "Isolation and fine mapping of 16 novel human zinc finger-encoding
RT cDNAs identify putative candidate genes for developmental and
RT malignant disorders.";
RL Genomics 27:259-264(1995).
CC -!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
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CC -----
DR EMBL; D87073; BAAL3242.1; -.
DR EMBL; U09849; AAC50265.1; -.
DR Genew; HGNC:12927; ZNF142.
DR MIM; 604083; -.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 35.
DR PRINTS; PR00048; ZINCFINGER.
DR SMART; SM00355; Znf_C2H2; 34.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 17.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 18.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT DOMAIN 163 1643 ZINC_FINGERS.
FT ZN_FING 163 185 C2H2-TYPE.
FT ZN_FING 219 242 C2H2-TYPE.
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FT ZN_FING 253 275 C2H2-TYPE.
FT ZN_FING 286 311 C2H2-TYPE (ATYPICAL).
FT ZN_FING 316 340 C2H2-TYPE.
FT ZN_FING 343 366 C2H2-TYPE.
FT ZN_FING 372 395 C2H2-TYPE.
FT ZN_FING 401 423 C2H2-TYPE.
FT ZN_FING 429 451 C2H2-TYPE.
FT ZN_FING 457 479 C2H2-TYPE.
FT ZN_FING 485 507 C2H2-TYPE.
FT ZN_FING 512 536 C2H2-TYPE.
FT ZN_FING 544 567 C2H2-TYPE.
FT ZN_FING 573 596 C2H2-TYPE.
FT ZN_FING 1135 1158 C2H2-TYPE.
FT ZN_FING 1171 1194 C2H2-TYPE.
FT ZN_FING 1200 1222 C2H2-TYPE.
FT ZN_FING 1228 1251 C2H2-TYPE.
FT ZN_FING 1257 1280 C2H2-TYPE.
FT ZN_FING 1286 1309 C2H2-TYPE.
FT ZN_FING 1328 1351 C2H2-TYPE.
FT ZN_FING 1354 1377 C2H2-TYPE.
FT ZN_FING 1380 1403 C2H2-TYPE.
FT ZN_FING 1424 1446 C2H2-TYPE.
FT ZN_FING 1452 1474 C2H2-TYPE.
FT ZN_FING 1480 1502 C2H2-TYPE.
FT ZN_FING 1508 1530 C2H2-TYPE.
FT ZN_FING 1536 1559 C2H2-TYPE.
FT ZN_FING 1565 1587 C2H2-TYPE.
FT ZN_FING 1593 1615 C2H2-TYPE.
FT ZN_FING 1621 1643 C2H2-TYPE.
FT CONFLICT 460 463 TECG -> LKGS (IN REF. 2).
FT CONFLICT 541 541 S -> A (IN REF. 2).
SQ SEQUENCE 1687 AA; 187865 MW; 42847520F04D38E7 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 1687;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OHHYGTP 7
Db 534 QHHPGP 540

RESULT 8
APC_RAT STANDARD; PRT; 2842 AA.
AC P70478;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenomatous polyposis coli protein (APC protein).
GN APC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344/N; TISSUE=Brain;
RX MEDLINE=96116966; PubMed=8563176;
RA Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
RA Sugimura T., Nagao M.;
RT "cDNA cloning of the rat APC gene and assignment to chromosome 18.";
RL Mamm. Genome 6:745-748(1995).
RN [2]
RP MUTAGENESIS.
RC STRAIN=Sprague-Dawley, and FISCHER 344/N;
RX MEDLINE=95148647; PubMed=7846077;
RA Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
RA Weisburger J.H., Sugimura T., Nagao M.;
RT "Specific 5'-GGGA-3'-->5'-GGA-3' mutation of the APC gene in rat colon
RT tumors induced by 2-amino-1-methyl-6-phenylimidazo(4,5-b)pyridine.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
CC -!- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-
```

CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE  
 ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY  
 SIMILARITY).  
 CC -1- SUBUNIT: FORMS HOMOLOGOMERS AND ASSOCIATES WITH CATENINS (BY  
 SIMILARITY).  
 CC -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 7 ARM REPEATS.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D38629; BAA07609.1; --  
 DR HSSP: Q02248; 3BCT.  
 DR InterPro: IPR000225; Armadillo.  
 DR Pfam: PF00514; Armadillo\_seg; 6.  
 DR SMART: SM00185; ARM; 5.  
 DR PROSITE: PS00176; ARM\_REPEAT; 1.  
 KW Anti-oncogene; Phosphorylation; Coiled coil; Repeat.  
 FT DOMAIN 1 728 LEU-RICH.  
 FT DOMAIN 1 62 COILED COIL (POTENTIAL).  
 FT DOMAIN 125 260 COILED COIL (POTENTIAL).  
 FT REPEAT 451 493 ARM 1.  
 FT REPEAT 503 545 ARM 2.  
 FT REPEAT 546 589 ARM 3.  
 FT REPEAT 590 636 ARM 4.  
 FT REPEAT 637 681 ARM 5.  
 FT REPEAT 682 723 ARM 6.  
 FT REPEAT 724 765 ARM 7.  
 FT DOMAIN 739 2831 SER-RICH.  
 FT DOMAIN 1130 1155 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 1864 1891 HIGHLY CHARGED.  
 FT MUTAGEN 523 523 C->R: IN AN IQ-INDUCED COLON TUMOR.  
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 Best Local Similarity 63.6%; Pred. No. 2.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 QY 2 HHY----GTPY 8  
 Db 1842 HHYAPIEGTPY 1852  
 RESULT 9  
 APC HUMAN  
 ID APC\_HUMAN STANDARD; PRT; 2843 AA.  
 AC P25054; Q15162; Q15163;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Adenomatous polyposis coli protein (APC protein).  
 GN APC OR DP2.5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=91335210; PubMed=1651562;  
 RA Kinzler K.W., Nilbert M.C., Su L.-K., Vogelstein B., Bryan T.M.,  
 RA Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D.,  
 RA Finnear R., Markham A., Groffen J., Boguski M.S., Altschul S.F.,  
 RA Horii A., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.;  
 RT "Identification of FAP locus genes from chromosome 5q21.";  
 RL Science 253:661-665(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=Petal brain;  
 RX MEDLINE=91330307; PubMed=1678319;  
 RA Joslyn G., Carlson M., Thliveris A., Albertsen H., Gelbert L.,  
 RA Samowitz W., Groden J., Stevens J., Spirio L., Robertson M.,  
 RA Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P.,  
 RA Warrington J., McPherson J.D., Wasmuth J., Le Paslier D.,  
 RA Abderrahim H., Cohen D., Leppert M., White R.;  
 RT "Identification of deletion mutations and three new genes at the  
 RT familial polyposis locus.";  
 RL Cell 66:601-613(1991).  
 RN [3]  
 RP ASSOCIATION WITH CATENINS.  
 RX MEDLINE=94082295; PubMed=8259519;  
 RA Su L.-K., Vogelstein B., Kinzler K.W.;  
 RT "Association of the APC tumor suppressor protein with catenins.";  
 RL Science 262:1734-1737(1993).  
 RN [4]  
 RP DISEASE.  
 RX MEDLINE=95174843; PubMed=7661930;  
 RA Hamilton S.R., Liu B., Parsons R.E., Papadopoulos N., Jen J.,  
 RA Powell S.M., Krush A.J., Berk T., Cohen Z., Tetu B., Burger P.C.,  
 RA Wood P.A., Taqi F., Booker S.V., Petersen G.M., Offerhaus G.J.A.,  
 RA Tersmette A.C., Giardiello F.M., Vogelstein B., Kinzler K.W.;  
 RT "The molecular basis of Turcot's syndrome.";  
 RL New Engl. J. Med. 332:839-847(1995).  
 RN [5]  
 RP DISEASE.  
 RX MEDLINE=97094176; PubMed=8940264;  
 RA Eccles D.M., van der Luijt R., Breukel C., Bullman H., Bunyan D.,  
 RA Fisher A., Barber J., du Boulay C., Primrose J., Burn J., Fodde R.;  
 RT "Hereditary desmoid disease due to a frameshift mutation at codon 1924  
 RT of the APC gene.";  
 RL Am. J. Hum. Genet. 59:1193-1201(1996).  
 RN [6]  
 RP DISEASE.  
 RX MEDLINE=20243021; PubMed=10782927;  
 RA Couture J., Matri A., Lagace R., Smits R., Berk T., Bouchard H.-L.,  
 RA Fodde R., Alman B., Bapat B.;  
 RT "A germline mutation at the extreme 3-prime end of the APC gene  
 RT results in a severe desmoid phenotype and is associated with  
 RT overexpression of beta-catenin in the desmoid tumor.";  
 RL Clin. Genet. 57:205-212(2000).  
 RN [7]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=94154728; PubMed=8111410;  
 RA Nagae H., Nakamura Y.;  
 RT "Mutations of the APC (adenomatous polyposis coli) gene.";  
 RL Hum. Mutat. 2:425-434(1993).  
 RN [8]  
 RP VARIANTS FAP.  
 RX MEDLINE=91335211; PubMed=1651563;  
 RA Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A.,  
 RA Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.,  
 RA Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,  
 RA Preisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B.;  
 RT "Mutations of chromosome 5q21 genes in FAP and colorectal cancer  
 RT patients.";  
 RL Science 253:665-669(1991).  
 RN [9]  
 RP VARIANTS FAP.  
 RX MEDLINE=93265030; PubMed=1338904;  
 RA Miyoshi Y., Nagase H., Ando H., Ichii S., Nakatsuru S., Aoki T.,  
 RA Miki Y., Mori T., Nakamura Y.;  
 RT "Somatic mutations of the APC gene in colorectal tumors: mutation  
 RT cluster region in the APC gene.";  
 RL Hum. Mol. Genet. 1:229-233(1992).  
 RN [10]  
 RP VARIANTS FAP.  
 RX MEDLINE=93244793; PubMed=1338691;  
 RA Nakatsuru S., Yanagisawa A., Ichii S., Tahara E., Kato Y.,  
 RA Nakamura Y., Horii A.;  
 RT "Somatic mutation of the APC gene in gastric cancer: frequent  
 RT mutations in very well differentiated adenocarcinoma and signet-ring

RT cell carcinoma.";  
 RL Hum. Mol. Genet. 1:559-563(1992).  
 RN [11]  
 RP VARIANT FAP W-1348, AND VARIANTS D-1118; M-1292; V-1304 AND S-2502.  
 RX MEDLINE=93250848; PubMed=1338764;  
 RA Nagase H., Miyoshi Y., Horii A., Aoki T., Petersen G.M.,  
 RA Vogelstein B., Maher E., Ogawa M., Maruyama M., Utsunomiya J.,  
 RA Baba S., Nakamura Y.;  
 RT "Screening for germ-line mutations in familial adenomatous polyposis  
 RT patients: 61 new patients and a summary of 150 unrelated patients.";  
 RL Hum. Mutat. 1:467-473(1992).  
 RN [12]  
 RP VARIANT FAP TRP-99.  
 RC TISSUE=Peripheral blood lymphocytes;  
 RX MEDLINE=95134544; PubMed=7833149;  
 RA Dobbie Z., Spycher M., Huerliman R., Ammann R., Roth J.,  
 RA Mueller A., Mueller H., Scott R.J.;  
 RT "Mutational analysis of the first 14 exons of the adenomatous  
 RT polyposis coli (APC) gene.";  
 RL Eur. J. Cancer 30A:1709-1713(1994).  
 RN [13]  
 RP VARIANT FAP GLY-722.  
 RX MEDLINE=95135430; PubMed=7833931;  
 RA Stella A., Montero M., Resta N., Marchese C., Susca F., Gentile M.,  
 RA Romio L., Pillia S., Prete F., Marenzi C., Guanti G.;  
 RT "Four novel mutations of the APC (adenomatous polyposis coli) gene in  
 RT FAP patients.";  
 RL Hum. Mol. Genet. 3:1687-1688(1994).  
 RN [14]  
 RP VARIANT FAP ILE-171.  
 RX MEDLINE=97144176; PubMed=8990002;  
 RA van der Luijt R.B., Meera Khan P., Vasen H.F.A., Tops C.M.J.,  
 RA van Leeuwen-Cornelisse I.S.J., Wijnen J.T., van der Klift H.M.,  
 RA Plug R.J., Griffioen G., Fodde R.;  
 RT "Molecular analysis of the APC gene in 105 Dutch kindreds with  
 RT familial adenomatous polyposis: 67 germline mutations identified by  
 RT DGGE, PTT, and southern analysis.";  
 RL Hum. Mutat. 9:7-16(1997).  
 RN [16]  
 RP VARIANTS COLORECTAL CARCINOMA THR-880; ILE-890 AND VAL-1508.  
 RX MEDLINE=98080146; PubMed=9419979;  
 RA Miyaki M., Nishio J., Konishi M., Kikuchi-Yanoshita R., Tanaka K.,  
 RA Muraoka M., Nagato M., Chong J.-M., Koike M., Terada T., Kawahara Y.,  
 RA Fukutome A., Tomiyama J., Chuganji Y., Momoi M., Utsunomiya J.;  
 RT "Drastic genetic instability of tumors and normal tissues in Turcot  
 RT syndrome.";  
 RL Oncogene 15:2877-2881(1997).  
 RN [17]  
 RP VARIANT LYS-1307.  
 RX MEDLINE=98400248; PubMed=9731522;  
 RA Redston M., Nathanson K.L., Iuan Z.O., Neuhausen S.L., Satagopan J.,  
 RA Wong N., Yang D., Nafia D., Abrahamson J., Ozcelik H.,  
 RA Antin-Ozgerkis D., Andrulis I., Daly M., Pinsky L., Schrag D.,  
 RA Gallinger S., Kabback M., King M.-C., Woodage T., Brody L.C.,  
 RA Godwin A., Warner E., Weber B., Foulkes W., Offit K.;  
 RT "The APC I1307K allele and breast cancer risk.";  
 RL Nat. Genet. 20:13-14(1998).  
 RN [18]  
 RP VARIANTS LYS-1307 AND GLN-1317.  
 RC TISSUE=Peripheral blood;  
 RX MEDLINE=98393712; PubMed=9724771;  
 RA Frayling I.M., Beck N.E., Ilyas M., Dove-Edwin I., Goodman P.,  
 RA Pack K., Bell J.A., Williams C.B., Hodgson S.V., Thomas H.J.W.,  
 RA Talbot I.C., Bodmer W.F., Tomlinson I.P.M.;  
 RT "The APC variants I1307K and E1317Q are associated with colorectal  
 RT tumors, but not always with a family history.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10722-10727(1998).  
 RN [19]

RP VARIANT LYS-1307.  
 RX MEDLINE=98400259; PubMed=9731533;  
 RA Woodage T., King S.M., Wacholder S., Hartge P., Struwing J.P.,  
 RA McAdams M., Laken S.J., Tucker M.A., Brody L.C.;  
 RT "The APC I1307K allele and cancer risk in a community-based study of  
 RT Ashkenazi Jews.";  
 RL Nat. Genet. 20:62-65(1998).  
 RN [20]  
 RP VARIANT LYS-1307.  
 RX MEDLINE=99138651; PubMed=9973276;  
 RA Gryfe R., Di Nicola N., Lal G., Gallinger S., Redston M.;  
 RT "Inherited colorectal polyposis and cancer risk of the APC I1307K  
 RT polymorphism.";  
 RL Am. J. Hum. Genet. 64:378-384(1999).  
 RN [21]  
 RP VARIANTS FAP CYS-1171 AND THR-2738; AND VARIANTS GLY-1057 AND  
 RP VAL-1822.  
 RX MEDLINE=99133859; PubMed=9950360;  
 RA Wallis Y.L., Morton D.G., McKeown C.M., Macdonald F.;  
 RT "Molecular analysis of the APC gene in 205 families: extended  
 RT genotype-phenotype correlations in FAP and evidence for the role of  
 RT APC amino acid changes in colorectal cancer predisposition.";  
 RL J. Med. Genet. 36:14-20(1999).  
 RN [22]  
 RP VARIANT FAP PRO-1184.  
 RX MEDLINE=99401091; PubMed=10470088;  
 RA Lamum H., Ilyas M., Rowan A., Clark S., Johnson V., Bell J.A.,  
 RA Frayling I.M., Efstathiou J., Pack K., Payne S., Roylance R.,  
 RA Gorman P., Sheer D., Neale K., Phillips R., Talbot I.C., Bodmer W.F.,  
 RA Tomlinson I.P.M.;  
 RT "The type of somatic mutation at APC in familial adenomatous polyposis  
 RT is determined by the site of the germline mutation: a new facet to  
 RT Query Match 62.1%; Score 36; DB 1; Length 2843;  
 Best Local Similarity 63.6%; Pred. NO. 2.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 QY 2 HHY---GTPY 8  
 Db 1844 HHYPIEGTPY 1854  
 RESULT 10  
 APC\_MOUSE STANDARD; PRT; 2845 AA.  
 ID AC 061315; Q62044;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Adenomatous polyposis coli protein (APC protein) (mAPC).  
 GN APC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.  
 RC STRAIN=C57BL/6J, and CAST/EI; TISSUE=Brain;  
 RX MEDLINE=92263101; PubMed=1350108;  
 RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,  
 RA Luongo C., Gould K.A., Dove W.F.;  
 RT "Multiple intestinal neoplasia caused by a mutation in the murine  
 RT homolog of the APC gene.";  
 RL Science 256:668-670(1992).  
 RN [2]  
 RP ERRATUM.  
 RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,  
 RA Luongo C., Gould K.A., Dove W.F.;  
 RL Science 256:1114-1114(1992).  
 RN [3]  
 RP SEQUENCE OF 1-45 FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RA Dicker F., Lambertz S., Reitmaier A., Ballhausen W.G.;

RT "The murine APC gene: alternative splicing of 5' untranslated  
RL region segments.";  
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN ALTERNATIVE SPLICING.  
RX MEDLINE=94061824; PubMed=8242607;  
RA Oshima M., Sugiyama H., Kitagawa K., Taketo M.;  
RT "APC gene messenger RNA: novel isoforms that lack exon 7.";  
RL Cancer Res. 53:5589-5591(1993).  
CC -1- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-  
CC CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STATE  
CC ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: FORMS HOMODIGOMERS AND ASSOCIATES WITH CATENINS (BY  
CC SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART,  
CC LUNG, BRAIN, STOMACH, INTESTINE, TESTIS AND OVARY.  
CC -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 7 ARM REPEATS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
EMBL; M88127; AAB59632.1; -;  
DR EMBL; U02937; AAA03443.1; -;  
DR HSSP; Q02248; 3BCT.  
DR MGD; MGI:88039; Apc.  
DR InterPro; IPR000225; Armadillo.  
DR Pfam; PF00514; Armadillo\_seg; 6.  
DR SMART; SM00185; ARM; 5.  
DR PROSITE; PS50176; ARM\_REPEAT; 1.  
KW Anti-oncogene; Phosphorylation; Alternative splicing; Repeat;  
KW Coiled coil.  
FT DOMAIN 1 61 COILED COIL (POTENTIAL).  
FT DOMAIN 125 245 COILED COIL (POTENTIAL).  
FT DOMAIN 1 728 LEU-RICH.  
FT REPEAT 451 493 ARM 1.  
FT REPEAT 503 545 ARM 2.  
FT REPEAT 546 589 ARM 3.  
FT REPEAT 590 636 ARM 4.  
FT REPEAT 637 681 ARM 5.  
FT REPEAT 682 723 ARM 6.  
FT REPEAT 724 765 ARM 7.  
FT DOMAIN 739 2834 SER-RICH.  
FT DOMAIN 1130 1156 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 1864 1891 HIGHLY CHARGED.  
FT VARSPIC 243 276 MISSING (IN ISOFORM 2 AND ISOFORM 4).  
FT VARSPIC 310 410 MISSING (IN ISOFORM 3 AND ISOFORM 4).  
FT VARIANT 120 120 T -> A (IN STRAIN CAST/EI).  
FT VARIANT 493 493 V -> I (IN STRAIN CAST/EI).  
FT VARIANT 797 797 Y -> F (IN STRAIN CAST/EI).  
FT VARIANT 1330 1330 A -> T (IN STRAIN CAST/EI).  
FT VARIANT 1618 1618 A -> S (IN STRAIN CAST/EI).  
FT VARIANT 2294 2294 G -> A (IN STRAIN CAST/EI).  
FT VARIANT 2496 2496 H -> Q (IN STRAIN CAST/EI).  
FT VARIANT 2523 2523 T -> A (IN STRAIN CAST/EI).  
FT VARIANT 2813 2813 T -> S (IN STRAIN CAST/EI).  
SQ SEQUENCE 2845 AA; 311086 MW; 145CA73CF570A499 CRC64;  
Query Match 62.1%; Score 36; DB 1; Length 2845;  
Best Local Similarity 63.6%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 2 HHY-----GTPY 8  
|||||

Db 1842 HHYTFIEGTPY 1852  
RESULT 11  
HBB2\_XENBO  
ID HBB2\_XENBO STANDARD; PRT; 145 AA.  
AC P07433;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-APR-1988 (Rel. 07, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hemoglobin beta-2 chain (Minor).  
GN HBB2.  
OS Xenopus borealis (Kenyan clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8354;  
RN [1]\_TaxID=8354;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87112760; PubMed=3100812;  
RA Knoechel W., Korge E., Basner A., Meyerhof W.;  
RT "Globin evolution in the genus Xenopus: comparative analysis of cDNAs  
RT coding for adult globin polypeptides of Xenopus borealis and Xenopus  
RT tropicalis.";  
RL J. Mol. Evol. 23:211-223(1986).  
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE  
CC VARIOUS PERIPHERAL TISSUES.  
CC -1- SUBUNIT: HETEROOTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.  
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.  
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.  
CC -----  
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CC -----  
EMBL; M32458; AAA49661.1; -;  
DR EIR; F25929; F25929.  
DR HSSP; P02118; 1A4F.  
DR InterPro; IPR002337; Beta haem.  
DR InterPro; IPR000971; Globin.  
DR Pfam; PF00042; globin; 1.  
DR PRINTS; PR00814; BETAHAEM.  
DR PROSITE; PS01033; GLOBIN; 1.  
KW Heme; Oxygen transport; Transport; Erythrocyte.  
FT INIT\_MET 0 0  
FT METAL 62 62 IRON (HEME DISTAL LIGAND).  
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).  
SQ SEQUENCE 145 AA; 15988 MW; 4F108FC787F397A7 CRC64;  
Query Match 60.3%; Score 35; DB 1; Length 145;  
Best Local Similarity 62.5%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 HHVGTPT 9  
|||

Db 115 HHFGEEYT 122  
RESULT 12  
KGUA\_THETN  
ID KGUA\_THETN STANDARD; PRT; 206 AA.  
AC Q8R956;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Guanylate kinase (EC 2.7.4.8) (GMP kinase).  
GN GSK OR TTE1511.  
OS Thermoanaerobacter tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;

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OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=1197336;
RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RA "A complete sequence of T. tengcongensis genome.";
RT Genome Res. 12:689-700(2002).
RL
RC STRAIN=cv. Columbia;
RX MEDLINE=92339744; PubMed=1634002;
RA Inze D., Ferreira P.C.G., Hemerly A.S., van Montagu M.;
RA "Control of cell division in plants.";
RL Biochem. Soc. Trans. 20:80-84(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansonge W., Unseld M.,
RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brotter P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner F.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Sasamoto S., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
CC -!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC
CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES
THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
CC -!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY
SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CDC2/CDKX SUBFAMILY.
CC -!- CAUTION: Ref.5 sequence differs from that shown due to erroneous
gene model prediction.
CC
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CC
CC EMBL; S45387; AAB23643.1; -
DR EMBL; M59198; AAA32831.1; -
DR EMBL; D10850; BAA01623.1; -
DR EMBL; X57839; CAA40971.1; -
DR EMBL; ALI32963; CAB87903.1; ALT_SEQ.
DR PIR; A48984; A48984.
DR PIR; JQ0967; JQ0967.
DR PIR; JQ1337; JQ1337.
DR PIR; S23095; S23095.
DR HSSP; P24941; IHCL.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.

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DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
KW Cell division; Mitosis; Phosphorylation.
FT DOMAIN 4 287 PROTEIN KINASE.
FT NP_BIND 10 18 ATP (BY SIMILARITY).
FT BINDING 33 33 ATP (BY SIMILARITY).
FT ACT_SITE 127 127 BY SIMILARITY.
FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 161 161 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
SQ SEQUENCE 294 AA; 34030 MW; B5FAE55FA9EC366E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 294;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTG 7
DB 179 HHYSTP 184

RESULT 14
META_CLOAB
ID META_CLOAB STANDARD; PRT; 301 AA.
AC Q97129;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homoserine O-succinyltransferase (EC 2.3.1.46) (Homoserine O-transuccinylase) (HTS).
GN META OR CAC1825.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AFCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=1146286;
RA Noelling J., Berton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
CC -|- CATALYTIC ACTIVITY: Succinyl-CoA + L-homoserine = CoA + O-succinyl-L-homoserine.
CC -|- PATHWAY: Methionine biosynthesis; HTS variant; first step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE HTS FAMILY.
CC -----
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CC -----
DR ENBL; AE007691; AAK79790.1; -.
DR TIGRFAMS; TIGR01001; meta; 1.
KW Methionine biosynthesis; Transferase; Acyltransferase;
KW Complete proteome.
FT ACT_SITE 142 142 POTENTIAL.
SQ SEQUENCE 301 AA; 35123 MW; ED40BA0DC247405D CRC64;

Query Match 60.3%; Score 35; DB 1; Length 301;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferrase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
Cell division; Mitosis; Phosphorylation.
DOMAIN 4 287 PROTEIN KINASE.
NP_BIND 10 18 ATP (BY SIMILARITY).
BINDING 33 33 ATP (BY SIMILARITY).
ACT_SITE 127 127 BY SIMILARITY.
MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
MOD_RES 161 161 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
SEQUENCE 294 AA; 34030 MW; B5FAE55FA9EC366E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 294;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTG 7
DB 179 HHYSTP 184

RESULT 15
HRG_BOVIN
ID HRG_BOVIN STANDARD; PRT; 396 AA.
AC P33733;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histidine-rich glycoprotein (Histidine-proline rich glycoprotein) (HPRG) (Fragments).
DE HRG.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=93351678; PubMed=8348977;
RA Soerensen C.B., Krogh-Pedersen H., Petersen T.E.;
RT "Determination of the disulphide bridge arrangement of bovine histidine-rich glycoprotein."
RL FEBS Lett. 328:285-290(1993).
CC -|- FUNCTION: THE PHYSIOLOGICAL FUNCTION IS NOT YET KNOWN. IT BINDS HEME, DYES AND DIVALENT METAL IONS. IT CAN INHIBIT ROSETTE FORMATION AND IS KNOWN TO INTERACT WITH HEPARIN, THROMBOSPONDIN, AND THE LYSINE-BINDING SITE OF PLASMINOGEN. ON THE BASIS OF ITS HOMOLOGY WITH HMW KININOGEN, THE HIS-RICH REGION OF THIS PROTEIN MAY MEDIATE THE CONTACT ACTIVATION PHASE OF INTRINSIC BLOOD COAGULATION CASCADE.
CC -|- DOMAIN: IN ADDITION TO HAVING A HIGH HIS AND PRO CONTENT, THIS PROTEIN HAS MANY INTERNAL REPEATS. 12 TANDEM REPEATS OF A 5-RESIDUE SEQUENCE (GHPH, CONSENSUS) FORM A HISTIDINE-RICH REGION.
CC -|- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.
DR PIR; S35687; S35687.
KW Glycoprotein; Heparin-binding; Repeat.
FT DOMAIN 1 102 CYSTATIN-LIKE 1.
FT DOMAIN 103 169 CYSTATIN-LIKE 2.
FT DOMAIN 191 238 PRO-RICH.
FT DOMAIN 243 368 PRO/HIS-RICH.
FT DISULFID 7 375
FT DISULFID 56 67
FT DISULFID 77 92
FT DISULFID 123 297
FT DISULFID 137 160
FT DISULFID 212 242
FT NON_CONS 52 53
FT CARBOHYD 70 70
FT NON_CONS 71 72
FT NON_CONS 78 79
FT CARBOHYD 91 91
FT NON_CONS 103 104
FT CARBOHYD 122 122
FT NON_CONS 163 164
FT CARBOHYD 220 220
FT NON_CONS 263 264
FT NON_CONS 303 304
FT VARIANT 86 86 S -> R.
FT VARIANT 309 309 S -> Q.
FT VARIANT 322 322 H -> Y.
SQ SEQUENCE 396 AA; 44470 MW; 128A8223499DE6FC CRC64;

Query Match 60.3%; Score 35; DB 1; Length 396;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTGY 8
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Db 171 QHHLGRPF 178

RESULT 16
ENO DEIRA
ID ENO DEIRA STANDARD; PRT; 422 AA.
AC QPR60;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
glycerate hydro-lyase).
GN ENO OR DR2637.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL;
RA MEDLINE=20036896; PubMed=10567266;
RX White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL; AE002092; AAF12173.1; -.
DR HSP; P56252; IPDZ.
DR TIGR; DR2637; -.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; enolase; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR Lyase; Glycolysis; Magnesium; Complete proteome.
KW ACT SITE 153
FT METAL 240 240 MAGNESIUM (BY SIMILARITY).
FT METAL 283 283 MAGNESIUM (BY SIMILARITY).
FT METAL 310 310 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 422 AA; 45541 MW; 7FE6C766E2A3AC0D CRC64;

Query Match 60.3%; Score 35; DB 1; Length 422;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGT 6
:|||||
Db 354 RHHYGT 359
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RESULT 17
YAAO_BACSU
ID YAAO_BACSU STANDARD; PRT; 480 AA.
AC P37536;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yaaO.
GN YAAO.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7594024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
subtilis chromosome containing the replication origin.";
RL DNA Res. 1:11-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chou S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.P., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone E.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.P., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF ORNITHINE, LYSINE, AND ARGININE
DECARBOXYLASES.
CC -----
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CC -----
DR EMBL; D26185; BAA05263.1; -.
DR EMBL; Z99104; CAB11803.1; -.
DR Subtilist; BG10091; yaaO.
DR InterPro; IPR000310; Decarboxylase1.
DR Pfam; PF01276; OKR_DC_1; 1.
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DR Pfam; PF03711; OKR_DC_1_C; 1.
DR PROSITE; PS00703; OKR_DC_1; FALSE NEG.
KW Hypothetical protein; Lyase; Decarboxylase; Pyridoxal phosphate;
FT BINDING 222 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 480 AA; 53163 MW; 0166EE309B32AFB1 CRC64;

Query Match
Best Local Similarity 60.3%; Score 35; DB 1; Length 480;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTTP 7
Db 182 HHYGIP 187

RESULT 18
PIXB_HUMAN STANDARD; PRT; 646 AA.
AC Q14155;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange
DE factor beta) (Beta-Pix) (COOL-1) (p85).
GN ARHGGEF7 OR PAK3BP OR PIXB OR COOL1 OR KIAA0142.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RX MEDLINE=96127530; PubMed=8590280;
RA Nagase T.; Seki N.; Tanaka A.; Ishikawa K.-I.; Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 2:167-174 (1995).
RN [2]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=98395067; PubMed=9726964;
RA Bagrodia S.; Taylor S.J.; Jordan K.A.; Van Aelst L.; Cerione R.A.;
RT "A novel regulator of p21-activated kinases."
RL J. Biol. Chem. 273:23633-23636 (1998).
CC -!- FUNCTION: Acts as a RAC1 guanine nucleotide exchange factor (GEF)
CC and can induce membrane ruffling (By similarity).
CC -!- SUBUNIT: Interacts with PAK kinases through the SH3 domain.
CC -!- ALTERNATIVE PRODUCTS: At least 2 isoforms are produced by
CC alternative splicing.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC
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DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RHOGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00741; DH_1; FALSE_NEG.
DR PROSITE; PS001010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW Guanine-nucleotide releasing factor; SH3 domain; Alternative splicing.
FT DOMAIN 6 65
FT DOMAIN 93 273
FT DOMAIN 295 400
SQ SEQUENCE 646 AA; 73140 MW; B5B5A83F0BEC28D2 CRC64;

Query Match
Best Local Similarity 60.3%; Score 35; DB 1; Length 646;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGTTPYT 9
Db 450 HHGTPHT 456

RESULT 19
PIXB_RAT STANDARD; PRT; 646 AA.
AC O55043;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange
DE factor beta) (Beta-Pix).
GN ARHGFE7 OR PAK3BP OR PIXB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98324100; PubMed=9659915;
RA Manser E.; Loo T.-H.; Koh C.-G.; Zhao Z.-S.; Chen X.-Q.; Tan L.;
RA Tan I.; Leung T.; Lim L.;
RT "PAK kinases are directly coupled to the PIX family of nucleotide
RT exchange factors."
RL Mol. Cell 1:183-192 (1998).
CC -!- FUNCTION: Acts as a RAC1 guanine nucleotide exchange factor (GEF)
CC and can induce membrane ruffling.
CC -!- SUBUNIT: Interacts with PAK kinases through the SH3 domain.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC
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DR PROSITE; PS00741; DH 1; FALSE_NEG.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW Guanine-nucleotide releasing factor; SH3 domain.
FT DOMAIN 6 65
FT DOMAIN 93 273
FT DOMAIN 295 400
FT DOMAIN 400 400
SQ SEQUENCE 646 AA; 73140 MW; 17CDE7D96ADEA53 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 646;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HYGTPYT 9
Db 450 HHGTPHT 456

RESULT 20
UL17_HSV11 STANDARD; PRT; 703 AA.
AC PI0201;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Protein UL17.
GN UL17.
OS Herpes simplex virus (type 1 / strain 17).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88274327; PubMed=2839594;
RA McGeoch D.J., Dairymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA McNab D., Perry L.J., Scott J.E., Taylor P.;
RT "The complete DNA sequence of the long unique region in the genome of
RT herpes simplex virus type 1.";
RL J. Gen. Virol. 69:1531-1574(1988).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL17,
CC HSV-6 ORF108, EBV-1 45, HCMV UL93, EBV BGLF1, AND VZV 43.
CC -----
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CC -----
DR EMBL; D10879; BAA01663.1; -
DR EMBL; X14112; CAA32329.1; -
DR PR; H30083; WMBET7.
SQ SEQUENCE 703 AA; 74582 MW; 536DAF5421BD6B4E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 703;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGT 6
Db 388 RHHYGT 393

RESULT 21
ID_PIXB_MOUSE STANDARD; PRT; 705 AA.
AC Q9ES28; Q9ES27; O08757;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rho guanine nucleotide exchange factor 7 (PAK-interacting exchange.

factor beta) (Beta-Pix) (p85SPR).
GN ARHGEF7 OR PAK3BP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Thymus;
RX MEDLINE=97350865; PubMed=9207241;
RA Oh W.K., Yoo J.C., Jo D., Song Y.H., Kim M.G., Park D.;
RT "Cloning of a SH3 domain-containing proline-rich protein, p85SPR, and
RT its localization in focal adhesion.";
RL Biochem. Biophys. Res. Commun. 235:794-798(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=20318354; PubMed=10860822;
RA Kim S., Kim T., Lee D., Park S.H., Kim H., Park D.;
RT "Molecular cloning of neuronally expressed mouse betaPix isoforms.";
RL Biochem. Biophys. Res. Commun. 272:721-725(2000).
CC -1- FUNCTION: Acts as a RAC1 guanine nucleotide exchange factor (GEF)
CC and can induce membrane ruffling (By similarity).
CC -1- SUBUNIT: Interacts with PAK kinases through the SH3 domain (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; a, b (shown here) and c; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Seems to be expressed in the central nervous
CC system.
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL; U96634; AAB57691.1; -
DR EMBL; AF247654; AAG18017.1; -
DR EMBL; AF247655; AAG18018.1; -
DR HSSP; P19174; 2HSP.
DR MGD; MGI:1860493; Arhgef7.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; Rhogef.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; Rhogef; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRODOM; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; Rhogef; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00741; DH 1; FALSE_NEG.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW Guanine-nucleotide releasing factor; SH3 domain; Alternative splicing.
FT DOMAIN 6 65
FT DOMAIN 93 273
FT DOMAIN 295 400
FT VARSPPLIC 419 493
FT VARSPPLIC 555 614
FT CONFLICT 467 468
FT CONFLICT 471 473
FT CONFLICT 478 479
SQ SEQUENCE 705 AA; 79832 MW; 10D12117D98BE77D2 CRC64;
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Query Match 60.3%; Score 35; DB 1; Length 705;  
Best Local Similarity 71.4%; Pred. No. 74;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HYGTPYT 9  
DB 450 HHGTPHT 456

RESULT 22  
AMPN RABIT STANDARD; PRT; 965 AA.  
AC P15541; 1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Aminopeptidase N (EC 3.4.11.2) (Microsomal aminopeptidase) (Leukemia antigen CD13).  
GN ANPEP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA MEDLINE=9409942; PubMed=7903857;  
RX Yang X.F., Milhiet P.E., Gaudoux F., Crine P., Boileau G.;  
RT "Complete sequence of rabbit kidney aminopeptidase N and mRNA localization in rabbit kidney by in situ hybridization.";  
RL Biochem. Cell Biol. 71:278-287(1993).  
RN [2]  
RP SEQUENCE OF 5-18.  
RX MEDLINE=82113673; PubMed=6120002;  
RA Peracci H., Maroux S., Bonicel J., Desnuelle P.;  
RT "The amino acid sequence of the hydrophobic anchor of rabbit intestinal brush border aminopeptidase N.";  
RL Biochim. Biophys. Acta 684:133-136(1982).  
RN [3]  
RP SEQUENCE OF 177-965 FROM N.A.  
RX MEDLINE=90092508; PubMed=2574692;  
RA Noren O., Dabelsteen E., Hoeyer P.E., Olsen J., Sjoestrom H., Hansen G.H.;  
RT "Onset of transcription of the aminopeptidase N (leukemia antigen CD 13) gene at the crypt/villus transition zone during rabbit enterocyte differentiation.";  
RL FEBS Lett. 259:107-112(1989).  
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, preferably a neutral or hydrophobic one, from a polypeptide. Aminoacyl-arylamides are poor substrates.  
CC -1- COFACTOR: BINDS 1 ZINC ION.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- PTM: SULFATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1.

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DR EMBL; S68687; AAB29534.1; -;  
DR EMBL; X51508; CAA35873.1; -;  
DR PIR; B25985; B25985.  
DR PIR; S07099; S07099.  
DR MEROPS; M01.001; -;  
DR InterPro; IPR001930; Ala.peptase.  
DR InterPro; IPR000130; Zn.MTpeptidase.  
DR Pfam; PF01433; Peptidase\_M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.

DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc; Glycoprotein;  
KW Sulfation; Transmembrane; Repeat; Signal-anchor.  
FT INIT MET 0  
FT DOMAIN 1 7  
FT TRANSMEM 8 31  
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
FT CYTOSOLIC SER/THR-RICH JUNCTION.  
FT METALLOPROTEASE.  
FT ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 384 384  
FT METAL 387 387  
FT ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 406 406  
FT MOD\_RES 172 172  
FT MOD\_RES 414 414  
FT MOD\_RES 419 419  
FT MOD\_RES 911 911  
FT CARBOHYD 39 39  
FT CARBOHYD 124 124  
FT CARBOHYD 258 258  
FT CARBOHYD 314 314  
FT CARBOHYD 551 551  
FT CARBOHYD 569 569  
FT CARBOHYD 623 623  
FT CARBOHYD 733 733  
FT CARBOHYD 816 816  
FT CONFLICT 9 9  
FT CONFLICT 15 15  
FT CONFLICT 209 209  
FT CONFLICT 225 225  
FT CONFLICT 233 233  
FT CONFLICT 592 593  
SQ SEQUENCE 965 AA; 109186 MW; 012D1895D4B57A96 CRC64;  
Query Match 60.3%; Score 35; DB 1; Length 965;  
Best Local Similarity 71.4%; Pred. No. 16+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYTPY 8  
DB 325 NHYTPY 331

RESULT 23  
VAPD BACNO STANDARD; PRT; 93 AA.  
AC Q46565; Q46556; Q46566; Q46570; Q46572;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Virulence-associated protein D.  
GN VAPD.  
OS Bacteroides nodosus (Dichelobacter nodosus).  
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;  
OC Dichelobacter.  
OX NCBI\_TaxID=870;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Al98;  
RX MEDLINE=92085031; PubMed=1748867;  
RA Katz M.E., Howarth P.M., Yong W.K., Riffkin G.G., Depiazzi L.J., Rood J.I.;  
RT "Identification of three gene regions associated with virulence in Dichelobacter nodosus, the causative agent of ovine footrot.";  
RL J. Gen. Microbiol. 137:2117-2124(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Al98;  
RX MEDLINE=93014173; PubMed=1398971;  
RA Katz M.E., Rood J.I., Strugnell R.A.;  
RT "Molecular characterization of a genomic region associated with virulence in Dichelobacter nodosus.";

RL Infect. Immun. 60:4586-4592(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Al98.  
RX MEDLINE=94222846; PubMed=8169216;  
RA Katz M.E., Wright C.L., Gartside T.S., Cheetham B.F., Doidge C.V.,  
RA Moses E.K., Rood J.I.;  
RT "Genetic organization of the duplicated vap region of the  
RT Dichelobacter nodosus genome.";  
RL J. Bacteriol. 176:2663-2669(1994).  
CC -1- SIMILARITY: BELONGS TO THE VAPD FAMILY.  
CC -----  
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CC -----  
CC EMBL; L31763; AAB00950.1; -;  
DR EMBL; L31763; AAB00940.1; -;  
DR EMBL; L22308; AAA20204.1; -;  
DR EMBL; L22307; AAA20123.1; -;  
DR EMBL; M74565; AAA22348.1; -;  
KW Virulence. 93 AA; 10590 MW; 15112582A678D9B0 CRC64;  
SQ SEQUENCE 93 AA; 10590 MW; 15112582A678D9B0 CRC64;  
  
Query Match 58.6%; Score 34; DB 1; Length 93;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 HYGTPY 8  
DB 16 HYGEPY 21  
  
RESULT 24  
VAPD\_ACTAC STANDARD; PRT; 95 AA.  
ID VAPD\_ACTAC  
AC Q52243;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Virulence-associated protein D homolog.  
OS Actinobacillus actinomycetemcomitans (Haemophilus  
OS actinomycetemcomitans).  
OG Plasmid pVT736-1.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Actinobacillus.  
OX NCBI\_TaxID=714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95362676; PubMed=7543479;  
RA Galli D.M., Leblanc D.J.;  
RT "Transcriptional analysis of rolling circle replicating plasmid  
RT pVT736-1: evidence for replication control by antisense RNA.";  
RL J. Bacteriol. 177:4474-4480(1995).  
CC -1- SIMILARITY: BELONGS TO THE VAPD FAMILY.  
CC -----  
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CC -----  
CC EMBL; L24000; AAC37126.1; -;  
DR EMBL; L24000; AAC37126.1; -;  
KW Plasmid; Virulence.  
SQ SEQUENCE 95 AA; 11190 MW; 3424348E815BF62A CRC64;  
  
Query Match 58.6%; Score 34; DB 1; Length 95;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 HYGTPY 8  
DB 16 HYGDPY 21  
  
RESULT 25  
KV4A\_HUMAN STANDARD; PRT; 114 AA.  
ID KV4A\_HUMAN  
AC P01625;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-IV region Len.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76004342; PubMed=50995;  
RA Schneider M., Hilschmann N.;  
RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
RT subgroup IV of the kappa type (Bence-Jones protein Len).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
RN [2]  
RP REVISION TO 9.  
RA Salomon A.;  
RL Submitted (AUG-1996) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01903; K4HULN.  
DR HSSP; P01607; LREI.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; ig\_1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 41 55 FRAMEWORK-2.  
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 63 94 FRAMEWORK-3.  
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 102 113 FRAMEWORK-4.  
FT DISULFID 23 94 BY SIMILARITY.  
FT NON TER 114 114  
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;  
  
Query Match 58.6%; Score 34; DB 1; Length 114;  
Best Local Similarity 55.6%; Pred. No. 16;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QHHYGTPT 9  
DB 95 QQYISTPY 103  
  
RESULT 26  
TYRT\_STRLN STANDARD; PRT; 140 AA.  
ID TYRT\_STRLN  
AC P55048;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Tyrosinase co-factor.  
GN MELC1.  
OS Streptomyces lincolnensis.  
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1915;

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NN  SEQUENCE FROM N.A.
RP  STRAIN=78-11;
RA  Zhang H.Z., Piepersberg W.;
RL  Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC  -I- FUNCTION: THIS PROTEIN MAY FUNCTION TO DELIVER COPPER TO
CC  TYROSINASE.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; X95703; CAA64999.1; -.
KW  Melanin biosynthesis; Copper.
SQ  SEQUENCE 140 AA; 14189 MW; 8752156617FD15A6 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 140;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPT 8
Db 80 HHHGTGY 86

RESULT 27
KVSA_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Colclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689 (1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187 (1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Biochem. J. 171:337-347 (1978).
CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC -----
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CC
CC EMBL; J00561; AAA38776.1; -.
DR PIR; A01916; KVM511.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29 IG KAPPA CHAIN V-V REGION MPC11.
FT CHAIN 30 149 FRAMEWORK-1.
FT DOMAIN 42 64 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 65 75 FRAMEWORK-2.
FT DOMAIN 76 90 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 91 97 FRAMEWORK-3.
FT DOMAIN 98 129 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 130 138 FRAMEWORK-4.
FT DOMAIN 139 148
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 58.6%; Score 34; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OHHYGTPT 9
Db 130 QOHYSTPPT 138

RESULT 28
KGUA_DEIRA STANDARD; PRT; 239 AA.
ID KGUA_DEIRA
AC Q9RS38;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate kinase (EC 2.7.4.8) (GMP kinase).
GN GMP OR DR2289.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pauphilet W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577 (1999).
CC -I- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
CC -I- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
CC -----
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CC -----

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DR EMBL; AE002061; AAF11836.1; ALT_INIT.
DR HSP; P15454; IGKY.
DR TIGR; DR2289;
DR InterPro; IPR000619; Guanylate_kin.
DR Pfam; PF00625; Guanylate_kin; 1.
DR SMART; SM00072; GuKc; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS00852; GUANYLATE_KINASE_2; 1.
DR TRANSFERASE; Kinase; ATP-binding; Complete proteome.
FT NF_BIND 26 33 ATP (BY SIMILARITY).
SQ SEQUENCE 239 AA; 26528 MW; 930AE5040D622722 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 239;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHYGTG 7
DB 92 NHYGTP 97

RESULT 29
HXA9 MORSA
ID HXA9 MORSA STANDARD; PRT; 269 AA.
AC Q9PMD5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A9.
GN HoxA9.
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9259633; PubMed=10327649;
RA Snell E.A., Scemama J.L., Stollwag E.J.;
RT "Genomic organization of the HoxA4-HoxA10 region from Morone saxatilis: implications for Hox gene evolution among vertebrates.";
RL J. Exp. Zool. 285:41-49 (1999).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ABD-B HOMEODOMAIN FAMILY.
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CC EMBL; AF089743; AAD46396.1;
DR HSP; P02833; 9ANT.
DR InterPro; IPR000047; HTH repressor.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
GN Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DNA_BIND 202 261 HOMEBOX.
SQ SEQUENCE 269 AA; 29600 MW; 8D49DCE0597D2A4C CRC64;

Query Match 58.6%; Score 34; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYG 5
DB 238 QHHYG 242

RESULT 31
SPEB STRCL
ID SPEB STRCL STANDARD; PRT; 313 AA.
AC F37819; P72400;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Possible agmatinase (EC 3.5.3.11) (Agmatine ureohydrolase) (AUH) (Proclavaminc acid amidino hydrolase).
GN PAH.
OS Streptomyces clavuligerus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.

Query Match 58.6%; Score 34; DB 1; Length 269;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTG 7
DB 82 HHYGHP 87

RESULT 30
COX3 CVACA
ID COX3 CVACA STANDARD; PRT; 270 AA.
AC P48873;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide III (EC 1.9.3.1).
GN COX3 OR COXIII.
OS Cyanidium caldarium.
OC Mitochondrion.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1;
RA Viehmann S.;
RL Thesis (1995), Justus Liebig University / Frankfurt, Germany.
CC -!- FUNCTION: Subunits I, II and III form the functional core of the enzyme complex.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferrocyclochrome c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
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CC EMBL; Z48930; CAA88770.1;
DR InterPro; IPR000298; CytC_oxdse_III.
DR Pfam; PF00510; COX3; 1.
DR ProDom; PD000382; CytC_oxdse_III; 1.
DR PROSITE; PS00253; COX3; 1.
DR Oxidoreductase; Mitochondrion; Transmembrane.
KW OXIDOREDUCTASE; MITOCHONDRION; TRANSMEMBRANE.
SQ SEQUENCE 270 AA; 31564 MW; 52917FBDCAE953C5 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYG 5
DB 238 QHHYG 242
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OX NCBI_TaxID=1901;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
RX MDLINE=94374706; PubMed=8088547;
RA Aldoo K.A., Wong A., Alexander D.C., Rittammer R.A.R., Jensen S.E.;
RT "Cloning, sequencing and disruption of a gene from Streptomyces
RL clavuligerus involved in clavulanic acid biosynthesis.";
RL Gene 147:41-46(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Hodgson J.E., Fosberry A., Rawlinson N.S., Ross H.N.M., Neal R.J.,
RA Arnell J.C., Earl A.J., Lawlor E.J.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: POSSIBLY INVOLVED IN CLAVULANIC ACID BIOSYNTHESIS.
CC -!- CATALYTIC ACTIVITY: Agmatine + H2O = putrescine + urea.
CC -!- COFACTOR: MANGANESE (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
CC -----
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CC -----
DR EMBL; U87786; AAA62451.1; -
DR EMBL; X84101; CAA58904.1; -
DR InterPro; IPR000287; Arginase.
DR Pfam; PF00491; arginase; 1.
DR TIGRFAMS; TIGR01230; agmatinase; 1.
DR PROSITE; PS00147; ARGINASE 1; 1.
DR PROSITE; PS00148; ARGINASE 2; 1.
DR PROSITE; PS01053; ARGINASE_3; 1.
KW Hydrolase; Manganese.
FT METAL 121
FT METAL 121
FT METAL 144
FT METAL 144
FT METAL 146
FT METAL 146
FT METAL 148
FT METAL 148
FT METAL 235
FT METAL 235
FT METAL 237
FT METAL 237
SQ SEQUENCE 313 AA; 33401 MW; 75959B564488B5E CRC64;

Query Match 58.6%; Score 34; DB 1; Length 313;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHYHGTPY 8
Db 157 RYHHGTPF 164
:::|::|:

RESULT 32
ID1 _ARATH STANDARD; PRT; 315 AA.
AC P42774; Q96263;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE G-box binding factor 1.
GN GBF1 OR AT4G36730 OR C7A10.630.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia; TISSUE=Leaf, and Stem;
RX MDLINE=9224864; PubMed=1373374;
RA Schindler U., Menkens A.E., Beckmann H., Ecker J.R., Cashmore A.R.;
RT "Heterodimerization between light-regulated and ubiquitously

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expressed Arabidopsis GBF bZIP proteins.";
RL EMBL J. 11:1261-1273(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Terryn N., Villarroel R., Neyt P., de Clercq R., Ardiles W.,
RA Terryn N., van den Daele H., Rouze P., Gielen J., van Montagu M.;
RT "Nucleotide sequence of the Arabidopsis thaliana gene encoding the G-
RL box-binding factor 1 (GBF1).";
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgathner M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Vost M., Bastiaens I., Aert R., Defoor E.,
RA Weitzensegger T., Bothé G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., de Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loeckert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Feilber R.,
RA Schnabl S., Hiller R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Maria M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RL thaliana.";
RL Nature 402:769-777(1999).
CC -!- FUNCTION: BINDS TO THE G-BOX MOTIF (5'-CCACGTGG-3') OF THE RBGS-1A
CC GENE PROMOTER. G-BOX AND G-BOX-LIKE MOTIFS ARE CIS-ACTING ELEMENTS
CC DEFINED IN PROMOTERS OF CERTAIN PLANT GENES WHICH ARE REGULATED
CC BY SUCH DIVERSE STIMULI AS LIGHT-INDUCTION OR HORMONE CONTROL.
CC -!- SUBUNIT: DNA-BINDING HETERODIMER.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: FOUND IN BOTH LIGHT AND DARK GROWN LEAVES.
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
CC -----
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DR EMBL; X63894; CAA45356.1; -  
DR EMBL; X99941; CAA68197.1; -  
DR EMBL; Z99708; CAB16806.1; -  
DR EMBL; AL161589; CAB80339.1; -  
DR HSSP; P03069; IYSA.  
DR TRANSFAC; T01078; -  
DR InterPro; IPR004827; TF\_BZIP.  
DR Pfam; PF00170; bZIP; 1.  
DR SMART; SM00338; BRLZ; 1.  
DR PROSITE; PS00036; BZIP\_BASIC; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 9 106 PRO-RICH.  
FT DNA\_BIND 224 243 BASIC MOTIF.  
FT DOMAIN 250 278 LEUCINE-ZIPPER.  
FT CONFLICT 43 43 T -> S (IN REF. 1).  
SQ SEQUENCE 315 AA; 33932 MW; 8585EF0249C91C21 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 315;  
Best Local Similarity 63.6%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 QHH-----YCTP 7  
Db 65 QHHMMPYGTGP 75

RESULT 33

HMDDL BRAFL  
ID \_HMDDL BRAFL STANDARD; PRT; 321 AA.  
AC PS3772;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Homeobox protein DLL homolog.  
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).  
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
OC Branchiostoma.  
OX NCBI\_TaxID=7739;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96378751; PubMed=8787764;  
RA Holland N.D., Panganiban G.E., Henvey E.L., Holland L.Z.;  
RT "Sequence and developmental expression of Amphidil, an amphioxus  
RT Distal-less gene transcribed in the ectoderm, epidermis and nervous  
RT system: insights into evolution of cranial forebrain and neural  
RT crest";  
RL Development 122:2911-2920(1996).  
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -1- SIMILARITY: BELONGS TO THE DISTAL-LESS HOMEOBOX FAMILY.  
CC PROTEINS.  
CC -----

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DR EMBL; U47058; AAB36860.1; -  
DR HSSP; P14653; 1B72.  
DR InterPro; IPR000047; HTH\_repressor.  
DR InterPro; IPR001356; Homeobox.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEOBOX.  
DR PRINTS; PR00031; HTHREPRESSR.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEOBOX\_1; 1.

DR PROSITE; PS50071; HOMEOBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
FT DNA\_BIND 116 175 HOMEOBOX.  
SQ SEQUENCE 321 AA; 35436 MW; F408D46FE1443C7 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 321;  
Best Local Similarity 62.5%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HHYGTPTPT 9  
Db 62 HPGNPGYS 69

RESULT 34

KITH\_HSVSM  
ID KITH\_HSVSM STANDARD; PRT; 361 AA.  
AC P04408;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Thymidine kinase (EC 2.7.1.21).  
GN TK.  
OS Herpesvirus saimiri (type 1 / strain MV-5-4-PSL) (Marmoset  
OS herpesvirus).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae.  
OX NCBI\_TaxID=10353;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84251697; PubMed=6330976;  
RA Otsuka H., Kit S.;  
RT "Nucleotide sequence of the marmoset herpesvirus thymidine kinase  
RT gene and predicted amino acid sequence of thymidine kinase  
RT polypeptide";  
RL Virology 135:316-330(1984).  
RN [2]  
RP REVISIONS.  
RA Kit S.;  
RL Submitted (JUN-1989) to the EMBL/GenBank/DBDJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + thymidine = ADP + thymidine 5'-  
CC phosphate.  
CC -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES THYMIDINE KINASE FAMILY.  
CC -----

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CC -----

DR EMBL; K02122; AAA67102.1; -  
DR PIR; A00614; KIBETM.  
DR HSSP; P03176; 2K15.  
DR InterPro; IPR001889; TK\_herpes.  
DR Pfam; PF00693; TK\_herpes; 1.  
DR ProDom; PD001519; TK\_herpes; 1.  
KW Transferase; Kinase; DNA synthesis; ATP-binding.  
FT NP\_BIND 17 24 ATP (PROBABLE).  
SQ SEQUENCE 361 AA; 39458 MW; B2E32DB1D5542DB CRC64;

Query Match 58.6%; Score 34; DB 1; Length 361;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8  
Db 88 QLHWGTPT 95

RESULT 35

LG1\_MAIZE

ID LGL\_MAIZE STANDARD; PRT; 399 AA.  
AC O04003;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE LIGULELESS1 protein.  
GN LGL.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. W22; TISSUE=Leaf;  
RX MEDLINE=97230364; PubMed=9119226;  
RA Moreno M.A., Harper L.C., Krueger R.W., Dellaporta S.L., Freeling M.;  
RT "Liguleless encodes a nuclear-localized protein required for  
RL induction of ligules and auricles during maize leaf organogenesis.";  
RL Genes Dev. 11:616-628(1997).  
CC -1- FUNCTION: INVOLVED IN THE FORMATION OF LIGULES AND AURICLES DURING  
CC LEAF ORGANOGENESIS.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: LEAF LIGULAR REGION, BLADE AND SHEATH.  
CC -1- DEVELOPMENTAL STAGE: DEVELOPING LEAVES. PRESENT AT HIGHEST  
CC LEVELS IN VERY YOUNG LIGULES AND AURICLES. PRESENT PRE- AND POST-  
CC LIGULE AND AURICLE DEVELOPMENT.  
CC -1- SIMILARITY: CONTAINS 1 SBP DOMAIN.  
CC -----  
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CC -----  
DR EMBL; U89496; AB51071.1; -;  
DR InterPro; IPR004333; SBP\_plant\_prot.  
DR Pfam; PF03110; SBP; 1.  
KW Nuclear protein; Developmental protein.  
FT DOMAIN 243 259 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 185 260 SBP.  
SQ SEQUENCE 399 AA; 43367 MW; 1E89F304232D7B8C CRC64;  
  
Query Match 58.6%; Score 34; DB 1; Length 399;  
Best Local Similarity 62.5%; Pred. No. 62;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 QHNYGTPY 8  
| | | | |  
Db 335 QOHYGRPF 342  
  
RESULT 36  
PAAH\_ECOLI STANDARD; PRT; 475 AA.  
AC P76083; P78289; O53016;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Probable 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (Beta-  
DE hydroxybutyryl-CoA dehydrogenase) (BHBD).  
GN PAAH OR B1395.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W / ATCC 11105;  
RX MEDLINE=98421522; PubMed=9748275;  
RA Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,

RA Garcia J.L., Diaz E.;  
RT "Catabolism of phenylacetic acid in Escherichia coli. Characterization  
RL of a new aerobic hybrid pathway.";  
RN J. Biol. Chem. 273:25974-25986(1998).  
RP [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shaoy Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sampaio G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome  
RL corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [4]  
RP TRANSCRIPTIONAL REGULATION.  
RX MEDLINE=20229831; PubMed=10766858;  
RA Ferrandez A., Garcia J.L., Diaz E.;  
RT "Transcriptional regulation of the divergent paa catabolic operons for  
RL phenylacetic acid degradation in Escherichia coli.";  
RL J. Biol. Chem. 275:12214-12222(2000).  
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxybutanoyl-CoA + NADP(+) = 3-  
CC acetoacetyl-CoA + NADPH.  
CC -1- PATHWAY: BUTYRATE/BUTANOL-PRODUCING PATHWAY.  
CC -1- PATHWAY: Phenylacetic acid aerobic catabolism.  
CC -1- INDUCTION: ACTIVATED BY CAMP RECEPTOR PROTEIN (CRP) AND  
CC INTEGRATION HOST FACTOR (IHF). INHIBITED BY PAA.  
CC -1- SIMILARITY: BELONGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; X97452; CAA66097.1; -;  
DR EMBL; AE000236; AAC74477.1; -;  
DR EMBL; D90778; BAA15006.1; ALT\_INIT.  
DR EMBL; D90777; BAA15001.1; ALT\_INIT.  
DR HSSP; P00348; 3HDH.  
DR EcoGene; EG13742; paaH.  
DR InterPro; IPR002135; 3HCDH.  
DR InterPro; IPR000205; NAD\_binding.  
DR Pfam; PF00725; 3HCDH; 2.  
DR Pfam; PF02737; 3HCDH\_N; 1.  
DR PROSITE; PS00067; 3HCDH; FALSE\_NEG.  
KW Oxidoreductase; NADP; Fatty acid metabolism; Repeat;  
KW Complete proteome.  
FT DOMAIN 1 284 BHBD 1.  
FT DOMAIN 285 475 BHBD 2.  
FT VARIANT 132 132 I -> V (IN STRAIN W).  
FT VARIANT 344 344 I -> V (IN STRAIN W).  
SQ SEQUENCE 475 AA; 51732 MW; DEB6190F08D527C6 CRC64;  
  
Query Match 58.6%; Score 34; DB 1; Length 475;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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CC -----  
 DR EMBL; X07017; CAA30069.1; -;  
 DR PIR; S00644; S00644.  
 DR HSP; P04049; 1FAR.  
 DR InterPro; IPR002219; DAG PE-bind.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR003116; RBD.  
 DR InterPro; IPR004040; STY\_pkinase.  
 DR InterPro; IPR002290; Ser Thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00130; DAG PE-bind; 1.  
 DR Pfam; PF02196; RBD; 1.  
 DR PRINTS; PR00008; DAGPEDOMAIN.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00455; RBD; 1.  
 DR SMART; SM00221; STYKG; 1.  
 DR PROSITE; PS00479; DAG PE BIND DOM 1; 1.  
 DR PROSITE; PS00081; DAG PE BIND DOM 2; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;  
 KW ATP-binding; Phorbol-ester binding.  
 FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.  
 FT DOMAIN 349 609 PROTEIN KINASE.  
 FT NP BIND 355 363 ATP (BY SIMILARITY).  
 FT BINDING 375 375 ATP (BY SIMILARITY).  
 FT ACT SITE 468 468 BY SIMILARITY.  
 SQ SEQUENCE 647 AA; 73124 MW; 8E1443667312DFC0 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 647;  
 Best Local Similarity 62.5%; Pred. No. 1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OHYGYTPY 8  
 Db 229 QHRYSTPH 236

RESULT 40  
 ID KRAF\_HUMAN STANDARD; PRT; 648 AA.  
 AC P04049;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)  
 DE (RAF-1) (C-RAF).  
 GN RAF1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86120351; PubMed=3003687;  
 RA Bonner T.I., Oppermann H., Seeburg P., Kerby S.B., Gunnell M.A.,  
 RA Young A.C., Rapp U.R.;  
 RT "The complete coding sequence of the human raf oncogene and the  
 RT corresponding structure of the c-raf-1 gene.";  
 RL Nucleic Acids Res. 14:1009-1015(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Strausberg R.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.  
 [3]  
 RN PHOSPHORYLATION.  
 RX MEDLINE=99039505; PubMed=9823899;  
 RA King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S.,  
 RA Marshall M.S.;  
 RT "The protein kinase Pak3 positively regulates Raf-1 activity through  
 RT phosphorylation of serine 338.";  
 RL Nature 396:180-183(1998).  
 RN [4]  
 RN ERRATUM.  
 RA King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S.,  
 RA Marshall M.S.;  
 RL Nature 406:439-439(2000).  
 RN [5]  
 RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 51-131.  
 RA MEDLINE=95312074; PubMed=7791872;  
 RA Nassar N., Horn G., Herrmann C., Scherer A., McCormick F.,  
 RA Wittinghofer A.;  
 RT "The 2.2 A crystal structure of the Ras-binding domain of the  
 RT serine/threonine kinase c-Raf1 in complex with Rap1A and a GTP  
 RT analogue.";  
 RL Nature 375:554-560(1995).  
 RN [6]  
 RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 56-131.  
 RA MEDLINE=96313130; PubMed=8756332;  
 RA Nassar N., Horn G., Herrmann C., Block C., Janknecht R.,  
 RA Wittinghofer A.;  
 RT "Ras/Rap effector specificity determined by charge reversal.";  
 RL Nat. Struct. Biol. 3:723-729(1996).  
 RN [7]  
 RN STRUCTURE BY NMR OF 55-132.  
 RX MEDLINE=95284022; PubMed=7766599;  
 RA Emerson S.D., Madison V.S., Palermo R.E., Waugh D.S., Scheffler J.E.,  
 RA Tsao K.L., Kiefer S.E., Liu S.P., Fry D.C.;  
 RT "Solution structure of the Ras-binding domain of c-Raf-1 and  
 RT identification of its Ras interaction surface.";  
 RL Biochemistry 34:6911-6918(1995).  
 RN [8]  
 RN STRUCTURE BY NMR OF 136-187.  
 RX MEDLINE=96323218; PubMed=8710867;  
 RA Mott H.R., Carpenter J.W., Zhong S., Ghosh S., Bell R.M.,  
 RA Campbell S.L.;  
 RT "The solution structure of the Raf-1 cysteine-rich domain: a novel  
 RT ras and phospholipid binding site.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8312-8317(1996).  
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM  
 CC THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT  
 CC SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 CC BINDING DOMAIN.  
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CC -----  
 DR EMBL; X03484; CAA27204.1; -;  
 DR EMBL; BC018119; AAH18119.1; -;  
 DR PIR; A00637; TVHUF6.  
 DR PDB; 1FAQ; 27-JAN-97.  
 DR PDB; 1FAR; 27-JAN-97.  
 DR PDB; 1RFA; 20-JUN-96.  
 DR PDB; 1GUA; 11-JAN-97.  
 DR Genew; HGNC:9829; RAF1.  
 DR MIM; 164760; -;  
 DR InterPro; IPR002219; DAG\_PE-bind.  
 DR InterPro; IPR000719; Euk\_pkinase.

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DR InterPro; IPR003116; RBD.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYKc; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding; Phosphorylation; 3D-structure.
FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
FT NP_BIND 349 609 PROTEIN_KINASE.
FT BINDING 355 363 ATP (BY SIMILARITY).
FT ACT_SITE 375 375 ATP (BY SIMILARITY).
FT MOD_RES 338 338 BY SIMILARITY.
SQ SEQUENCE 648 AA; 73051 MW; EF821B5349711BC3 CRC64;
Query Match 58.6%; Score 34; DB 1; Length 648;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QHHYGTPT 8
Db 229 QHRYSTPH 236

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Search completed: July 18, 2003, 15:07:20  
 Job time : 6.58 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:40 ; Search time 23.22 Seconds  
(without alignments)  
79.863 Million cell updates/sec

Title: US-10-007-790-10  
Perfect score: 58  
Sequence: 1 QHHYGTPT 9

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPRTEMBL 21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp Unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	44	75.9	235	4 Q8WZ18	Q8WZ18 homo sapien
2	42	72.4	332	5 Q9XWK6	Q9XWK6 caenorhabdi
3	42	72.4	411	5 Q9XWK8	Q9XWK8 caenorhabdi
4	40	69.0	228	12 Q8QRV8	Q8QRV8 chimpanzee
5	40	69.0	237	16 Q9K1P1	Q9K1P1 neisseria m
6	40	69.0	386	16 Q92NE3	Q92NE3 rhizobium m
7	40	69.0	750	10 Q9SDB1	Q9SDB1 arabidopsis
8	40	69.0	1222	10 Q8S8T6	Q8S8T6 arabidopsis
9	40	69.0	1884	10 Q8W010	Q8W010 arabidopsis
10	39	67.2	234	11 Q8VCP0	Q8VCP0 mus musculu
11	39	67.2	713	5 Q9N8N5	Q9N8N5 trypanosoma
12	38	65.5	107	11 Q9ERZ9	Q9ERZ9 mus musculu
13	38	65.5	287	17 Q27992	Q27992 archaeoglob
14	38	65.5	786	2 P95466	P95466 pancoea cit
15	38	65.5	849	10 Q9SVZ7	Q9SVZ7 arabidopsis
16	38	65.5	861	10 Q9C5E7	Q9C5E7 arabidopsis

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17 38 65.5 1168 10 Q8S7C7
18 38 65.5 1392 10 Q9SDG9
19 37 63.8 199 16 Q9CIT2
20 37 63.8 279 10 Q9FM02
21 37 63.8 416 16 Q8RB97
22 37 63.8 439 17 Q8U1V4
23 37 63.8 450 17 Q58798
24 37 63.8 451 17 Q9V076
25 37 63.8 517 5 Q8SSF5
26 37 63.8 547 17 Q972Y4
27 37 63.8 575 5 Q9GYL1
28 37 63.8 1086 5 Q9N976
29 36 62.1 90 4 Q9BYK1
30 36 62.1 211 3 Q9HEF6
31 36 62.1 223 16 Q31432
32 36 62.1 236 16 Q98FG8
33 36 62.1 298 11 Q9QYF0
34 36 62.1 299 16 Q8ZB12
35 36 62.1 303 12 Q993G9
36 36 62.1 309 16 Q9JXG8
37 36 62.1 309 16 Q9JWG7
38 36 62.1 416 5 Q9VDA7
39 36 62.1 439 10 Q9C865
40 36 62.1 448 16 Q8Y1V0
41 36 62.1 460 10 Q9LIF8
42 36 62.1 464 10 Q94EA9
43 36 62.1 487 17 Q9HHU7
44 36 62.1 589 16 Q06827
45 36 62.1 599 5 Q9V9H7

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#### ALIGNMENTS

##### RESULT 1

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Q8WZ18 ID Q8WZ18 PRELIMINARY; PRT; 235 AA.
AC Q8WZ18;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Hypothetical 24.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jiang H.Q., Zhou X.M., Zhang P.P., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289574; AAL55758.1; -
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 24633 MW; C76D6CCEC05EB17A CRC64;

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Query Match 75.9%; Score 44; DB 4; Length 235;
Best Local Similarity 87.5%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QHHYGTPT 8
Db 70 QSHYGTPT 77

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##### RESULT 2

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Q9XWK6 ID Q9XWK6 PRELIMINARY; PRT; 332 AA.
AC Q9XWK6;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)

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DE Y48A6C.3 protein.  
GN Y48A6C.3  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gardner A.E.;  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: A platform for  
RT investigating biology."  
RL Science 282:2012-2018(1998).  
DR EMBL; AL032642; CAA21653.1; -.  
DR InterPro; IPR001440; TPR.  
DR InterPro; IPR000822; Znf\_C2H2.  
DR Pfam; PF00096; zf-C2H2; 2.  
DR SMART; SM00355; Znf\_C2H2; 1.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_1.  
DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 1.  
KW DNA-binding; Zinc-finger.  
SQ SEQUENCE 332 AA; 37819 MW; DEA92762ED8745D4 CRC64;  
  
Query Match 72.4%; Score 42; DB 5; Length 332;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 HHYGTPT 8  
DB 256 HHYATPY 262  
|||||  
  
RESULT 3  
Q9XWK8 PRELIMINARY; PRT; 461 AA.  
AC Q9XWK8  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Y48A6C.1 protein.  
GN Y48A6C.1  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gardner A.E.;  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: A platform for  
RT investigating biology."  
RL Science 282:2012-2018(1998).  
DR EMBL; AL032642; CAA21651.2; -.  
DR InterPro; IPR000822; Znf\_C2H2.  
DR Pfam; PF00096; zf-C2H2; 2.  
DR SMART; SM00355; Znf\_C2H2; 1.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_2.  
DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 2.  
KW DNA-binding; Zinc-finger.  
SQ SEQUENCE 461 AA; 53033 MW; 310B2510C869AF57 CRC64;  
  
Query Match 72.4%; Score 42; DB 5; Length 461;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPT 8  
DB 260 HHYATPY 266  
|||||  
  
RESULT 4  
Q8QRV8 PRELIMINARY; PRT; 228 AA.  
AC Q8QRV8  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE UL157.  
OS chimpanzee cytomegalovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=188763;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Davison A.J., Akter P., Dolan A., Wright K.M., Addison C.,  
RA Alcendor D.J., Hayward G.S., McGeoch D.J.;  
RT "The human cytomegalovirus genome revisited";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF480884; AAM00780.1; -.  
SQ SEQUENCE 228 AA; 25902 MW; 42D8D01531D6939D CRC64;  
  
Query Match 69.0%; Score 40; DB 12; Length 228;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QHHYGTPT 7  
DB 26 QHHYNTPT 32  
|||||  
  
RESULT 5  
Q9K1P1 PRELIMINARY; PRT; 237 AA.  
AC Q9K1P1  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hydrolyase, putative.  
GN NMB0040.  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,  
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,  
RA Gill J., Starlato V., Masignani V., Pizza M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
RT MC58";  
RL Science 287:1809-1815(2000).  
DR EMBL; AE002362; AAF40511.1; -.  
DR TIGR; NMB0040; -.  
DR InterPro; IPR001454; Hlg\_nase/hydrlase.  
DR Pfam; PF00702; Hydrolyase; 1.  
KW Complete proteome.  
SQ SEQUENCE 237 AA; 26836 MW; E9059942D1D907D5 CRC64;  
  
Query Match 69.0%; Score 40; DB 16; Length 237;  
Best Local Similarity 75.0%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 QHHYTPY 8
DB 220 QNHNTFY 227

RESULT 6
Q92NE3 PRELIMINARY; PRT; 386 AA.
AC Q92NE3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative ABC transporter protein.
GN R02264 OR SMC01652.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capella D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591790; CAC46843.1; -;
DR InterPro; IPR000567; SBP_bac.1.
DR Pfam; PF01547; SBP_bacterial_1; 1.
KW Complete proteome.
SQ SEQUENCE 386 AA; 42673 MW; 0FC10131CD1BA8A CRC64;

Query Match 69.0%; Score 40; DB 16; Length 386;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HYGTPY 8
DB 138 HYGTPY 143

RESULT 7
Q9SDB1 PRELIMINARY; PRT; 750 AA.
AC Q9SDB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 83.8 kDa protein (Fragment).
GN AT2G41700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002510; AAM14842.1; -;
FT NON_TER 1
SQ SEQUENCE 1222 AA; 134754 MW; 5C41200C427F2F4E CRC64;

Query Match 69.0%; Score 40; DB 10; Length 1222;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QHHYTPY 9
DB 100 KHHYGVGYT 108

RESULT 9
Q8W010 PRELIMINARY; PRT; 1884 AA.
AC Q8W010;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ATP-binding cassette transporter ABCA1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002510; AAM14842.1; -;
FT NON_TER 1
SQ SEQUENCE 1222 AA; 134754 MW; 5C41200C427F2F4E CRC64;

Query Match 69.0%; Score 40; DB 10; Length 1222;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QHHYTPY 9
DB 100 KHHYGVGYT 108

RESULT 8
Q8S8T6 PRELIMINARY; PRT; 1222 AA.
AC Q8S8T6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ABC transporter (Fragment).
GN AT2G41700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002510; AAM14842.1; -;
FT NON_TER 1
SQ SEQUENCE 1222 AA; 134754 MW; 5C41200C427F2F4E CRC64;

Query Match 69.0%; Score 40; DB 10; Length 750;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QHHYTPY 9
DB 704 KHHYGVGYT 712
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OX NCBI\_TaxID=3702;  
RN [1]  
RA SEQUENCE FROM N.A.  
RA Forestier C.;  
RT "AtARCA1, a full size ABC transporter homolog of the mammalian  
RT cholesterol efflux regulatory protein ABCA1.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AV032590; AAK39643.1; -;  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR003439; ABC\_transporter.  
DR Pfam; PF00005; ABC\_tran; 2.  
DR ProDom; PD000006; ABC\_transporter; 2.  
DR SMART; SM00382; AAA; 2.  
DR PROSITE; PS00211; ABC\_TRANSPORTER; UNKNOWN\_2.  
KW ATP-binding.  
SQ SEQUENCE 1884 AA; 209477 MW; 93CA7AB44D65D588 CRC64;

Query Match 69.0%; Score 40; DB 10; Length 1884;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
:|||||  
Db 734 KHHYGVGYT 742

RESULT 10  
Q8VCP0 PRELIMINARY; PRT; 234 AA.  
ID Q8VCP0  
AC Q8VCP0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 25.7 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RA SEQUENCE FROM N.A.  
RA TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR ENBL; BC019474; AAH19474.1; -;  
DR InterPro; IPR003599; Ig\_c1.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25702 MW; 102551CS8AC2FA9F CRC64;

Query Match 67.2%; Score 39; DB 11; Length 234;  
Best Local Similarity 66.7%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
:|||||  
Db 109 QHHGIPPT 117

RESULT 11  
Q9N8N5 PRELIMINARY; PRT; 713 AA.  
ID Q9N8N5  
AC Q9N8N5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical 76.0 kDa protein.

GN CHR1.240.  
OS Trypanosoma brucei  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RA SEQUENCE FROM N.A.  
RC STRAIN=TREU927;  
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,  
RA Lennard N.O., Clark L.N., Harris B.R., Melville S., Lawson D.,  
RA Gerrard C., Rajandream M.A., Barrall B.G.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AL359782; CAB95508.1; -;  
DR InterPro; IPR000194; ATPase\_a/bcentre.  
DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 713 AA; 75955 MW; 5D9F2057727E79EA CRC64;

Query Match 67.2%; Score 39; DB 5; Length 713;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGT 6  
:|||||  
Db 612 QHHYGT 617

RESULT 12  
Q9ERZ9 PRELIMINARY; PRT; 107 AA.  
ID Q9ERZ9  
AC Q9ERZ9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Anti human TNF-alpha light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RA SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
RT "Cloning and sequencing of the light chain fragment of variable region  
RT J. Genes of an anti-hTNF-a monoclonal antibody.";  
RL J. Cell. Mol. Immunol. 12:21-26(1996).  
RN [2]  
RA SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RT "Construction and sequencing of the single-chain antibody gene of a  
RT human TNF-alpha specific monoclonal antibody.";  
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).  
RN [3]  
RA SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AF262753; AAG23804.1; -;  
DR HSP; P80362; 1WTL.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGv; 1.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 65.5%; Score 38; DB 11; Length 107;  
Best Local Similarity 66.7%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
:|||||  
Db 92 QOHYRTPT 100

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RESULT 13
O27992
ID O27992 PRELIMINARY; PRT; 287 AA.
AC O27992;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Hypothetical protein AF2292.
GN AF2292.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton P.M., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AE000946; AAB88967.1; -.
DR TIGR; AF2292; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 287 AA; 33541 MW; 8DA315595CE2AC58 CRC64;

Query Match 65.5%; Score 38; DB 17; Length 287;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHMYGTPY 8
DB 212 QHMYGAPF 219

RESULT 14
P95466
ID P95466 PRELIMINARY; PRT; 786 AA.
AC P95466;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Glucose dehydrogenase [pyrroloquinoline-quinone] (EC 1.1.99.17).
GN GDH.
OS Pantoea citrea.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pantoea.
OX NCBI_TaxID=53336;
RN [1]
RC SEQUENCE FROM N.A., AND ACTIVITY.
RX STRAIN=1056R;
RX MEDLINE=97133947; PubMed=8979341;
RA Cha J.-S., Pujol C., Kado C.I.;
RT "Identification and characterization of a Pantoea citrea gene encoding
RT glucose dehydrogenase that is essential for causing pink disease of
RT pineapple."
RL Appl. Environ. Microbiol. 63:71-76(1997).
CC -1- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE +
CC REDUCED ACCEPTOR.
CC -1- COPACTOR: PQO.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC (BY SIMILARITY).
CC -1- MISCELLANEOUS: RESPONSIBLE FOR PINK TO BROWN DISCOLORATIONS OF

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CC CC INFECTED PINEAPPLES UPON HEATING DURING THE CANNING PROCEDURE.
CC CC INFECTED BATCHES HAVE TO BE DISCARDED.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQO DEHYDROGENASE FAMILY.
DR EMBL; X95985; CAA65229.1; -.
DR InterPro; IPR001479; Bac_PQO.
DR InterPro; IPR002372; Bac_PQO_repeat.
DR Pfam; PF01011; Bacterial_PQO; 6.
DR PROSITE; PS00364; BACTERIAL_PQO_2; 1.
KW Oxidoreductase; PQO; Transmembrane; Periplasmic.
FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 14 55 POTENTIAL.
FT DOMAIN 56 59 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 60 80 POTENTIAL.
FT DOMAIN 81 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 POTENTIAL.
FT DOMAIN 107 115 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 116 136 POTENTIAL.
FT DOMAIN 137 431 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 432 452 POTENTIAL.
FT DOMAIN 453 652 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 653 673 POTENTIAL.
FT DOMAIN 674 700 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 701 721 POTENTIAL.
FT DOMAIN 722 786 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 724 770 PQO-BINDING.
FT ACT_SITE 462 462 BY SIMILARITY.
SQ SEQUENCE 786 AA; 86038 MW; 372402AAD8B067CC CRC64;

Query Match 65.5%; Score 38; DB 2; Length 786;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHMYGTPY 8
DB 640 QHMYGVYP 647

RESULT 15
Q9SVZ7
ID Q9SVZ7 PRELIMINARY; PRT; 849 AA.
AC Q9SVZ7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Pumilio-like protein.
GN PUM19.160 OR AT4G25880.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RC SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Hohnel J., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049480; CAB39609.1; -.
DR EMBL; AL161564; CAB79443.1; -.
DR InterPro; IPR001313; Pumilio/Puf.
DR Pfam; PF00806; PUF; 8.

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DR SMART: SM00025; Pumilio; 8.  
SQ SEQUENCE 849 AA; 94894 MW; 74EFC4593EB7B498 CRC64;  
Query Match 65.5%; Score 38; DB 10; Length 849;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 8  
Db 267 QFHYGQPY 274  
RESULT 16  
Q9C5E7 PRELIMINARY; PRT; 861 AA.  
AC Q9C5E7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Putative pumilio protein.  
GN A4G25880.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
RA Theologis A.;  
RT "Full length cDNA of gene AT4g25880 (GI:7269439).";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF360298; AAK26008.1; -;  
DR InterPro: IPR001313; Pumilio/Puf.  
DR Pfam: PF00806; PUF; 8.  
DR SMART: SM00025; Pumilio; 8.  
SQ SEQUENCE 861 AA; 96105 MW; 44555848AAFCDESA CRC64;  
Query Match 65.5%; Score 38; DB 10; Length 861;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 8  
Db 287 QFHYGQPY 294  
RESULT 17  
Q8S7C7 PRELIMINARY; PRT; 1168 AA.  
AC Q8S7C7;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative gag-pol polyprotein.  
GN OSJNBA0057L21.25.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Buehl C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,  
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,  
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,  
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,

RA Salzberg S.L., White O., Fraser C.M.;  
RT "Oryza sativa chromosome 10 BAC OSJNBA0057L21 genomic sequence.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC087599; AAL79695.1; -;  
KW Polyprotein.  
SQ SEQUENCE 1168 AA; 128502 MW; B3ED6E5C79954CAA CRC64;  
Query Match 65.5%; Score 38; DB 10; Length 1168;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 9  
Db 455 QRHYTTPYS 463  
RESULT 18  
Q9SDG9 PRELIMINARY; PRT; 1392 AA.  
AC Q9SDG9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Similar to putative polyprotein.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Sasaki T., Matsuoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
clone: P0038F12.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF000836; BAA88175.1; -;  
DR InterPro: IPR001584; Rve.  
DR InterPro: IPR001878; Znf\_CCHC.  
DR Pfam: PF00865; rve; 1.  
DR Pfam: PF00098; zf-CCHC; 1.  
DR SMART: SM00343; Znf\_C2HC; 1.  
KW Polyprotein.  
SQ SEQUENCE 1392 AA; 154506 MW; 7188F034FDA07AAE CRC64;  
Query Match 65.5%; Score 38; DB 10; Length 1392;  
Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 9  
Db 588 QRHYTTPYS 596  
RESULT 19  
Q9CIT2 PRELIMINARY; PRT; 199 AA.  
AC Q9CIT2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Anaerobic ribonucleoside-triphosphate reductase activating  
DE protein.  
GN NR04 OR L20274.  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
OC Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IL1403;  
RX MEDLINE=21235196; PubMed=11337471;  
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarre K.,

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RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RL Lactis esp. lactis IL1403."
RL Genome Res. 11:731-753 (2001).
DR EMBL: AE006264; AAK04372.1; -.
DR InterPro: IPR001989; Radical_activat.
DR Pfam: PF02143; Radical_activat; 1.
KW Complete proteome.
SQ SEQUENCE 199 AA; 23268 MW; 9D7D9794EC065813 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 199;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9
DB 59 YGTPYT 64

RESULT 20
Q9FW02 PRELIMINARY; PRT; 279 AA.
AC Q9FW02;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 32.4 kDa protein.
GN FljE17.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoids II; Brassicales; Brassicaceae; Arabidopses.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 1 BAC FljE17 genomic sequence.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC074284; AAG12615.1; -.
KW Hypothetical protein.
SQ SEQUENCE 279 AA; 32364 MW; E4698FAC34C61C0C CRC64;

Query Match 63.8%; Score 37; DB 10; Length 279;
Best Local Similarity 83.3%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHYGTG 7
DB 192 HHFGTP 197

RESULT 21
Q8RB97 PRELIMINARY; PRT; 416 AA.
AC Q8RB97;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE D-alanyl-D-alanine carboxypeptidase.
GN DACC OR TTE0925.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacterales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

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RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700 (2002).
DR EMBL: AE013058; AAM24181.1; -.
DR Carboxypeptidase; Complete proteome.
SQ SEQUENCE 416 AA; 46794 MW; 586681D1A33FC870 CRC64;

Query Match 63.8%; Score 37; DB 16; Length 416;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
DB 161 ENHYSTPT 168

RESULT 22
Q8UIV4 PRELIMINARY; PRT; 439 AA.
AC Q8UIV4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF1101.
GN PF1101.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE010220; AAL81225.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 439 AA; 49079 MW; B3ABA93A7F06CE68 CRC64;

Query Match 63.8%; Score 37; DB 17; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9
DB 100 YGTPYT 105

RESULT 23
O58798 PRELIMINARY; PRT; 450 AA.
AC O58798;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PH1071.
GN PH1071.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";

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RL DNA Res. 5:55-76(1998).
DR EMBL: APO00004; BAA30170.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR InterPro; IPR004613; MG423.
DR InterPro; IPR001587; UPF0036.
DR Pfam; PF00753; lactamase_B; 1.
DR Pfam; PF02147; UPF0036; 1.
DR TIGRFAMs; TIGR00649; MG423; 1.
DR PROSITE; PS01292; UPF0036; UNKNOWN 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 450 AA; 50341 MW; 4F8833725B966DFB CRC64;

Query Match 63.8%; Score 37; DB 17; Length 450;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9
Db 110 YGTPYT 111

RESULT 24
Q9V076 PRELIMINARY; PRT; 451 AA.
AC Q9V076;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PAB1751.
GN PAB1751.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248285; CAB49829.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR InterPro; IPR004613; MG423.
DR InterPro; IPR001587; UPF0036.
DR Pfam; PF00753; lactamase_B; 1.
DR Pfam; PF02147; UPF0036; 1.
DR TIGRFAMs; TIGR00649; MG423; 1.
DR PROSITE; PS01292; UPF0036; UNKNOWN 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 451 AA; 50517 MW; AA689437804BC24E CRC64;

Query Match 63.8%; Score 37; DB 17; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9
Db 106 YGTPYT 111

RESULT 25
Q8SSFS PRELIMINARY; PRT; 517 AA.
AC Q8SSFS;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein disulfide isomerase.
GN ECU02_0850.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
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RNA SEQUENCE FROM N.A.
RP STRAIN=GB-M1;
RA Genoscope; (APR-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL: AL590442; CAD25114.1; -.
SQ SEQUENCE 517 AA; 59068 MW; 87CB15737957BE3B CRC64;

Query Match 63.8%; Score 37; DB 5; Length 517;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGTPYT 9
Db 407 HLGTPYT 413

RESULT 26
Q972Y4 PRELIMINARY; PRT; 547 AA.
ID Q972Y4;
AC Q972Y4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein ST1005.
GN ST1005.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000984; BAB66029.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 547 AA; 63567 MW; A888D7EAD99CEDCC CRC64;

Query Match 63.8%; Score 37; DB 17; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9
Db 162 YGTPYT 167

RESULT 27
Q9GYL1 PRELIMINARY; PRT; 575 AA.
ID Q9GYL1;
AC Q9GYL1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 66.7 kDa protein.
GN R04E5.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Miller N.;
RT "The sequence of C. elegans cosmid R04E5.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41538; AAG00007.2; -.
DR InterPro; IPR001664; IF.
DR Pfam; PF00038; filament; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 575 AA; 66699 MW; DCD9581BEC52C01 CRC64;

Query Match 63.8%; Score 37; DB 5; Length 575;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPT 9
Db 427 HHYGSYS 434

RESULT 28
Q9N976 PRELIMINARY; PRT; 1086 AA.
ID Q9N976;
AC Q9N976;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 116.1 kDa protein.
GN P1295.12.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Masuy D.; Purnelle B.; Goffeau A.; Ivens A.C.; Quail M.;
RA Rajandream M.A.; Barrell B.G.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C.; Lewis S.M.; Bagherzadeh A.; Zhang L.; Chan H.M.;
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL359773; CAB95220.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1086 AA; 116056 MW; 19C4A930165C3415 CRC64;

Query Match 63.8%; Score 37; DB 5; Length 1086;

Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 7
Db 566 QHHAGTPT 572

RESULT 29
Q9BYK1 PRELIMINARY; PRT; 90 AA.
ID Q9BYK1;
AC Q9BYK1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE DJ908M14.1.3 (ribosomal protein S21, isoform 3).
GN RPS21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121832; CAC29248.1; -.
DR InterPro; IPR001931; Ribosomal_S21E.
DR Pfam; PF01249; Ribosomal_S21e; 1.
DR ProDom; PD006584; Ribosomal_S21E; 1.
DR PROSITE; PS00996; RIBOSOMAL_S21E; 1.
KW Ribosomal protein.
SQ SEQUENCE 90 AA; 9894 MW; 2A2466BC91A1F556 CRC64;

Query Match 62.1%; Score 36; DB 4; Length 90;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPT 9
Db 71 HHFGTSWT 78

RESULT 30
Q9HEF6 PRELIMINARY; PRT; 211 AA.
ID Q9HEF6;
AC Q9HEF6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 23.4 kDa protein.
GN 65E11.100.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U.; Aign V.; Hoheisel J.; Brandt P.; Fartmann B.; Holland R.;
RA Nyakatura G.; Mewes H.W.; Mannhaupt G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451021; CAC18294.2; -.
KW Hypothetical protein.
SQ SEQUENCE 211 AA; 23425 MW; B75964FD26EC5C4F CRC64;

Query Match 62.1%; Score 36; DB 3; Length 211;
Best Local Similarity 71.4%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGTPT 7
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Db          29 ENHYGTP 35
:::|||||
RESULT 31
O31432      PRELIMINARY;      PRT; 223 AA.
AC O31432;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE YBDJ protein.
GN YBDJ
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Avevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karasata D., Kaahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinio S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
RP [2]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
RA "Sequence analysis of the 70kb region between 17 and 23 degree of the
RT Bacillus subtilis chromosome";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
CC -!- SIMILARITY: TO BACTERIAL REGULATORY PROTEINS INVOLVED IN SIGNAL
CC TRANSDUCTION.
DR EMBL; Z99105; CAB11994.1; -.
DR EMBL; AB006424; BAA33098.1; -.
DR HSSP; P08402; 1800.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
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DR Pfam; PF00072; response\_reg; 1.  
DR Pfam; PF00486; trans\_reg\_C; 1.  
DR ProDom; PD000039; Response\_reg; 1.  
DR ProDom; PD000329; Trans\_reg\_C; 1.  
DR SMART; SM00448; REC; 1.  
KW DNA-binding; Phosphorylation; Sensory transduction;  
KW Transcription regulation; Complete proteome.  
SQ SEQUENCE 223 AA; 26173 MW; 9DB646AD90675A86 CRC64;

Query Match 62.1%; Score 36; DB 16; Length 223;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGT 6  
Db 117 EHHYGT 122

RESULT 32  
Q98FG8 PRELIMINARY; PRT; 236 AA.  
AC Q98FG8;  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Peptidoglycan transglycosylase.  
GN MLI3783.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NAF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti";  
RL DNA Res. 7:331-338(2000).  
DR EMBL; AP003002; BAB50599.1; -.  
DR InterPro; IPR001264; GT\_51.  
DR Pfam; PF00312; Transglycosyl; 1.  
DR ProDom; PD001895; GT\_51; 1.  
KW Complete proteome.  
SQ SEQUENCE 236 AA; 26042 MW; 4A5FFFD098A371C0 CRC64;

Query Match 62.1%; Score 36; DB 16; Length 236;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGT 7  
Db 177 QHHFGIP 183

RESULT 33  
Q9QYF0 PRELIMINARY; PRT; 298 AA.  
AC Q9QYF0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CN 8 scfv.  
GN CN 8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig; 2.
DR SMART; SM00406; IGV; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 62.1%; Score 36; DB 11; Length 298;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9
Db 261 QHFWTPT 269

RESULT 34
Q82B12 PRELIMINARY; PRT; 299 AA.
ID Q82B12
AC Q82B12
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein YPO3617.
GN YPO3617.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414158; CAC93086.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 299 AA; 33184 MW; DFD537C95DE4C86 CRC64;

Query Match 62.1%; Score 36; DB 16; Length 299;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HYGTPY 8
Db 98 HFGTPY 103

RESULT 35
Q993G9 PRELIMINARY; PRT; 303 AA.
ID Q993G9
AC Q993G9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ORF41.
OS callitriche herpesvirus 3.

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OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=106331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CJ0149;
RX MEDLINE=21107697; PubMed=11158621;
RA Cho Y., Ramer J., Rivallier P., Quink C., Garber R.L., Beier D.R.,
RA Wang F.;
RT "An Epstein-Barr-related herpesvirus from marmoset lymphomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1224-1229(2001).
DR EMBL; AF319782; AAK38249.1; -.
SQ SEQUENCE 303 AA; 34855 MW; D6BFB90656294623 CRC64;

Query Match 62.1%; Score 36; DB 12; Length 303;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HHYGTPT 8
Db 89 HHVSDPY 95

RESULT 36
Q9JXG8 PRELIMINARY; PRT; 309 AA.
ID Q9JXG8
AC Q9JXG8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transcriptional regulator, LysR family.
GN NMB2055.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
CC -1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
DR EMBL; AE002555; AAF42375.1; -.
DR TIGR; NMB2055; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH 1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 309 AA; 34831 MW; 7086861A2DE26637 CRC64;

Query Match 62.1%; Score 36; DB 16; Length 309;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGTPT 7
Db 44 ENHYGTPT 50

RESULT 37
Q9JWG7

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ID O9JWG7 PRELIMINARY; PRT; 309 AA.
AC O9JWG7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transcriptional activator protein METR.
GN METR OR NMA0381.
OS Neisseria meningitidis (serogroup A)
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROTYPE A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
DR ENBL; AL162753; CAB83682.1; -
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN 1.
DR DNA-binding; Transcription_regulation; Complete proteome.
SQ SEQUENCE 309 AA; 34835 MW; 74D2137E7BA00601 CRC64;

Query Match 62.1%; Score 36; DB 16; Length 309;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHNYGTP 7
Db 44 ENHYGTP 50

RESULT 38
Q9VDA7 PRELIMINARY; PRT; 416 AA.
ID Q9VDA7 PRELIMINARY;
AC Q9VDA7; Q9TY85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE TIN protein (CG7895 protein).
DE TIN OR NK-4 OR CG7895.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer J.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Baou A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fostler C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE OF 1-15 FROM N.A.
RP STRAIN=CANTON-S;
RC STRAIN=CANTON-S;
RX MEDLINE=90046666; PubMed=2573058;
RA Kim Y., Nirenberg M.;
RT "Drosophila NK-homeobox genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:7716-7720(1989).
RN [3]
RN SEQUENCE OF 1-15 FROM N.A.
RP STRAIN=CANTON-S;
RC STRAIN=CANTON-S;
RA Lee Y., Park T., Schulz R., Kim Y.;
RT "Twist-mediated activation of the NK-4 homeobox gene in the visceral
RT mesoderm of Drosophila requires two distinct clusters of E-box
RT regulatory elements."
RL J. Biol. Chem. 0:0-0(1997).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR ENBL; AF003734; AAF55890.1; -
DR EMBL; AF004336; AAD09865.1; -
DR HSSP; P23441; 1FTT.
DR FlyBase; FBgn0004110; tin.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 416 AA; 46066 MW; F58A4F92324A7E2B CRC64;

Query Match 62.1%; Score 36; DB 5; Length 416;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHNYGTP 8
Db 140 QHHGHGP 147

RESULT 39
Q9C865 PRELIMINARY; PRT; 439 AA.
ID Q9C865 PRELIMINARY;
AC Q9C865;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 49.3 kDa protein (SH3 domain-containing protein 1).

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GN T8E3.10 OR AT1G31440.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RX MEDLINE=21016719; PubMed=11130712;  
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,  
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,  
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
RT thaliana.";  
RL Nature 408:816-820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21558796; PubMed=11701894;  
RA Lam B.C.-H., Sage T.L., Bianchi F., Blumwald E.;  
RA "Role of SH3 domain-containing proteins in clathrin-mediated vesicle  
RT trafficking in Arabidopsis.";  
RL Plant Cell 13:2499-2512(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
RA Theologis A.;  
RT "Arabidopsis Full Length cDNA Clones.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
DR EMBL; AC027135; AAG51264.1; -.  
DR EMBL; AF367773; AAL32438.1; -.  
DR EMBL; AY080835; AAL87310.1; -.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PSS0002; SH3; 1.  
KW Hypothetical protein; SH3 domain.  
SQ SEQUENCE 439 AA; 49258 MW; 41A42B784BE8AC25 CRC64;  
  
Query Match 62.1%; Score 36; DB 10; Length 439;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 HHYGTPT 8  
Db 108 HHFGTST 114  
  
RESULT 40  
Q8Y1V0 PRELIMINARY; PRT; 448 AA.  
AC Q8Y1V0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative amidotransferase amidase protein (EC 3.5.1.-).  
GN RSC0589 OR RS04871.  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
OC Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,  
RA Weissenbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
RL Nature 415:497-502(2002).  
DR EMBL; AL646060; CAD14119.1; -.  
DR InterPro; IPR000120; Amidase.  
DR Pfam; PF01425; Amidase; 1.  
KW Hydrolase; Complete proteome.  
SQ SEQUENCE 448 AA; 45899 MW; 5FD24B29FCCDIE9A CRC64;  
  
Query Match 62.1%; Score 36; DB 16; Length 448;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 HYGTPPT 9  
Db 140 HYGTPPT 146  
  
Search completed: July 18, 2003, 15:09:50  
Job time : 25.22 secs



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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:01:44 ; Search time 23.66 Seconds  
(without alignments)  
39.423 Million cell updates/sec

Title: US-10-007-790-5

Perfect score: 41

Sequence: 1 GYSFTGY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	7	21	AAV87657 Murine PIP3 recogn
2	41	100.0	20	21	AAV70805 Murine anti-PAB-42
3	41	100.0	20	23	AAU70794 Hepatitis B virus
4	41	100.0	98	13	AAU70708 Hypercalcaemia age
5	41	100.0	99	14	AAU70771 Murine anti-CD3 MA
6	41	100.0	108	20	AAU70361 HBV specific singl
7	41	100.0	111	18	AAW04593 Anti-DNA antibody
8	41	100.0	114	16	AAU79244 Heavy chain variab
9	41	100.0	114	22	AAU50793 Murine antibody S2
10	41	100.0	115	13	AAU21267 Murine VH group 1

11	41	100.0	116	13	AAU27010 Hypercalcaemia age
12	41	100.0	119	13	AAU25730 Humanised VH regio
13	41	100.0	119	22	AAU69680 Humanised CMV5 ant
14	41	100.0	119	22	AAU69682 Human anti-PAB-42
15	41	100.0	120	15	AAU59985 U7.6 heavy chain v
16	41	100.0	120	17	AAU88752 scFv U7.6 VH Uns
17	41	100.0	120	17	AAU88752 scFv U7.6 VH (K19N
18	41	100.0	122	14	AAU30772 huxCD3v9, humanise
19	41	100.0	124	21	AAU87655 Murine PIP3 recogn
20	41	100.0	130	21	AAU70791 Murine anti-PAB-42
21	41	100.0	130	23	AAU70768 Hepatitis B virus
22	41	100.0	136	17	AAU06446 HuM3 VH region BR
23	41	100.0	136	17	AAU06442 HuM3 VH region..
24	41	100.0	139	14	AAU38259 Chimeric 128.1 VH,
25	41	100.0	233	14	AAU41710 Chimeric antibody c
26	41	100.0	235	14	AAU41682 Murine 128.1 VH/hu
27	41	100.0	235	14	AAU41707 Murine 128.1 VH/hu
28	41	100.0	235	14	AAU41715 Anti-mesothelin sc
29	41	100.0	241	20	AAU76197 Antimesothelin ant
30	41	100.0	241	22	AAU50019 Human BLYS binding
31	41	100.0	241	23	AAU45937 Fv(GP-4) immunosup
32	41	100.0	243	15	AAU60781 Anti-5T4 secreted
33	41	100.0	243	20	AAU42294 5T4 scFv antibody
34	41	100.0	243	20	AAU27407 Murine anti-5T4 an
35	41	100.0	243	20	AAU86002 Amino acid sequenc
36	41	100.0	243	22	AAU83835 Human BLYS binding
37	41	100.0	245	23	AAU45889 HBV specific singl
38	41	100.0	297	20	AAU05363 Bispecific CD3-L6F
39	41	100.0	302	15	AAU60206 Human B7-1.5T4.1 p
40	41	100.0	488	20	AAU86004 Amino acid sequenc
41	41	100.0	488	22	AAU83836 Anti-5T4 single ch
42	41	100.0	592	22	AAU86003 An immunotoxin com
43	41	100.0	595	20	AAU86003 Diphtheria toxin/U
44	41	100.0	601	21	AAU07461
45	41	100.0	637	23	AAU75365

#### ALIGNMENTS

#### RESULT 1

AAU87657

ID AAY87657 standard; Protein; 7 AA.

XX AAY87657;

XX AC

XX AAY87657;

XX DT

XX 11-AUG-2000 (first entry)

XX DE Murine PIP3 recognizing Mab variable region heavy chain CDR1 region.

XX DE PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR1;

XX KW immunogen; antibody; heavy chain; complementarity determining region.

XX KW

XX OS Mus sp.

XX XX

XX JP2000083664-A.

XX XX

XX 28-MAR-2000.

XX XX

XX 07-SEP-1998; 98JP-0252921.

XX XX

XX 07-SEP-1998; 98JP-0252921.

XX XX

XX (FUKU/) FUKUI Y.

XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.

XX A monoclonal antibody recognizing

XX PT phosphatidylinositol-3,4,5-triphosphate

XX Claim 7; Page 12; 15pp; Japanese.

XX PS

XX XX

CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain complementarity determining region, CDRI described in the method of  
 CC the invention.

XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 41; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. NO. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 1 GYSFTGY 7

RESULT 2  
 AAY70805  
 ID AAY70805 standard; peptide; 20 AA.

AC AAY70805;  
 XX  
 XX 31-JUL-2000 (first entry)  
 DT  
 XX Murine anti-PAB-421 IDI-2 mAb heavy chain CDR based peptide IDI-2 H1.  
 DE  
 XX Murine, p53 protein; monoclonal antibody; mAb; PAB-421; IDI-2 H1;  
 KW heavy chain variable region; VH; complementarity determining region; CDR;  
 KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;  
 KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;  
 KW DNA-binding domain; anti-idiotypic antibody.

XX Mus sp.

XX WO200023082-A1.

XX 27-APR-2000.

XX 19-OCT-1999; 99WO-US24443.

XX 19-OCT-1998; 98US-0104816.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;

XX WPI; 2000-339512/29.

XX Treatment of systemic lupus erythematosus by down-regulating the  
 PT autoimmune response to the C-terminal DNA-binding domain of the p53  
 PT protein by an active compound comprising of antibodies to p53 or  
 PT fragments of p53 -

XX Claim 78; Fig 10; 87pp; English.

XX The patent discloses a method for the treatment of systemic lupus  
 CC erythematosus (SLE) by down-regulating the autoimmune response to the  
 CC C-terminal DNA-binding domain of p53 protein by an active compound.  
 CC The present sequence is a IDI-2 H1 peptide which comprises the  
 CC complementarity determining region (CDR) of the heavy chain of  
 CC IDI-2 monoclonal antibody (mAb). The IDI-2 mAb is an anti-idiotypic  
 CC antibody/Ab2 mAb specific for PAB-421 which is an Ab1 mAb specific  
 CC to the C-terminal DNA-binding domain of murine p53 protein.  
 CC The peptide corresponds to residues 19-38 of IDI-2 heavy chain  
 CC variable region. It is an example of the active compound useful in  
 CC the diagnosis, prevention and treatment of SLE in humans.

XX SQ Sequence 20 AA;  
 Query Match 100.0%; Score 41; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 0.68;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 8 GYSFTGY 14

RESULT 3  
 AAU70794  
 ID AAU70794 standard; Peptide; 20 AA.  
 XX  
 XX AAU70794;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX Hepatitis B virus antigen binding partner #26.

XX Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;  
 KW antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;  
 KW B cell mediated processing; T cell proliferation; cytokine production;  
 KW immune system response.

XX Synthetic.

XX WO200181421-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-IB00844.

XX 21-APR-2000; 2000US-0556605.

XX (TRIP-) TRIPEP AB.

XX Sallberg M;

XX WPI; 2002-055347/07.

XX Novel peptide that binds to hepatitis B virus core or E antigen, useful  
 PT for treating and preventing hepatitis B virus infection -

XX Claim 2; Page 33; 82pp; English.

XX The invention relates to an isolated or purified peptide (I) which binds  
 CC Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).  
 CC (I) is useful for treating or preventing Hepatitis B virus (HBV)  
 CC infection, by identifying a subject in need of a molecule that inhibits  
 CC HBV infection, and providing the subject with (I). (I) is also useful  
 CC for determining the presence of HBV in a biological sample, and for  
 CC inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,  
 CC by determining whether (I) inhibits B cell mediated processing and  
 CC uptake of HBcAg and/or HBeAg by performing an assay of T cell  
 CC proliferation or cytokine production. (I) is also useful for modulating  
 CC an immune system response. (I) is useful as a template for a design of  
 CC synthetic molecules including peptides, derivatives or modified peptides,  
 CC peptidomimetics and chemicals. (I) is also useful as biotechnological  
 CC tool, diagnostic reagent and as active ingredient in pharmaceuticals.  
 CC (I) is also useful as detection reagents in conventional  
 CC immunochemical techniques, as diagnostic reagents to detect HBV in  
 CC biological sample, and to determine the efficacy of an HBV treatment  
 CC protocol by monitoring the levels of HBcAg and/or HBeAg during and after  
 CC treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core  
 CC antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described  
 CC in the invention.

XX SQ Sequence 20 AA;

XX Query Match 100.0%; Score 41; DB 23; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 5 GYSFTGY 11

RESULT 4  
AAR27008  
ID AAR27008 standard; peptide; 98 AA.  
AC AAR27008;  
XX  
XX 20-MAY-1998 (first entry)  
XX  
XX Hypercalcaemia agent portion 1.  
XX  
XX Antihuman parathyroid hormone-related protein; monoclonal antibody;  
KW variable region; rodent/human chimeric MAb; constant region; PTHrP.  
XX  
XX Synthetic.  
XX  
XX JP04228089-A.  
XX  
XX 18-AUG-1992.  
XX  
XX 15-MAY-1991; 91JP-0110565.  
XX  
XX 15-MAY-1990; 90JP-0124581.  
XX  
XX (KANF ) KANEKA CORP.  
XX  
XX WPI; 1992-320987/39.  
XX  
XX Treatment and preventive agent for hypercalcaemia - contg. one of  
PT anti-human para-thyroid-hormone-related protein monoclonal antibody,  
PT a rodent or chimera monoclonal antibody, fused gene and cell  
PT line, etc.  
XX  
XX Disclosure; Page 13; 18pp; Japanese.  
XX  
XX The sequences given in AAR27008-11 are fragments which were used in  
CC the construction of an agent for the treating and prevention of  
CC hypercalcaemia. The agent contained a portion of the antihuman  
CC parathyroid hormone-related protein monoclonal antibody (antihuman  
CC PTHrP Mab). The Mab was used as the active component in the agent.  
CC The agent further comprises a rodent/human chimeric MAB which has a  
CC rodent variable region and a human constant region and recognises  
CC human PTHrP.  
XX  
XX  
SQ Sequence 98 AA;

Query Match 100.0%; Score 41; DB 13; Length 98;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 18 GYSFTGY 24

RESULT 5  
AAR30771  
ID AAR30771 standard; protein; 99 AA.  
XX  
XX AAR30771;  
XX  
XX 12-MAY-1993 (first entry)  
XX  
XX Murine anti-CD3 MAB UCHT1 heavy chain variable domain.  
DE  
XX Humanisation; rapid; monoclonal antibody; muxCD3.

XX Mus musculus.  
OS  
XX WO9222653-A.  
PN  
XX 23-DEC-1992.  
PD  
XX  
XX 15-JUN-1992; 92WO-US05126.  
PF  
XX 14-JUN-1991; 91US-0715272.  
PR  
XX (GETH ) GENENTECH INC.  
XX  
XX Carter PJ, Presta LG;  
PI  
XX WPI; 1993-018139/02.  
DR  
XX Humanisation of antibodies - by molecular modelling of the variable  
PT domains and alteration by gene conversion mutagenesis .  
PT  
XX Disclosure; Fig 5; 126pp; English.  
PS  
XX The sequence is that of the heavy chain variable domain of murine  
CC anti-CD3 monoclonal antibody UCHL1 (muxCD3, Shalaby 1992).  
CC  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 41; DB 14; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 6  
AAY05361  
ID AAY05361 standard; Protein; 108 AA.  
XX  
XX AAY05361;  
AC  
XX  
XX 30-JUN-1999 (first entry)  
DT  
XX HBV specific single stranded antibody.  
DE  
XX  
XX Single stranded antibody; hepatitis B virus; HBV core protein;  
KW HBV infection; viral proliferation inhibitor; viral DNA synthesis;  
KW gene therapy.  
XX  
XX Mus sp.  
OS  
XX  
XX WO9911792-A1.  
PN  
XX 11-MAR-1999.  
PD  
XX  
XX 02-SEP-1998; 98WO-JP03921.  
PF  
XX  
XX 02-SEP-1997; 97JP-0237054.  
PR  
XX  
XX (HAYA/) HAYASHI N.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
PA  
XX  
XX Hayashi N, Tohdoh N, Yamamoto H, Yamamoto M;  
PI  
XX WPI; 1999-243623/20.  
XX  
XX N-PSDB; AAX33929.  
DR  
XX  
XX Single-stranded antibody against hepatitis B virus core protein,  
PT applicable as (gene) therapeutic agents for treatment of hepatitis B  
PT viral infections  
XX  
XX Claim 2; Page 60-61; 72pp; English.  
PS



CC chain expressed by the hybridoma of interest, or to the 5' and of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &  
 CC AAR7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.

XX SQ Sequence 114 AA;

Query Match 100.0%; Score 41; DB 16; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 DB 20 GYSFTGY 26  
 |||||

RESULT 9  
 AAB50793  
 ID AAB50793 standard; Protein; 114 AA.  
 XX  
 AC AAB50793;  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Murine antibody S2C6 heavy chain variable region.  
 XX  
 KW Mouse; antibody; S2C6; heavy chain variable region; CD40; cancer;  
 KW inflammatory disease; immune system disorder.  
 XX  
 OS Mus musculus.

PN WO200075348-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 08-JUN-2000; 2000WO-US15749.  
 XX  
 PR 08-JUN-1999; 99US-0328296.  
 XX  
 PA (SEAT-) SEATTLE GENETICS INC.  
 XX  
 PI Siegal CB, Wahl AF, Francisco JA, Fell HP;  
 XX  
 DR WPI; 2001-071080/08.  
 DR N-PSDB; AAC91890.  
 XX  
 PT Anti-CD40 antibodies which immunospecifically bind CD40, useful for  
 PT prevention and treatment of cancer, inflammatory diseases and disorders  
 PT or deficiencies of immune system -  
 XX  
 PS Claim 3; Fig 2; 91pp; English.

XX  
 CC The present invention provides the protein and coding sequences of  
 CC anti-CD40 antibodies. These can be used in the treatment of cancer and  
 CC inflammatory and immune system diseases, including systemic lupus  
 CC erythematosus, scleroderma, inflammatory myositis, Sjogren's syndrome,  
 CC mixed connective tissue disease, rheumatoid arthritis, multiple  
 CC sclerosis, inflammatory bowel disease, acute respiratory distress  
 CC syndrome, pulmonary inflammation, osteoporosis, delayed type  
 CC hypersensitivity, asthma, primary biliary cirrhosis and idiopathic  
 CC thrombocytopenic purpura.

XX SQ Sequence 114 AA;

Query Match 100.0%; Score 41; DB 22; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 DB 26 GYSFTGY 32  
 |||||

RESULT 10  
 AAR21267  
 ID AAR21267 standard; Protein; 115 AA.

XX  
 AC AAR21267;  
 DT 21-MAY-1992 (first entry)  
 XX  
 DE Murine VH group 1 chain D specific for pHOX.

XX  
 KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;  
 KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;  
 KW specific binding pairs; replicable genetic display package.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Binding-site 31..35  
 FT /label= CDR1  
 FT Binding-site 50..86  
 FT /label= CDR2  
 FT Binding-site 99..105  
 FT /label= CDR3  
 FT /note=" D/N-X-G-X-X motif "  
 XX

PN WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1991; 91WO-GB01134.

XX 15-MAY-1991; 91GB-0010549.

XX 10-JUL-1990; 90GB-0015198.

XX 19-OCT-1990; 90GB-0022845.

XX 12-NOV-1990; 90GB-0024503.

XX 06-MAR-1991; 91GB-0004744.

XX (CAMP-) CAMBRIDGE ANTIBODY.

XX (MEDI-) MED RES COUNCIL.

XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 XX Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;  
 XX Winter GP, Bonnert TP;

XX WPI; 1992-056862/07.

XX Producing members of specific binding pairs - by expression in  
 XX recombinant host cells with a secreting replicable genetic  
 XX display package.

XX Example 21; Fig 24; 209pp; English.

XX  
 CC The VH sequence is one of eight (AAR21264-71) found to be expressed  
 CC from a single chain Fv library from an immunised mouse. The  
 CC library produces a diverse repertoire of antibody fragments specific  
 CC for 2-phenyl-5-oxazolone (phox). It was prep'd. using cDNA generated  
 CC from mRNA from mice immunised with phox coupled to chicked serum  
 CC albumin. The VH and VL kappa sequences were separately amplified by  
 CC PCR (see AAQ23474-84) and ligated into fdCAT2 (see AAQ23463) for  
 CC expression on the phage surface as fusions with gene III. The  
 CC resulting library of clones was diverse. Twenty three hapten binding  
 CC clones were sequenced revealing the eight different VH genes (A-H)  
 CC in a variety of pairings with seven different Vk genes (a-g) (see  
 CC AAR21264-92). Nearly all the VH genes belonged to gp 1, with only

CC one, "E", being of gp 2 (VHox1). Of the twenty three clones  
 CC sequenced, three were of type "D". Most of the clones were V<sub>k</sub>-d  
 CC combinations. The K<sub>d</sub> of V<sub>H</sub>-E/V<sub>k</sub>-d for pHOX-GABA was 10 nM. Only two  
 CC other combinations (of eleven tested) were found to have higher  
 CC values. This suggests that phage bearing scFv fragments having  
 CC weak affinities can be selected with antigen, probably due to the  
 CC avidity of the multiple antibody heads on the phage.  
 CC See also AAR21260-307, 309-311; AAR22450, 565-581.

XX SQ Sequence 115 AA;

Query Match 100.0%; Score 41; DB 13; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTGY 7  
 Db 26 GYSFTGY 32  
 |||||

# RESULT 11

AAR27010  
 ID AAR27010 standard; peptide; 116 AA.

XX AC

XX AAR27010;

XX DT 23-FEB-1993 (first entry)

XX DE Hypercalcaemia agent portion 3.

XX KW Antihuman parathyroid hormone-related protein; monoclonal antibody;

XX OS variable region; rodent/human chimeric MAB; constant region; PTHR-P.

XX PN Synthetic.

XX PD JP04228089-A.

XX PF 18-AUG-1992.

XX PR 15-MAY-1991; 91JP-0110565.

XX PR 15-MAY-1990; 90JP-0124581.

XX PA (KANF ) KANEKA CORP.

XX DR WPI; 1992-320987/39.

XX DR N-PSDB; AAQ28522.

XX PT Treatment and preventive agent for hypercalcaemia - contg. one of  
 PT anti-human para-thyroid-hormone-related protein monoclonal antibody,  
 PT a rodent or chimera monoclonal antibody, fused gene and cell  
 PT line, etc.

XX PS Disclosure; Page 13; 18pp; Japanese.

XX CC The sequences given in AAR27008-11 are fragments which were used in  
 CC the construction of an agent for the treating and prevention of  
 CC hypercalcaemia. The agent contained a portion of the antihuman  
 CC parathyroid hormone-related protein monoclonal antibody (antihuman  
 CC PTHR-P MAB). The MAB was used as the active component in the agent.  
 CC The agent further comprises a rodent/human chimeric MAB which has a  
 CC rodent variable region and a human constant region and recognises  
 CC human PTHR-P.

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 41; DB 13; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTGY 7  
 Db 27 GYSFTGY 33  
 |||||

# RESULT 12

AAR25730  
 ID AAR25730 standard; Protein; 119 AA.

XX AC AAR25730;

XX DT 13-JAN-1993 (first entry)

XX DE Humanised VH region of the mouse CMV5 antibody.

XX KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;

XX OS gH; heavy chain; variable region; framework; human; Wol.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

XX FT Region 31..35

XX FT /note= "CDR"

XX FT Region 50..66

XX FT /note= "CDR"

XX FT Region 99..108

XX FT /note= "CDR"

XX FT Misc-difference 5 /note= "mutated residue"

XX FT Misc-difference 24 /note= "mutated residue"

XX FT Misc-difference 27 /note= "mutated residue"

XX FT Misc-difference 28 /note= "mutated residue"

XX FT Misc-difference 30 /note= "mutated residue"

XX FT Misc-difference 69 /note= "mutated residue"

XX FT Misc-difference 80 /note= "mutated residue"

XX FT Misc-difference 97 /note= "mutated residue"

XX FT /note= "mutated residue"

XX PN WO9211018-A.

XX PD 09-JUL-1992.

XX PF 19-DEC-1991; 91WO-US09711.

XX PR 19-DEC-1990; 90US-0634278.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;

XX DR WPI; 1992-249842/30.

XX PT New immunoglobulin(s) having murine CDRs in human framework  
 PT regions - have lower antigenicity; useful for treating e.g. HSV,  
 PT CMV, T-cell disorders, myeloid disorders and auto-immune  
 PT conditions

XX PS Claim 40; Fig 27B; 141pp; English.

XX CC The sequence shows the humanised mature heavy chain variable  
 CC region of the mouse CMV5 antibody. Murine CDRs were used  
 CC in a human Wol framework to produce a pure humanised immunoglobulin  
 CC (Ig) which is capable of binding to the gH glycoprotein of  
 CC cytomegalovirus. The Ig is non immunogenic, due to the human  
 CC framework, and has a strong affinity for its predetermined  
 CC antigen. They can be produced in large quantities via recombinant  
 CC DNA and monoclonal antibody technology. The humanised Igs may be  
 CC used alone or in combination with chemotherapeutic agents such as  
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.  
 CC See also AAR25721-32.

```

XX SQ Sequence 119 AA;
Query Match 100.0%; Score 41; DB 13; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYSFTGY 32
|||||

RESULT 13
AAB69680
ID AAB69680 standard; Protein; 119 AA.
XX AC AAB69680;
XX DT 30-APR-2001 (first entry)
XX DE Humanised CMV5 antibody heavy chain SEQ ID NO: 65.
XX KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX KW light chain; graft versus host disease; transplant; autoimmune disease;
XX KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX OS Mus sp.
XX OS Homo sapiens.
XX PN US6180370-B1.
XX PD 30-JAN-2001.
XX PF 07-JUN-1995; 95US-0484537.
XX PR 28-DEC-1988; 88US-0290975.
XX PR 13-FEB-1989; 89US-0310252.
XX PR 28-SEP-1990; 90US-0590274.
XX PR 19-DEC-1990; 90US-0634278.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Queen CL, Selick HE;
XX DR WPI; 2001-190856/19.
XX CC Producing humanized immunoglobulin, involves producing a cell
XX PT containing DNA segments encoding humanized heavy and light chain
XX PT variable regions, and expressing the DNA segments in the cell -
XX PS Disclosure; Fig 6; 145pp; English.
XX CC The present invention describes a method of producing humanised
XX CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX CC humanised version of an immunoglobulin. This is obtained by comparing a
XX CC donor and human immunoglobulin and producing a combined antibody which
XX CC contains part of each. These are useful in the treatment of
XX CC graft-versus-host disease, transplant rejection, autoimmune diseases such
XX CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
XX CC and systemic lupus erythematosus, herpes infections, CMV virus infections
XX CC and myeloid leukaemia. The present sequence is an antibody used to
XX CC demonstrate the method of the invention.
XX SQ Sequence 119 AA;
Query Match 100.0%; Score 41; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYSFTGY 32
|||||

RESULT 14
AAB69692
ID AAB69692 standard; Protein; 119 AA.
XX AC AAB69692;
XX DT 30-APR-2001 (first entry)
XX DE Human WOI antibody heavy chain SEQ ID NO: 89.
XX KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX KW light chain; graft versus host disease; transplant; autoimmune disease;
XX KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX OS Homo sapiens.
XX PN US6180370-B1.
XX PD 30-JAN-2001.
XX PF 07-JUN-1995; 95US-0484537.
XX PR 28-DEC-1988; 88US-0290975.
XX PR 13-FEB-1989; 89US-0310252.
XX PR 28-SEP-1990; 90US-0590274.
XX PR 19-DEC-1990; 90US-0634278.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Queen CL, Selick HE;
XX DR WPI; 2001-190856/19.
XX CC Producing humanized immunoglobulin, involves producing a cell
XX PT containing DNA segments encoding humanized heavy and light chain
XX PT variable regions, and expressing the DNA segments in the cell -
XX PS Example 8; Fig 40; 145pp; English.
XX CC The present invention describes a method of producing humanised
XX CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX CC humanised version of an immunoglobulin. This is obtained by comparing a
XX CC donor and human immunoglobulin and producing a combined antibody which
XX CC contains part of each. These are useful in the treatment of
XX CC graft-versus-host disease, transplant rejection, autoimmune diseases such
XX CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
XX CC and systemic lupus erythematosus, herpes infections, CMV virus infections
XX CC and myeloid leukaemia. The present sequence is an antibody used to
XX CC demonstrate the method of the invention.
XX SQ Sequence 119 AA;
Query Match 100.0%; Score 41; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYSFTGY 32
|||||

RESULT 15
AAR59985
ID AAR59985 standard; Protein; 120 AA.
XX AC AAR59985;
XX DT 26-MAR-1995 (first entry)
XX DE U7.6 heavy chain variable region.

```

XX Marker; antibody; single chain Fv fusion protein; scFv.

XX Mus musculus.

XX WO9415642-A.

XX 21-JUL-1994.

XX 07-JAN-1994; 94WO-US000261.

XX 08-JAN-1993; 93US-0002324.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX George AJT, Huston JS, Segal DM;

XX WPI; 1994-248905/30.

XX N-PSDB; AAQ69933.

XX Delivering agents to target cells - where monospecific binding  
PT proteins are administered to a host and bind to target cells,  
PT followed by admin. of multivalent antibodies to direct the agents  
PT to the target cells

XX Disclosure; Fig 3; 80pp; English.

XX The sequence is that of the U7.6 heavy chain variable region  
CC produced by PCR from murine mRNA using the CH1-Xba primers. The  
CC protein was used to produce a fusion protein of light chain variable  
CC region-linker-heavy chain variable region.  
CC See also AAR59984-6.

XX Sequence 120 AA;

Query Match 100.0%; Score 41; DB 15; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 GYSFTGY 7

DB 26 GYSFTGY 32

RESULT 16

AAR88752

ID AAR88752 standard; Protein; 120 AA.

XX AC AAR88752;

XX 20-JUL-1996 (first entry)

XX scFv U7.6 VH.

XX Single-chain Fv; scFv; glycosylation; protein secretion;  
KW endoplasmic reticulum; antibody engineering.

XX Unspecified.

XX WO9605228-A1.

XX 22-FEB-1996.

XX 14-AUG-1995; 95WO-US10348.

XX 17-AUG-1994; 94US-0292124.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Huston JS, Jost CR, Segal DM;

XX

DR WPI; 1996-139645/14.

DR N-PSDB; AAT12612.

XX Single-chain Fv molecules with additional glycosylation sites - have  
PT increased rates of secretion, decreased antigenicity, modified  
PT ligand binding affinity and are protected from proteolytic  
PT degradation

XX Claim 6; Page 40-41; 65pp; English.

XX When the VH (AAR88752) and VL (AAR88753) regions of anti-DNP scFv U7.6  
CC were expressed in COS-7 cells transfected with a vector carrying  
CC the encoding DNA sequences (AAT12612 and AAT12613), only low levels of  
CC secretion were achieved; exit from the endoplasmic reticulum was  
CC identified as the rate-limiting step. Increasing the degree of  
CC glycosylation of the scFv, by replacing VH lys19 with Asn (see also  
CC AAR88754), increased the secretion rate. Additional glycosylation can  
CC also decrease antigenicity, modify ligand binding affinity and  
CC protect from proteolysis.

XX Sequence 120 AA;

Query Match 100.0%; Score 41; DB 17; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7

DB 26 GYSFTGY 32

RESULT 17

AAR88754

ID AAR88754 standard; Protein; 120 AA.

XX AC AAR88754;

XX 20-JUL-1996 (first entry)

XX scFv U7.6 VH (K19N).

XX Single-chain Fv; scFv; glycosylation; protein secretion;  
KW endoplasmic reticulum; antibody engineering.

XX Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 19 /label= Glycosylation\_site

FT WO9605228-A1.

XX 22-FEB-1996.

XX 14-AUG-1995; 95WO-US10348.

XX 17-AUG-1994; 94US-0292124.

XX (CREA-) CREATIVE BIOMOLECULES INC.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Huston JS, Jost CR, Segal DM;

XX WPI; 1996-139645/14.

XX Single-chain Fv molecules with additional glycosylation sites - have  
PT increased rates of secretion, decreased antigenicity, modified  
PT ligand binding affinity and are protected from proteolytic  
PT degradation

XX Claim 7; Page 42; 65pp; English.

XX A modified VH chain (AAR88754) of anti-DAP scFv U7.6 (see also

CC AAR88752) has asparagine substituting for lysine at amino acid  
 CC position 19. The asparagine site increases the degree of  
 CC glycosylation of recombinant scfv U7.6 produced by COS-7 cell  
 CC transfectants, leading to an increased rate of glycosylation from  
 CC the endoplasmic reticulum. The method allows scfv molecules  
 CC capable of binding to specific ligands to be produced in, and  
 CC secreted by, eukaryotic cells. Decreased antigenicity and  
 CC increased resistance to proteolysis may also result from  
 CC additional glycosylation sites.

XX SQ Sequence 120 AA;

Query Match 100.0%; Score 41; DB 17; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 3.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 26 GYSFTGY 32

## RESULT 18

AAR30772  
 ID AAR30772 standard; protein; 122 AA.

XX AC AAR30772;

XX DT 12-MAY-1993 (first entry)

XX DE huxCD3v9, humanised muxCD3 heavy chain variable domain.

XX KW Humanisation; rapid; monoclonal antibody; anti-CD3.

XX OS Mus musculus.

XX PN W09222653-A.

XX PD 23-DEC-1992.

XX PF 15-JUN-1992; 92WO-US05126.

XX PR 14-JUN-1991; 91US-0715272.

XX PA (GETH ) GENENTECH INC.

XX PI Carter PJ, Presta LG;

XX PS WPI; 1993-018139/02.

XX PT Humanisation of antibodies - by molecular modelling of the variable  
 domains and alteration by gene conversion mutagenesis

XX PS Disclosure; Fig 5; 126pp; English.

XX CC The sequence is that of the heavy chain variable domain of huxCD3v9,  
 CC a humanised variant of murine anti-CD3 monoclonal antibody UCHT1  
 CC (muxCD3, Shalaby 1992).

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 41; DB 14; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 26 GYSFTGY 32

## RESULT 19

AAY87655  
 ID AAY87655 standard; Protein; 124 AA.

XX

AC AAY87655;

XX DT 11-AUG-2000 (first entry)

XX DE Murine PIP3 recognizing Mab variable region heavy chain protein.

XX KW PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;  
 immunogen; antibody; heavy chain.

XX OS Mus sp.

XX PN JP2000083664-A.

XX PD 28-MAR-2000.

XX PF 07-SEP-1998; 98JP-0252921.

XX PR 07-SEP-1998; 98JP-0252921.

XX PA (FUKU/) FUKUI Y.

XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.

XX N-PSDB; AAA12202.

XX PT A monoclonal antibody recognizing  
 phosphatidylinositol-3,4,5-triphosphate

XX PS Claim 5; Page 11; 15pp; Japanese.

XX CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunosay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain described in the method of the invention.

XX SQ Sequence 124 AA;

Query Match 100.0%; Score 41; DB 21; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 4.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 26 GYSFTGY 32

## RESULT 20

AAY70791  
 ID AAY70791 standard; Protein; 130 AA.

XX AC AAY70791;

XX DT 31-JUL-2000 (first entry)

XX DE Murine anti-PAB-421 IDI-2 mAb heavy chain variable region.

XX KW Murine; p53 protein; PAB-421; monoclonal antibody; mAb; IDI-2;

XX KW anti-idiotypic antibody; DNA-binding domain;

XX KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;  
 KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;

XX KW heavy chain variable region; VH; complementarity determining region; CDR.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Region 26..35

XX FT /label= CDR

FT Region /note= "Complementarity determining region"  
 FT 50..66  
 FT /label= CDR  
 FT /note= "Complementarity determining region"  
 FT 99..113  
 FT /label= CDR  
 FT /note= "Complementarity determining region"  
 XX  
 XX WO200023082-A1.  
 XX  
 XX 27-APR-2000.  
 XX  
 XX 19-OCT-1999; 99WO-US24443.  
 XX  
 XX 19-OCT-1998; 98US-0104816.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;  
 XX WPI; 2000-339512/29.  
 XX  
 XX Treatment of systemic lupus erythematosus by down-regulating the  
 PT autoimmune response to the C-terminal DNA-binding domain of the p53  
 PT protein by an active compound comprising of antibodies to p53 or  
 PT fragments of p53 -  
 XX  
 XX Claim 78; Fig 9; 87pp; English.  
 XX  
 XX The patent discloses a method for the treatment of systemic lupus  
 CC erythematosus (SLE) by down-regulating the autoimmune response to the  
 CC C-terminal DNA-binding domain of p53 protein by an active compound.  
 CC The present sequence is a heavy chain variable region of IDI-2 an  
 CC anti-idiotypic antibody/Ab2 monoclonal antibody (mAb) specific for  
 CC pAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain  
 CC of murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on  
 CC complementarity determining regions of light and heavy chain variable  
 CC regions of these antibodies, are examples of active compounds useful in  
 CC the diagnosis, prevention and treatment of SLE in humans.  
 XX  
 XX Sequence 130 AA;  
 Query Match 100.0%; Score 41; DB 21; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 DB 26 GYSFTGY 32  
 |||||  
 RESULT 21  
 AAU70768  
 ID AAU70768 standard; Peptide; 130 AA.  
 XX  
 XX AAU70768;  
 XX  
 XX 14-FEB-2002 (first entry)  
 XX  
 XX Hepatitis B virus antigen binding partner 9C8 VH.  
 DE  
 DE Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;  
 KW antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;  
 KW B cell mediated processing; T cell proliferation; cytokine production;  
 KW immune system response.  
 XX  
 XX Synthetic.  
 OS  
 OS WO200181421-A2.  
 PN  
 XX 01-NOV-2001.  
 PD  
 XX 20-APR-2001; 2001WO-IB00844.  
 XX  
 XX PF

XX 21-APR-2000; 2000US-0556605.  
 PR (TRIP-) TRIPEP AB.  
 PA  
 XX Sallberg M;  
 PI  
 XX WPI; 2002-055347/07.  
 DR  
 XX  
 XX Novel peptide that binds to hepatitis B virus core or E antigen, useful  
 PT for treating and preventing hepatitis B virus infection -  
 PT  
 XX Claim 2; Page 11; 82pp; English.  
 PS  
 XX The invention relates to an isolated or purified peptide (I) which binds  
 CC Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).  
 CC (I) is useful for treating or preventing Hepatitis B virus (HBV)  
 CC infection, by identifying a subject in need of a molecule that inhibits  
 CC HBV infection, and providing the subject with (I). (I) is also useful  
 CC for determining the presence of HBV in a biological sample, and for  
 CC inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,  
 CC by determining whether (I) inhibits B cell mediated processing and  
 CC uptake of HBcAg and/or HBeAg by performing an assay of T cell  
 CC proliferation or cytokine production. (I) is also useful for modulating  
 CC an immune system response. (I) is useful as a template for a design of  
 CC synthetic molecules including peptides, derivatives or modified peptides,  
 CC peptidomimetics and chemicals. (I) is also useful as biotechnological  
 CC tool, diagnostic reagent and as active ingredient in pharmaceuticals.  
 CC (I) is also useful as detection reagents in conventional  
 CC immunohistochemical techniques, as diagnostic reagents to detect HBV in  
 CC biological sample, and to determine the efficacy of an HBV treatment  
 CC protocol by monitoring the levels of HBcAg and/or HBeAg during and after  
 CC treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core  
 CC antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described  
 CC in the invention.  
 XX  
 XX Sequence 130 AA;  
 Query Match 100.0%; Score 41; DB 23; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 DB 25 GYSFTGY 31  
 |||||  
 RESULT 22  
 AAW06446  
 ID AAW06446 standard; Protein; 136 AA.  
 XX  
 XX AAW06446;  
 AC  
 XX 05-FEB-1997 (first entry)  
 DT  
 XX HuMc3 VH region BR-R version.  
 DE  
 XX Humanised antibody; variable heavy region; buried residue modification;  
 KW VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMFg; lactation;  
 KW fat globule membrane; murine; mammal; epithelial cell; breast cancer;  
 KW breast membrane glycoprotein; therapy; immunotherapy.  
 XX  
 XX Synthetic.  
 OS  
 OS WO96080565-A2.  
 PN  
 XX 21-MAR-1996.  
 XX  
 XX 14-SEP-1995; 95WO-US11683.  
 PF  
 XX 07-JUN-1995; 95US-0487598.  
 PR  
 XX 16-SEP-1994; 94US-0307868.  
 XX  
 XX

(CANC-) CANCER RES FUND CONTRA COSTA.

Ceriani RI, Do Couto FJR, Peterson JA;  
WPI; 1996-179941/18.

Recombinant Mc3 antibody which binds BA46 antigen of HMFG - comprises a modified heavy or light chain variable region, useful in the diagnosis and therapy of breast cancer

Example 7; Fig 14; 91pp; English.

This sequence represents the variable heavy (VH) chain of the humanised murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the buried residue retention (BR-R) technique. The Mc3 sequences can also be modified using the buried residue modification, where important non-human framework residues are unaffected (see AAW06442 and AAW06443).

The Mc3 antibody binds to the BA46 antigen of the human milk fat globule (HMFG). The milk fat globule membrane is derived from the apical surface of the mammalian epithelial cell during lactation, and therefore is a source for breast membrane glycoproteins. The antibody can be used in an in vitro method to detect a HMFG antigen (or antigen fragment), and to diagnose the presence of the antigen in a subject. The antibody can also be used to deliver an agent to a target (within a subjects body), containing a HMFG antigen. The antibodies can also be used for diagnosis, prognosis, and therapeutic applications of breast cancer. As the humanised antibodies retain their high affinity binding to the antigen, they are useful for immunodiagnostic and immunotherapeutic applications in humans.

Sequence 136 AA;

Query Match 100.0%; Score 41; DB 17; Length 136;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 23  
AAW06442  
ID AAW06442 standard; Protein; 136 AA.

AC AAW06442;  
AC AAW06442;  
DT 04-FEB-1997 (first entry)  
XX HuMc3 VH region.

XX Humanised antibody; variable heavy region; buried residue modification;  
KW HuMc3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation;  
KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;  
KW breast membrane glycoprotein; therapy; immunotherapy.

OS Synthetic.  
XX WO9608565-A2.  
XX 21-MAR-1996.  
XX 14-SEP-1995; 95WO-US11683.  
XX 07-JUN-1995; 95US-0487598.  
XX 16-SEP-1994; 94US-0307868.  
XX (CANC-) CANCER RES FUND CONTRA COSTA.  
XX Ceriani RI, Do Couto FJR, Peterson JA;  
XX WPI; 1996-179941/18.  
XX N-PSDB; AAT42717.

XX Recombinant Mc3 antibody which binds BA46 antigen of HMFG - comprises a modified heavy or light chain variable region, useful in the diagnosis and therapy of breast cancer

Claim 13; Fig 18; 91pp; English.

This sequence represents the variable heavy (VH) chain of the humanised murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the buried residue modification technique, where important non-human framework residues are unaffected. The Mc3 antibody binds to the BA46 antigen of the human milk fat globule (HMFG). The milk fat globule membrane is derived from the apical surface of the mammalian epithelial cell during lactation, and therefore is a source for breast membrane glycoproteins. The antibody can be used in an in vitro method to detect a HMFG antigen (or antigen fragment), and to diagnose the presence of the antigen in a subject. The antibody can also be used to deliver an agent to a target (within a subjects body), containing a HMFG antigen. The antibodies can also be used for diagnosis, prognosis, and therapeutic applications of breast cancer. As the humanised antibodies retain their high affinity binding to the antigen, they are useful for immunodiagnostic and immunotherapeutic applications in humans.

Sequence 136 AA;

Query Match 100.0%; Score 41; DB 17; Length 136;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 24  
AAR38259  
ID AAR38259 standard; Protein; 139 AA.

AC AAR38259;  
AC AAR38259;  
DT 20-OCT-1993 (first entry)  
XX Chimeric 128.1 VH, mouse kappa subgroup IIB.

XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy;  
KW light; chain; variable; constant; region; anti-human; transferrin;  
KW receptor; antibody; brain; capillary; endothelial cell; conjugate;  
KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke;  
KW epilepsy; Parkinsons disease; Alzheimers disease.

OS Synthetic.  
XX Location/Qualifiers  
FH Key 1..19 /note= "Leader peptide"  
FT Region 20..50 /label= FR1  
FT Region 51..55 /label= CDR1  
FT Region 56..68 /label= FR2  
FT Region 69..85 /label= CDR2  
FT Region 86..117 /label= FR3  
FT Region 118..126 /label= CDR3  
FT Region 127..139 /label= FR4  
XX WO9310819-A.  
XX 10-JUN-1993.



```
FT Region 20..137
FT /note= "128.1 HV"
FT Region 20..49
FT /label= FR1
FT Region 50..56
FT /label= CDR1
FT Region 57..85
FT /label= CDR2
FT Region 86..117
FT /label= FR3
FT Region 118..126
FT /label= CDR3
FT Region 127..137
FT /label= FR4
FT Region 138..235
FT /note= "Human gammal CH"
XX
XX WO9310819-A.
XX
XX 10-JUN-1993.
XX
XX 24-NOV-1992; 92WO-US10206.
XX
XX 26-NOV-1991; 91US-0800458.
XX
XX (ALKE-) ALKERMES INC.
XX
XX F-riden PM;
XX
XX WPI; 1993-196742/24.
XX N-PSDB; AAQ43844.
XX
XX Antibody conjugates specific for transferrin receptor - used
XX for diagnosis and treatment of cancer, AIDS and neurological
XX disorders
XX
XX Disclosure; Fig 11H-I; 15lpp; English.
XX
XX The sequences given in AAR41682-85 are encoded by the expression vector,
XX pAH4602. This vector contains open reading frames encoding the heavy
XX chain variable region (VH) of the antibody 128.1, an ampicillin
XX resistance gene and a histidine (histidinol) selection marker.
XX Transcription of the VH gene is from the VH promoter of the murine
XX 27.44 gene. The vector also includes a heavy chain immunoglobulin
XX enhancer and the human gammal constant region (CH). The VH region of
XX 128.1 was isolated by polymerase chain reaction and cloned into plasmid
XX pAH4274. This was achieved by digesting the plasmid and the product
XX with EcoRV and NheI. The VH gene was inserted in-frame with the human
XX gammal CH region CH at the 3' end of the VH-J region by means of a NheI
XX site. 128.1 is an anti-human transferrin receptor antibody which binds
XX to the transferrin receptor on brain capillary endothelial cells. This
XX antibody may be used in a conjugate in which it is linked to a neuro-
XX pharmaceutical or diagnostic agent. The conjugate may be used to treat
XX or prevent neurological disorders eg. brain tumours, AIDS, stroke,
XX epilepsy, Parkinsons and Alzheimers disease. It may also be used for
XX diagnostic methods.
XX
XX Sequence 235 AA;
XX
XX Query Match 100.0%; Score 41; DB 14; Length 235;
XX Best Local Similarity 100.0%; Pred. NO. 7.6;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYSFTGY 7
XX |||||
XX 45 GYSFTGY 51
XX
XX RESULT 27
XX AAR41707
XX ID AAR41707 standard; Protein; 235 AA.
XX
XX AC AAR41707;
```

```
XX
DT 20-OCT-1993 (first entry)
XX
XX Murine 128.1 VH/human gamma-2 CH1 encoded by plasmid pAH4625.
XX
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;
XX heavy; light; chain; variable; constant; region; anti-human; pAH4807;
XX transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
XX endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
XX diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
XX Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX Region /note= "Leader peptide"
XX /label= FR1
XX Region 51..55
XX /label= CDR1
XX Region 56..68
XX /label= FR2
XX Region 69..85
XX /label= CDR2
XX Region 86..117
XX /label= FR3
XX Region 118..126
XX /label= CDR3
XX Region 127..137
XX /label= FR4
XX Region 138..235
XX /label= CH1
XX
XX WO9310819-A.
XX
XX 10-JUN-1993.
XX
XX 24-NOV-1992; 92WO-US10206.
XX
XX 26-NOV-1991; 91US-0800458.
XX
XX (ALKE-) ALKERMES INC.
XX
XX Friden PM;
XX
XX WPI; 1993-196742/24.
XX N-PSDB; AAQ43846.
XX
XX Antibody conjugates specific for transferrin receptor - used
XX for diagnosis and treatment of cancer, AIDS and neurological
XX disorders
XX
XX Disclosure; Fig 17G-H; 15lpp; English.
XX
XX The sequences given in AAR41707-09 are encoded by the expression vector
XX pAH4625. This vector represents the cloning of the human gamma
XX isotype, gamma-2, with the variable region of the murine monoclonal
XX antibody 128.1. This plasmid encodes a chimeric monoclonal antibody
XX in which the heavy chain (VH) is derived from a murine source and the
XX sequences encoding CH1, CH2 and CH3 are derived from a human source.
XX This vector, in combination with the chimeric light chain vector,
XX PAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones
XX were isolated. 128.1 is an anti-human transferrin receptor antibody
XX which binds to the transferrin receptor on brain capillary endothelial
XX cells. This antibody may be used in a conjugate in which it is linked
XX to a neuropharmaceutical or diagnostic agent. The conjugate may be
XX used to treat or prevent neurological disorders eg. brain tumours,
XX AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
XX also be used for diagnostic methods.
XX
XX Sequence 235 AA;
```

Query Match 100.0%; Score 41; DB 14; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.6; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 45 GYSFTGY 51  
|||||

RESULT 28  
AAR41715  
ID AAR41715 standard; Protein; 235 AA.  
XX  
AC AAR41715;  
XX  
DT 20-OCT-1993 (first entry)  
XX  
DE Murine 128.1 VH/human gamma-4 CH1 encoded by plasmid pAH4808.  
XX  
KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;  
KW heavy; light; chain; variable; constant; region; anti-human; pAH4807;  
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;  
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;  
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;  
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.  
XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "Leader peptide"  
FT Region 20..50  
FT /label= FR1  
FT Region 51..55  
FT /label= CDR1  
FT Region 56..68  
FT /label= FR2  
FT Region 69..85  
FT /label= CDR2  
FT Region 86..117  
FT /label= FR3  
FT Region 118..126  
FT /label= CDR3  
FT Region 127..137  
FT /label= FR4  
FT Region 138..235  
FT /label= CH1

XX  
XX WO9310819-A.  
XX  
XX 10-JUN-1993.  
XX  
XX 24-NOV-1992; 92WO-US10206.  
XX  
XX 26-NOV-1991; 91US-0800458.  
XX  
XX (ALKE-) ALKERMES INC.  
XX  
XX Friden PM;  
XX  
XX WPI; 1993-196742/24.  
XX  
XX N-PSDB; AAQ43848.  
XX  
XX Antibody conjugates specific for transferrin receptor - used  
XX for diagnosis and treatment of cancer, AIDS and neurological  
XX disorders  
XX  
XX Disclosure; Fig 19G-H; 151pp; English.  
XX  
XX The sequences given in AAR41715-18 are encoded by the expression vector  
XX pAH4808. This vector represents the cloning of the human gamma  
XX isotype, gamma-4, with the variable region of the murine monoclonal  
XX antibody 128.1. This plasmid encodes a chimeric monoclonal antibody

CC in which the heavy chain (VH) is derived from a murine source and the  
CC sequences encoding CH1, CH2 and CH3 are derived from a human source.  
CC This vector, in combination with the chimeric light chain vector,  
CC PAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones  
CC were isolated. 128.1 is an anti-human transferrin receptor antibody  
CC which binds to the transferrin receptor on brain capillary endothelial  
CC cells. This antibody may be used in a conjugate in which it is linked  
CC to a neuropharmaceutical or diagnostic agent. The conjugate may be  
CC used to treat or prevent neurological disorders eg. brain tumours,  
CC AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may  
CC also be used for diagnostic methods.  
XX  
SQ Sequence 235 AA;  
XX  
XX Query Match 100.0%; Score 41; DB 14; Length 235;  
XX Best Local Similarity 100.0%; Pred. No. 7.6; Indels 0; Gaps 0;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 45 GYSFTGY 51  
|||||

RESULT 29  
ABB76197  
ID ABB76197 standard; Protein; 241 AA.  
XX  
AC ABB76197;  
XX  
DT 05-AUG-2002 (first entry)  
XX  
DE Anti-mesothelin scFv SS.  
XX  
KW Mesothelin; antibody; scFv; mouse; mesothelioma; ovarian cancer;  
KW stomach cancer; squamous cell cancer; antitumour; therapy;  
KW diagnosis; immunotoxin.  
XX  
OS Mus sp.

XX  
FH Key Location/Qualifiers  
FT Region 1..31  
FT /note= "heavy chain framework region 1"  
FT Region 32..36  
FT /note= "heavy chain complementarity determining  
FT region 1"  
FT Region 37..50  
FT /note= "heavy chain framework region 2"  
FT Region 51..67  
FT /note= "heavy chain complementarity determining  
FT region 2"  
FT Region 68..99  
FT /note= "heavy chain framework region 3"  
FT Region 100..109  
FT /note= "heavy chain complementarity determining  
FT region 3"  
FT Region 110..120  
FT /note= "heavy chain framework region 4"  
FT Region 121..135  
FT /note= "linker"  
FT Region 136..158  
FT /note= "light chain framework region 1"  
FT Region 159..168  
FT /note= "light chain complementarity determining  
FT region 1"  
FT Region 169..183  
FT /note= "light chain framework region 2"  
FT Region 184..190  
FT /note= "light chain complementarity determining  
FT region 2"  
FT Region 191..222  
FT /note= "light chain framework region 3"  
FT Region 223..231  
FT /note= "light chain complementarity determining



XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
XX Claim 1; Page 2725-2726; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
XX  
XX Sequence 241 AA;  
SQ  
Query Match 100.0%; Score 41; DB 23; Length 241;  
Best Local Similarity 100.0%; Pred. NO. 7.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32  
RESULT 31  
AAR60781  
ID AAR60781 standard; Protein; 243 AA.  
XX  
AC AAR60781;  
XX  
XX 09-MAY-1995 (first entry)  
DT  
XX Fv(GP-4) immunosuppressive.  
DE  
XX MAb; monoclonal antibody; hybridoma; interleukin-2; IL-2;  
KW Fv; antibody variable region; GP-4; Fv(GP-4);  
KW immunosuppressive.  
XX  
OS Mus sp.  
XX  
XX EP621338-A.  
PN  
XX 26-OCT-1994.  
PD  
XX 21-APR-1994; 94EP-0106257.  
PF  
XX 21-APR-1993; 93JP-0094491.  
PR  
XX 07-MAR-1994; 94JP-0036065.  
PR  
XX (AJIN) AJINOMOTO KK.  
PA  
XX Hamura J, Kanayama Y, Nakazawa H, Shimamura T, Sugamura K;  
PI Takeshita T;  
XX WPI; 1994-325948/41.  
XX

DR N-PSDB; AAQ73679.  
XX Immunosuppressant polypeptide - has ability to block  
PT interleukin-2 response  
PT  
XX Claim 9; Page 27-28; 37pp; English.  
PS  
XX MAb capable of binding to the gamma chain of the IL-2 receptor, and  
CC thus of blocking the IL-2 response, is produced by mouse hybridoma  
CC line GP-4 (FERM BP-4640). DNA encoding the variable region of  
CC this MAb was expressed in E. coli, yielding Fv(GP-4) with  
CC immunosuppressive activity.  
XX  
XX Sequence 243 AA;  
SQ  
Query Match 100.0%; Score 41; DB 15; Length 243;  
Best Local Similarity 100.0%; Pred. NO. 7.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
Db 148 GYSFTGY 154  
RESULT 33  
AAY42294  
ID AAY42294 standard; Protein; 243 AA.  
XX  
AC AAY42294;  
XX  
XX 06-DEC-1999 (first entry)  
DT  
XX Anti-5T4 secreted single chain antibody Fv fragment.  
DE  
XX Cytochrome; targeting; localisation; cancer; tumour; prodrug; reduction;  
KW nucleus.  
KW  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO9945127-A2.  
PN  
XX 10-SEP-1999.  
PD  
XX 05-MAR-1999; 99WO-GB00674.  
PF  
XX 06-MAR-1998; 98GB-0004941.  
PR  
XX 19-AUG-1998; 98GB-0018103.  
PR  
XX 29-JAN-1999; 99GB-0002081.  
PR  
XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
PA  
XX Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;  
PI Mitrophanous K;  
PI  
XX WPI; 1999-551046/46.  
DR  
DR N-PSDB; AA219786.  
DR  
XX New prodrug activating agent targeted to selected cells or tissues,  
PT particularly hypoxic cells, for treating e.g. tumors -  
PT  
XX Example 9; Fig 3; 187pp; English.  
PS  
XX This sequence represents an example of a secreted single chain antibody  
CC Fv fragment (in this case, directed against the 5T4 antigen), which is  
CC involved in transcellular localisation. A secreted single chain  
CC antibody Fv fragment can be fused to cytochrome P450 reductase (P450R)  
CC derivatives such as anchorless P450R (AAY42287) or FN fragment  
CC (AAY42288). This enables the fusion protein to be delivered to other  
CC cells where it is then transported to the nucleus. Many drugs' sites of  
CC action are in the nucleus, rather than the cytoplasm, where P450R  
CC normally functions. P450R or its derivatives can be used to activate  
CC prodrugs to their active form via reduction. Administration of a prodrug

CC is useful where the active drug may be metabolised before it reaches its  
 CC site of action or where the active drug is cytotoxic, e.g., anticancer  
 CC drugs. Targeted delivery of such prodrug activators allows a reduction  
 CC in dose of the prodrug, and thus of systemic side-effects. P450R  
 CC derivative fusion proteins, or vectors that express them, are  
 CC specifically used to treat tumours, inflammation, atherosclerosis and  
 CC muscular dystrophy, but may also be used to treat many other conditions,  
 CC e.g., cerebral malaria, rheumatoid arthritis, or conditions associated  
 CC with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,  
 CC antiviral agents, analgesics, anaesthetics, anti-inflammatory agents,  
 CC antineoplastic agents and diagnostic agents.

XX SQ Sequence 243 AA;

Query Match 100.0%; Score 41; DB 20; Length 243;

Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGY 7

Db 26 GYSFTGY 32

RESULT 34

AA27407  
 ID AAY27407 standard; Protein; 243 AA.

XX AC AAY27407;

DT 23-NOV-1999 (first entry)

XX 5T4 scFv antibody signal peptide.

XX Prodrug; localization domain; tumor-selective antibody; cytochrome P450;  
 KW prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;  
 KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;  
 KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;  
 XX 5T4 scFv.

XX Unidentified.

XX WO9945126-A2.

XX 10-SEP-1999.

XX 05-MAR-1999; 99WO-GB00672.

XX 06-MAR-1998; 98GB-0004841.

XX 19-AUG-1998; 98GB-0018103.

XX 29-JAN-1999; 99GB-0002081.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;

PI Mitrophanous K;

XX WPI; 1999-540852/45.

DR N-PSDB; AA207810.

XX New prodrug activating agent targeted to selected cells or tissues,  
 PT particularly hypoxic cells, for treating e.g. tumors or inflammation -

XX Example 9; Fig 3F; 149pp; English.

XX The invention provides a new prodrug activating agent that comprises: (i)  
 CC a localization domain (Lb); other than a tumor-selective antibody) and a  
 CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding  
 CC a cytochrome P450 and under control of at least one constitutive or  
 CC inducible expression control sequence or (iii) a modified hematopoietic  
 CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and  
 CC under control of elements as in (ii). The prodrug activating agent or  
 CC vectors that express them, are specifically used to treat tumors,  
 CC inflammation, atherosclerosis and muscular dystrophy, but may also be

CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid  
 CC arthritis, or conditions associated with hypoxia, hypoglycemia or  
 CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,  
 CC anesthetics, anti-inflammatory agents, antineoplastic agents and diagnostic  
 CC agents. LD optimize activity of PAD, e.g. by delivering it to selected  
 CC locations or by delivering it to neighboring cells (bystander effect),  
 CC and allow a reduction in dose of prodrug, and thus of systemic side-  
 CC effects. Nucleic acids encoding the agent may be expressed selectively  
 CC in hypoxic cells. The present sequence represents the single chain  
 CC variable antibody fragment against the tumor antigen 5T4 (5T4 scFv).  
 CC 5T4 scFv is used in the construction of a fusion protein comprising  
 CC 5T4 scFv and a human P450 reductase derivative alP450R.

XX SQ Sequence 243 AA;

Query Match 100.0%; Score 41; DB 20; Length 243;

Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGY 7

Db 26 GYSFTGY 32

RESULT 35

AAW86002  
 ID AAW86002 standard; Protein; 243 AA.

XX AC AAW86002;

XX 15-MAR-1999 (first entry)

XX Murine anti-5T4 antigen monoclonal antibody scFv.

XX Tumour interacting protein; cancer; gene therapy; vector;  
 KW 5T4 antigen; monoclonal antibody; single chain antibody; scFv;  
 KW mouse; 5T4scFv.1.

XX Chimeric - Mus sp.

XX Chimeric - synthetic.

XX Key Location/Qualifiers

FT Misc-difference 169  
 FT /note= "encoded by GDT"

XX WO9855607-A2.

XX 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB01627.

XX 04-JUL-1997; 97GB-0014230.

XX 04-JUN-1997; 97GB-0011579.

XX 20-JUN-1997; 97GB-0013150.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Bebbington CR, Carroll MW, Ellard FM, Kingsman SM;

PI Myers KA;

XX WPI; 1999-059910/05.

DR N-PSDB; AAV80290.

XX New vector encoding a tumour interacting protein for treating cancer  
 PT - contains a desired nucleotide sequence and/or protein which  
 PT recognises tumours, and is used as a gene delivery system to treat  
 PT cancer

XX Example 1; Fig 1A; 82pp; English.

XX This amino acid sequence comprises an scFv, termed 5T4scFv.1,  
 CC comprising the heavy chain variable region (VH) from the murine 5T4  
 CC monoclonal antibody followed by a 15-amino acid flexible linker and

CC the light chain variable region (VL) of the mouse 5T4 antibody. The  
 CC trophoblast cell surface antigen defined by monoclonal antibody 5T4  
 CC is expressed at high levels on the cells of a wide variety of human  
 CC tumours. 5T4scFv.1 DNA (see AAW80290) can be used to construct  
 CC single-chain antibodies (see AAW86003) and scFv fusion constructs  
 CC (see AAW86004-05). The invention relates to a vector comprising a  
 CC nucleotide sequence coding for a tumour interacting protein (TIP)  
 CC and optionally a nucleotide sequence of interest (NOI) which  
 CC encodes a protein of interest (POI), the vector being capable of  
 CC delivering the NOI and/or POI to the tumour recognised by the TIP.  
 CC Delivery can be in vivo or ex vivo. The vector is used to treat  
 CC cancer, and may also be used as a gene delivery system for introducing  
 CC at least 1 gene encoding a TIP (preferably a tumour binding protein)  
 CC into a hematopoietic cell lineage.  
 CC  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 41; DB 20; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GYSFTGY 7  
 Db 26 GYSFTGY 32  
 RESULT 36  
 AAB83835  
 ID AAB83835 standard; Protein; 243 AA.  
 AC AAB83835;  
 DT 23-JUL-2001 (first entry)  
 XX  
 XX Amino acid sequence of a 5T4 ScFv designated 5T4ScFv.1.  
 DE  
 XX  
 XX Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;  
 KW hypersensitivity; autoimmune disease; central nervous system disorder;  
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;  
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;  
 KW Helicobacter-related disease; immune disorder.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 169  
 FT /note= "Ala encoded by GDT"  
 XX  
 PN WO200136486-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 XX 13-NOV-2000; 2000WO-GB04317.  
 XX  
 XX 18-NOV-1999; 99WO-GB03859.  
 PR 15-FEB-2000; 2000GB-0003527.  
 PR 02-MAR-2000; 2000GB-0005071.  
 XX  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 PA  
 XX Kingeman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;  
 PI Myers KA;  
 XX  
 XX WPI; 2001-343805/36.  
 DR N-PSDB; AAF89729.  
 XX  
 XX Use of single chain antibody capable of recognizing a disease  
 PT associated molecule for manufacturing a medicament for preventing  
 PT and/or treating a disease condition associated with disease associated  
 PT molecule -  
 XX  
 XX Claim 3; Fig 1; 118pp; English.

XX The specification describes the use of a single chain antibody (ScFv),  
 CC which is capable of recognizing a disease associated molecule in the  
 CC manufacture of a medicament for the prevention and treatment of a  
 CC disease condition. The ScFv antibody is useful in the manufacture of  
 CC a medicament, for affecting a disease in vivo, for preparing a  
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant  
 CC treatment of a disease. The ScFv antibody is also useful for  
 CC treating inflammatory diseases including arthritis, hypersensitivity,  
 CC autoimmune diseases, cancers, central nervous system disorders  
 CC including Parkinson's disease, periodontal diseases, cardiopulmonary  
 CC diseases, cardiovascular diseases, gastrointestinal disorders,  
 CC infections, diabetes, Helicobacter-related diseases, and other immune  
 CC disorders. The present sequence represents a 5T4 ScFv of the invention.  
 CC The antibody comprises the VH and VL regions from murine 5T4 monoclonal  
 CC antibody, joined by a linker sequence.  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 41; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GYSFTGY 7  
 Db 26 GYSFTGY 32  
 RESULT 37  
 ABP45889  
 ID ABP45889 standard; Protein; 245 AA.  
 XX  
 AC ABP45889;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 XX Human BlyS binding scFv SEQ ID 1900.  
 DE  
 XX  
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 XX 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI; 2002-114799/15.  
 XX  
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 XX Claim 1; Page 2668-2669; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antitumour and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 245 AA;

Query Match 100.0%; Score 41; DB 23; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 26 GYSFTGY 32

RESULT 38  
 AAY05363  
 ID AAY05363 standard; Protein; 297 AA.

AC AAY05363;  
 DT 30-JUN-1999 (first entry)  
 XX  
 DE HBV specific single stranded antibody.

KW Single stranded antibody; hepatitis B virus; HBV core protein;  
 KW HBV infection; viral proliferation inhibitor; viral DNA synthesis;  
 KW gene therapy.

OS Mus sp.  
 XX  
 XX WO9911792-A1.  
 XX  
 XX 11-MAR-1999.  
 XX  
 XX 02-SEP-1998; 98WO-JP03921.  
 XX  
 XX 02-SEP-1997; 97JP-0237054.

XX (HAYA/) HAYASHI N.  
 XX (SUMU) SUMITOMO PHARM CO LTD.

XX Hayashi N, Tohdoh N, Yamamoto H, Yamamoto M;

XX WPI; 1999-243623/20.  
 DR N-PSDB; AAX33931.

XX Single-stranded antibody against hepatitis B virus core protein,  
 PT applicable as (gene) therapeutic agents for treatment of hepatitis B  
 PT viral infections

XX Claim 5; Page 55-57; 72pp; English.

XX This sequence is the single-stranded antibody of the invention, that  
 CC has the capability of binding to a hepatitis B virus (HBV) core protein.  
 CC Therapeutic agents can be formulated with the antibody for treatment of  
 CC HBV infections by stopping proliferation of the virus through inhibition  
 CC of viral DNA synthesis, and the gene encoding the antibody can be applied  
 CC as an agent to gene therapy.

XX Sequence 297 AA;  
 SQ

Query Match 100.0%; Score 41; DB 20; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 9.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 65 GYSFTGY 71

RESULT 39  
 AAR60206  
 ID AAR60206 standard; Protein; 302 AA.

XX  
 AC AAR60206;  
 XX  
 XX 14-MAR-1995 (first entry)

XX Bispecific CD3-L6FvIg antibody derivative.

XX fusion protein; recombinant bispecific single chain antibody;  
 KW helical peptide linker; anti-L6 antibody; tumour cell antigen;  
 KW anti-CD3 antibody; variable region.

XX Synthetic.

XX Key Location/Qualifiers  
 FH 1..23  
 FT Peptide /label= L6\_VL\_leader  
 FT Region 24..271  
 FT /label= CD3\_VL-VH\_fusion  
 FT Region 134..148  
 FT /label= (Gly4Ser)3\_linker  
 FT Region 272..274  
 FT /label= hinge  
 FT Region 275..302  
 FT /label= Fv\_helical\_linker

XX EP610046-A.

XX 10-AUG-1994.

XX 31-JAN-1994; 94EP-0300692.

XX 01-FEB-1993; 93US-0013420.

PR 13-SEP-1993; 93US-0121054.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Bajorath J, Fell PH, Gilliland LK, Hayden MS, Ledbetter JA;  
 PI Linsley PS;

XX WPI; 1994-250885/31.  
 DR N-PSDB; AAQ81076.

XX Expression vector encoding bispecific fusion protein - having  
 PT binding domains for separate targets joined by helical peptide,  
 PT useful e.g. for diagnosis and treatment

XX Example 1; Fig 11 and Page 29-31; 50pp; English.

XX The VL and VH sequences of the anti-CD3 hybridoma G19-4 were  
 CC amplified by PCR methods. A gene fusion was constructed from the  
 CC two amplified domains and a (Gly4Ser)3 linker. The amino  
 CC terminus of the VL-VH fusion cassette was fused at the SalI site to  
 CC the L6 light chain variable region leader peptide and the  
 CC carboxy-terminus was fused directly to the hinge region of the Fc  
 CC domain at the BclI site and/or to a short "helical" peptide linker  
 CC to construct the bispecific CD3-L6FvIg antibody derivative. The  
 CC variable regions for L6 were fused in frame to the opposite end of  
 CC the helical linker (not included in AAR60206).

XX Sequence 302 AA;  
 SQ

Query Match 100.0%; Score 41; DB 15; Length 302;  
Best Local Similarity 100.0%; Pred. No. 9.7; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGY 7  
|||  
Db 176 GYSFTGY 182

RESULT 40  
AAW86004  
ID AAW86004 standard; Protein; 488 AA.

XX AAW86004;  
AC AAW86004;  
XX 15-MAR-1999 (first entry)  
XX Human B7-1.5T4.1 protein fusion, specific for human 5T4.  
DE  
XX Tumour interacting protein; cancer; gene therapy; vector;  
KW 5T4 antigen; monoclonal antibody; single chain antibody;  
KW mouse; human; B7-1; co-stimulatory molecule.  
XX

OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
OS Chimeric - synthetic.

XX WO9855607-A2.

PN 10-DEC-1998.

XX 04-JUN-1998; 98WO-GB01627.

XX 04-JUL-1997; 97GB-0014230.

PR 04-JUN-1997; 97GB-0011579.

PR 20-JUN-1997; 97GB-0013150.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Babbington CR, Carroll MW, Ellard FM, Kingsman SM;  
PI Myers KA;  
XX WPI: 1999-059910/05.  
DR N-PSDB; AAW80292.

XX New vector encoding a tumour interacting protein for treating cancer  
PT - contains a desired nucleotide sequence and/or protein which  
PT recognises tumours, and is used as a gene delivery system to treat  
PT cancer

XX Example 5; Fig 2; 82pp; English.

PS This is the amino acid sequence of B7-1.5T4.1, a fusion protein  
XX comprising the extracellular domain (amino acids 1-215) of human  
CC co-stimulatory molecule B7-1 joined via a flexible peptide linker  
CC to an scFv (see AAW86002) derived from murine 5T4 monoclonal  
CC antibody. B7-1.5T4.1 cDNA (see AAW80292) can be inserted into vector  
CC pCI to allow expression of the fusion protein in mammalian cells.  
CC The trophoblast cell surface antigen defined by 5T4 is expressed at  
CC high levels on the cells of a wide variety of human tumours. The  
CC invention relates to a vector comprising a nucleotide sequence  
CC coding for a tumour interacting protein (TIP) and optionally a  
CC nucleotide sequence of interest (NOI) which encodes a protein of  
CC interest (POI), the vector being capable of delivering the NOI  
CC and/or POI to the tumour recognised by the TIP. Delivery can be in  
CC vivo or ex vivo. The vector is used to treat cancer, and may also  
CC used as a gene delivery system for introducing at least 1 gene  
CC encoding a TIP (preferably a tumour binding protein) into a  
CC haematopoietic cell lineage. B7-1 is expected to bind specifically  
CC to CD28 and CTLA-4 present on human T-cells.

XX Sequence 488 AA;  
XX .SQ

Query Match 100.0%; Score 41; DB 20; Length 488;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGY 7  
|||  
Db 272 GYSFTGY 278

Search completed: July 18, 2003, 15:06:39  
Job time : 28.66 secs

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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:46 ; Search time 8.12 Seconds  
(without alignments)  
25.365 Million cell updates/sec

Title: US-10-007-790-5

Perfect score: 41  
Sequence: 1 GYSFTGY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2.6/prodata/1/iaa/5A COMB.pep:\*  
2: /cgn2.6/prodata/1/iaa/5B COMB.pep:\*  
3: /cgn2.6/prodata/1/iaa/6A COMB.pep:\*  
4: /cgn2.6/prodata/1/iaa/6B COMB.pep:\*  
5: /cgn2.6/prodata/1/iaa/6CTUS COMB.pep:\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	7	US-09-257-069-5	Sequence 5, Appli
2	41	100.0	20	US-09-556-605-29	Sequence 29, Appli
3	41	100.0	111	US-08-881-037-20	Sequence 20, Appli
4	41	100.0	114	US-08-888-366-8	Sequence 8, Appli
5	41	100.0	117	US-08-525-539A-76	Sequence 76, Appli
6	41	100.0	117	US-08-525-539A-78	Sequence 78, Appli
7	41	100.0	119	US-07-634-278-65	Sequence 65, Appli
8	41	100.0	119	US-07-634-278-89	Sequence 89, Appli
9	41	100.0	119	US-08-477-728-65	Sequence 65, Appli
10	41	100.0	119	US-08-477-728-89	Sequence 89, Appli
11	41	100.0	119	US-08-474-040-65	Sequence 65, Appli
12	41	100.0	119	US-08-474-040-89	Sequence 89, Appli
13	41	100.0	119	US-08-487-200-65	Sequence 65, Appli
14	41	100.0	119	US-08-487-200-89	Sequence 89, Appli
15	41	100.0	119	US-08-484-537-65	Sequence 65, Appli
16	41	100.0	119	US-08-484-537-89	Sequence 89, Appli
17	41	100.0	120	US-08-002-324-2	Sequence 2, Appli
18	41	100.0	120	PCT-US94-00261-2	Sequence 2, Appli
19	41	100.0	122	US-07-934-373C-19	Sequence 19, Appli
20	41	100.0	122	US-07-934-373C-20	Sequence 20, Appli
21	41	100.0	122	US-07-934-373C-45	Sequence 45, Appli
22	41	100.0	122	US-08-437-642B-19	Sequence 19, Appli
23	41	100.0	122	US-08-437-642B-20	Sequence 20, Appli
24	41	100.0	122	US-08-437-642B-45	Sequence 45, Appli
25	41	100.0	122	US-08-146-206C-19	Sequence 19, Appli
26	41	100.0	122	US-08-146-206C-20	Sequence 20, Appli
27	41	100.0	122	US-08-146-206C-26	Sequence 26, Appli

28 41 100.0 122 5 PCT-US93-07832-20 Sequence 20, Appli  
29 41 100.0 124 4 US-09-257-069-2 Sequence 2, Appli  
30 41 100.0 129 5 PCT-US93-07832-19 Sequence 19, Appli  
31 41 100.0 130 4 US-09-556-605-3 Sequence 3, Appli  
32 41 100.0 136 4 US-08-525-539A-47 Sequence 47, Appli  
33 41 100.0 136 4 US-08-525-539A-63 Sequence 63, Appli  
34 41 100.0 137 3 US-08-444-644-17 Sequence 17, Appli  
35 41 100.0 137 4 US-08-232-246A-17 Sequence 17, Appli  
36 41 100.0 233 3 US-08-444-644-33 Sequence 33, Appli  
37 41 100.0 233 4 US-08-232-246A-33 Sequence 33, Appli  
38 41 100.0 235 3 US-08-444-644-19 Sequence 19, Appli  
39 41 100.0 235 3 US-08-444-644-28 Sequence 28, Appli  
40 41 100.0 235 3 US-08-444-644-42 Sequence 42, Appli  
41 41 100.0 235 4 US-08-232-246A-19 Sequence 19, Appli  
42 41 100.0 235 4 US-08-232-246A-28 Sequence 28, Appli  
43 41 100.0 235 4 US-08-232-246A-42 Sequence 42, Appli  
44 41 100.0 243 1 US-08-230-843-4 Sequence 4, Appli  
45 41 100.0 243 2 US-08-636-936-4 Sequence 4, Appli

#### ALIGNMENTS

RESULT 1  
US-09-257-069-5  
; Sequence 5, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-257-069-5

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGY 7  
|||  
Db 1 GYSFTGY 7

RESULT 2  
US-09-556-605-29  
; Sequence 29, Application US/09556605  
; Patent No. 6417324  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; APPLICANT: Lazdina, Una  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE REFERENCE: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP.020A  
; CURRENT APPLICATION NUMBER: US/09/556,605  
; CURRENT FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Oligonucleotide

US-09-556-605-29

Query Match 100.0%; Score 41; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 5 GYSFTGY 11

RESULT 3

US-08-881-037-20  
; Sequence 20, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Klick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-881-037-20

Query Match 100.0%; Score 41; DB 3; Length 111;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 18 GYSFTGY 24

RESULT 4

US-08-888-366-8  
; Sequence 8, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.

; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,366  
FILING DATE: 03-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,407  
FILING DATE: 27-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,542  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/493,299  
FILING DATE: 14-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/324,392  
FILING DATE: 14-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.39USC1  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-8

Query Match 100.0%; Score 41; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 20 GYSFTGY 26

RESULT 5

US-08-525-539A-76  
; Sequence 76, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/525,539A
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DYLAN, TYLER
/ REGISTRATION NUMBER: 37,612
/ REFERENCE/DOCKET NUMBER: 27633-20001.21
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 76:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 117 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-525-539A-76
/
/ Query Match 100.0%; Score 41; DB 4; Length 117;
/ Best Local Similarity 100.0%; Pred. No. 0.92;
/ Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 GYSFTGY 7
/ Db 26 GYSFTGY 32
/
/ RESULT 6
/ US-08-525-539A-78
/ Sequence 78, Application US/08525539A
/ Patent No. 6309636
/ GENERAL INFORMATION:
/ APPLICANT: DO COUTO, FERNANDO J.R.
/ APPLICANT: CERIANI, ROBERTO L.
/ APPLICANT: PETERSON, JERRY A.
/ TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
/ TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
/ TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
/ NUMBER OF SEQUENCES: 81
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 755 Page Mill Road
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/525,539A
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DYLAN, TYLER
/ REGISTRATION NUMBER: 37,612
/ REFERENCE/DOCKET NUMBER: 27633-20001.21
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 78:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 117 amino acids
/
/ QY 1 GYSFTGY 7
/ Db 26 GYSFTGY 32
/
/ RESULT 7
/ US-07-634-278-65
/ Sequence 65, Application US/07634278
/ Patent No. 5530101
/ GENERAL INFORMATION:
/ APPLICANT: QUEEN, Cary L.
/ APPLICANT: CO, Man Sung
/ APPLICANT: SCHNEIDER, William P.
/ APPLICANT: LANDOLFI, Nicholas F.
/ APPLICANT: COELINGH, Kathleen L.
/ APPLICANT: SELICK, Harold E.
/ TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
/ NUMBER OF SEQUENCES: 113
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Khourie and Crew
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/634,278
/ FILING DATE: 19-DEC-1990
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/590,274
/ FILING DATE: 28-SEP-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/310,252
/ FILING DATE: 13-FEB-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/290,975
/ FILING DATE: 28-DEC-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 11823-002600
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 65:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-07-634-278-65
/
/ Query Match 100.0%; Score 41; DB 1; Length 119;
/ Best Local Similarity 100.0%; Pred. No. 0.94;
/ Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 GYSFTGY 7
```

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Db      26 GYSFTGY 32
|||||
RESULT 8
US-07-634-278-89
; Sequence 89, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: CORLINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 179 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-728-89
Query Match. 100.0%; Score 41; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYSFTGY 32
|||||
RESULT 10
US-08-477-728-89
; Sequence 89, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-634-278-89
Query Match. 100.0%; Score 41; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYSFTGY 32
|||||
RESULT 9
US-08-477-728-65
; Sequence 65, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
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ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-728-89

Query Match 100.0%; Score 41; DB 1; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 11  
US-08-474-040-65  
Sequence 65, Application US/08474040  
Patent No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO. Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-474-040-65

Query Match 100.0%; Score 41; DB 1; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 12  
US-08-474-040-89  
Sequence 89, Application US/08474040  
Patent No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO. Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990

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; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-487-200-65

Query Match 100.0%; Score 41; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYSFTGY 32
|||||

RESULT 14
US-08-487-200-89
; Sequence 89, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas P.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 89:

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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-487-200-89

Query Match 100.0%; Score 41; DB 1; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 15

US-08-484-537-65

; Sequence 65, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US/07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 65:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-537-65

Query Match 100.0%; Score 41; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 16

US-08-484-537-89  
; Sequence 89, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US/07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 89:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-537-89

Query Match 100.0%; Score 41; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 17  
US-08-002-324-2  
; Sequence 2, Application US/08002324  
; Patent No. 5861156  
; GENERAL INFORMATION:  
; APPLICANT: George, Andrew J.T.  
; APPLICANT: Segal, David M.  
; APPLICANT: Huston, James S.  
; TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO TARGET  
; TITLE OF INVENTION: CELLS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/002,324  
; FILING DATE: 19930108  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: CBM92-02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 981-6240  
; TELEFAX: (617) 981-9540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-002-324-2

Query Match 100.0%; Score 41; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.95; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

Qy 1 GYSFTGY 7  
Db 26 GYSFTGY 32

RESULT 18  
PCT-US94-00261-2  
; Sequence 2, Application PC/TUS9400261  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT: 1  
; TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/00261  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: CBM92-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 981-6240  
TELEFAX: (617) 981-9540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-00261-2

Query Match 100.0%; Score 41; DB 5; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.95; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

Qy 1 GYSFTGY 7  
Db 26 GYSFTGY 32

RESULT 19  
US-07-934-373C-19  
; Sequence 19, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-19

Query Match 100.0%; Score 41; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

## RESULT 20

US-07-934-373C-20  
; Sequence 20, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-20

Query Match 100.0%; Score 41; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

## RESULT 21

US-07-934-373C-45  
; Sequence 45, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-45

Query Match 100.0%; Score 41; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

## RESULT 22

US-08-437-642B-19  
; Sequence 19, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-Aug-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206

```
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; APPLICATION NUMBER: 40,378
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-19

Query Match 100.0%; Score 41; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYSFTGY 32

RESULT 23
US-08-437-642B-20
; Sequence 20, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-19

Query Match 100.0%; Score 41; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYSFTGY 32

RESULT 24
US-08-437-642B-45
; Sequence 45, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-45

Query Match 100.0%; Score 41; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
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```
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-20

Query Match 100.0%; Score 41; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYSFTGY 32

RESULT 24
US-08-437-642B-45
; Sequence 45, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-45

Query Match 100.0%; Score 41; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
```

```
Db          |||||
            26 GYSFTGY 32

RESULT 25
US-08-146-206C-19
; Sequence 19, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-19
;
Query Match          100.0%; Score 41; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GYSFTGY 7
            |||||
Db          26 GYSFTGY 32

RESULT 27
US-08-146-206C-26
; Sequence 26, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-19
;
Query Match          100.0%; Score 41; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GYSFTGY 7
            |||||
Db          26 GYSFTGY 32

RESULT 26
US-08-146-206C-20
; Sequence 20, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
```

US-08-146-206C-26

Query Match 100.0%; Score 41; DB 4; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 28

PCT-US93-07832-20  
; Sequence 20, Application PC/TUS9307832  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07832  
; FILING DATE: 19930820  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 709P2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US93-07832-20

Query Match 100.0%; Score 41; DB 5; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 29

US-09-257-069-2  
; Sequence 2, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.

; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-2

Query Match 100.0%; Score 41; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 0.98;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

RESULT 30

PCT-US93-07832-19  
; Sequence 19, Application PC/TUS9307832  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07832  
; FILING DATE: 19930820  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 709P2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 129 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US93-07832-19

Query Match 100.0%; Score 41; DB 5; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 26 GYSFTGY 32

## RESULT 31

US-09-556-605-3  
; Sequence 3, Application US/09556605  
; Patent No. 6417324  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; APPLICANT: Lardina, Una  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP.020A  
; CURRENT APPLICATION NUMBER: US/09/556,605  
; CURRENT FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Oligonucleotide  
US-09-556-605-3

Query Match 100.0%; Score 41; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 25 GYSFTGY 31

## RESULT 32

US-08-525-539A-47  
; Sequence 47, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; FILE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792

; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-525-539A-47

Query Match 100.0%; Score 41; DB 4; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 45 GYSFTGY 51

## RESULT 33

US-08-525-539A-63  
; Sequence 63, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; FILE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-525-539A-63

Query Match 100.0%; Score 41; DB 4; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||||  
Db 45 GYSFTGY 51

## RESULT 34

US-08-444-644-17

Sequence 17, Application US/08444644  
Patent No. 6015555  
GENERAL INFORMATION:  
APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,644  
FILING DATE: 26-NOV-1991  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/232,246  
FILING DATE: 07-JUL-1994  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..137  
OTHER INFORMATION: /note= "Chimeric 128.1 Heavy Chain  
V-Region"  
US-08-444-644-17

Query Match 100.0%; Score 41; DB 3; Length 137;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 35  
US-08-232-246A-17  
Sequence 17, Application US/08232246A  
Patent No. 6329508  
GENERAL INFORMATION:  
APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,246A  
FILING DATE: 04-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..137  
OTHER INFORMATION: /note= "Chimeric 128.1 Heavy Chain  
V-Region"  
US-08-232-246A-17

Query Match 100.0%; Score 41; DB 4; Length 137;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 36  
US-08-444-644-33  
Sequence 33, Application US/08444644  
Patent No. 6015555  
GENERAL INFORMATION:  
APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA

;; COUNTRY: USA  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/444,644  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/232,246  
;; FILING DATE: 07-JUL-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/800,458  
;; FILING DATE: 26-NOV-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US90/05077  
;; FILING DATE: 07-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/404,089  
;; FILING DATE: 07-SEP-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wagner, Richard W.  
;; REGISTRATION NUMBER: 34,480  
;; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540  
;; INFORMATION FOR SEQ ID NO: 33:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 233 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: N-terminal  
;; US-08-444-644-33

Query Match 100.0%; Score 41; DB 3; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 37  
US-08-232-246A-33  
; Sequence 33, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,246A  
; FILING DATE: 04-MAY-1994

;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/800,458  
;; FILING DATE: 26-NOV-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US90/05077  
;; FILING DATE: 07-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/404,089  
;; FILING DATE: 07-SEP-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wagner, Richard W.  
;; REGISTRATION NUMBER: 34,480  
;; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540  
;; INFORMATION FOR SEQ ID NO: 33:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 233 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: N-terminal  
;; US-08-232-246A-33

Query Match 100.0%; Score 41; DB 4; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 38  
US-08-444-644-19  
; Sequence 19, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/232,246  
;; FILING DATE: 07-JUL-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/800,458  
;; FILING DATE: 26-NOV-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US90/05077  
;; FILING DATE: 07-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/404,089  
;; FILING DATE: 07-SEP-1989

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; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-444-644-19

Query Match 100.0%; Score 41; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7
Db 45 GYSFTGY 51

RESULT 39
US-08-444-644-28
; Sequence 28, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-444-644-19
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-444-644-28

Query Match 100.0%; Score 41; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7
Db 45 GYSFTGY 51

RESULT 40
US-08-444-644-42
; Sequence 42, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-444-644-42

Query Match 100.0%; Score 41; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.9;
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Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GYSFTGY	7						
Db	45	GYSFTGY	51						

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Job time : 9.12 secs



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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:09:56 ; Search time 18.06 Seconds

(without alignments)  
46.031 Million cell updates/sec

Title: US-10-007-790-5

Perfect score: 41

Sequence: ~ 1 GYSFTGY 7

Scoring table: BLOSUM62

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

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Database : Published Applications AA.\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	20	10	US-09-839-447A-29
2	41	100.0	20	15	US-10-153-271-29
3	41	100.0	117	11	US-09-956-206A-76
4	41	100.0	117	11	US-09-956-206A-78
5	41	100.0	130	10	US-09-839-447A-3
6	41	100.0	130	15	US-10-153-271-3
7	41	100.0	136	11	US-09-956-206A-47
8	41	100.0	136	11	US-09-956-206A-63
9	41	100.0	241	12	US-09-880-748-1948
10	41	100.0	245	12	US-09-880-748-1900
11	41	100.0	259	15	US-10-207-655-13
12	41	100.0	274	10	US-09-813-659-30
13	41	100.0	302	10	US-09-813-659-18
14	41	100.0	302	10	US-09-813-659-32
15	41	100.0	504	15	US-10-207-655-348
16	41	100.0	601	11	US-09-480-236-1

17	38	100.0	672	12	US-09-900-766-1	Sequence 1, Appli
18	38	92.7	98	15	US-10-025-687-17	Sequence 17, Appl
19	38	92.7	98	15	US-10-194-975-1	Sequence 1, Appli
20	38	92.7	98	15	US-10-125-687-17	Sequence 17, Appl
21	38	92.7	241	12	US-09-880-748-2008	Sequence 2008, Ap
22	38	92.7	241	12	US-09-880-748-2031	Sequence 2031, Ap
23	38	92.7	241	12	US-09-880-748-2032	Sequence 2032, Ap
24	38	92.7	242	12	US-09-880-748-2021	Sequence 2021, Ap
25	38	92.7	242	12	US-09-880-748-2046	Sequence 2046, Ap
26	38	92.7	242	12	US-09-880-748-2106	Sequence 2106, Ap
27	38	92.7	243	12	US-09-880-748-2009	Sequence 2009, Ap
28	38	92.7	243	12	US-09-880-748-2012	Sequence 2012, Ap
29	38	92.7	243	12	US-09-880-748-2014	Sequence 2014, Ap
30	38	92.7	243	12	US-09-880-748-2063	Sequence 2063, Ap
31	38	92.7	243	12	US-09-880-748-2107	Sequence 2107, Ap
32	38	92.7	243	12	US-09-880-748-2109	Sequence 2109, Ap
33	38	92.7	244	12	US-09-880-748-1908	Sequence 1908, Ap
34	38	92.7	244	12	US-09-880-748-2011	Sequence 2011, Ap
35	38	92.7	244	12	US-09-880-748-2026	Sequence 2026, Ap
36	38	92.7	244	12	US-09-880-748-2037	Sequence 2037, Ap
37	38	92.7	245	12	US-09-880-748-1946	Sequence 1946, Ap
38	38	92.7	245	12	US-09-880-748-2004	Sequence 2004, Ap
39	38	92.7	245	12	US-09-880-748-2042	Sequence 2042, Ap
40	38	92.7	248	12	US-09-880-748-2116	Sequence 2116, Ap
41	38	92.7	248	12	US-09-880-748-1386	Sequence 1386, Ap
42	38	92.7	248	12	US-09-880-748-1388	Sequence 1388, Ap
43	38	92.7	249	8	US-08-779-457-48	Sequence 48, Appl
44	38	92.7	249	12	US-09-880-748-1635	Sequence 1635, Ap
45	38	92.7	250	12	US-09-880-748-1722	Sequence 1722, Ap

#### ALIGNMENTS

RESULT 1  
US-09-839-447A-29  
; Sequence 29, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP.020CPI  
; CURRENT APPLICATION NUMBER: US/09/839,447A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-09-839-447A-29

Query Match 100.0%; Score 41; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred.No.0.28; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

QY 1 GYSFTGY 7  
|||  
Db 5 GYSFTGY 11

RESULT 2  
US-10-153-271-29  
; Sequence 29, Application US/10153271  
; Publication No. US20030082186A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE

;; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
;; FILE REFERENCE: TRIPEP.020DVI  
;; CURRENT APPLICATION NUMBER: US/10/153,271  
;; CURRENT FILING DATE: 2002-05-21  
;; PRIOR APPLICATION NUMBER: 09/556,605  
;; PRIOR FILING DATE: 2000-04-21  
;; NUMBER OF SEQ ID NOS: 78  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 29  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Artificial Peptide  
US-10-153-271-29

Query Match 100.0%; Score 41; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 5 GYSFTGY 11

RESULT 3

US-09-956-206A-76  
; Sequence 76, Application US/09956206A  
; Patent No. US20020164339A1  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; CERIANI, ROBERTO L.  
; PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,206A  
FILING DATE: 19-Apr-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/525,539  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/US95/11683  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: 08/487,598  
FILING DATE: 7-JUNE-1995  
APPLICATION NUMBER: 08/307,868  
FILING DATE: 16-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WITT, ERIC  
REGISTRATION NUMBER: 44,408  
REFERENCE/DOCKET NUMBER: 276332000101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids

;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-956-206A-76  
Query Match 100.0%; Score 41; DB 11; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

RESULT 4

US-09-956-206A-78  
; Sequence 78, Application US/09956206A  
; Patent No. US20020164339A1  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; CERIANI, ROBERTO L.  
; PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; METHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,206A  
FILING DATE: 19-Apr-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/525,539  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/US95/11683  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: 08/487,598  
FILING DATE: 7-JUNE-1995  
APPLICATION NUMBER: 08/307,868  
FILING DATE: 16-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WITT, ERIC  
REGISTRATION NUMBER: 44,408  
REFERENCE/DOCKET NUMBER: 276332000101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
US-09-956-206A-78

Query Match 100.0%; Score 41; DB 11; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

## RESULT 5

US-09-839-447A-3  
; Sequence 3, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE REFERENCE: TRIPEP.020CP1  
; CURRENT APPLICATION NUMBER: US/09/839,447A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-09-839-447A-3

Query Match 100.0%; Score 41; DB 10; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 25 GYSFTGY 31

## RESULT 6

US-10-153-271-3  
; Sequence 3, Application US/10153271  
; Publication No. US20030082186A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE REFERENCE: TRIPEP.020DV1  
; CURRENT APPLICATION NUMBER: US/10/153,271  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: 09/556,605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-10-153-271-3

Query Match 100.0%; Score 41; DB 15; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 25 GYSFTGY 31

## RESULT 7

US-09-956-206A-47  
; Sequence 47, Application US/09956206A  
; Patent No. US20020164339A1

## GENERAL INFORMATION:

APPLICANT: DO COUTO, FERNANDO J.R.  
CERIANI, ROBERTO L.  
PETERSON, JERRY A.  
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
METHODS OF HUMANIZING ANTIBODY PEPTIDES  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,206A  
FILING DATE: 19-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/525,539  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/US95/11683  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: 08/487,598  
FILING DATE: 7-JUNE-1995  
APPLICATION NUMBER: 08/307,868  
FILING DATE: 16-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WITT, ERIC  
REGISTRATION NUMBER: 44,408  
REFERENCE/DOCKET NUMBER: 276332000101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-09-956-206A-47  
Query Match 100.0%; Score 41; DB 11; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
Db 45 GYSFTGY 51  
RESULT 8  
US-09-956-206A-63  
; Sequence 63, Application US/09956206A  
; Patent No. US20020164339A1  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; CERIANI, ROBERTO L.  
; PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; METHODS OF HUMANIZING ANTIBODY PEPTIDES  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,206A  
FILING DATE: 19-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/525,539  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/US95/11683  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: 08/487,598  
FILING DATE: 7-JUNE-1995  
APPLICATION NUMBER: 08/307,868  
FILING DATE: 16-SEPT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WITT, ERIC  
REGISTRATION NUMBER: 44,408  
REFERENCE/DOCKET NUMBER: 276332000101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 63:  
US-09-956-206A-63

Query Match 100.0%; Score 41; DB 11; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
Db 45 GYSFTGY 51

RESULT 9  
US-09-880-748-1948  
; Sequence 1948, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1948  
; LENGTH: 241

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1948  
Query Match 100.0%; Score 41; DB 12; Length 241;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

RESULT 10  
US-09-880-748-1900  
; Sequence 1900, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1900  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1900

Query Match 100.0%; Score 41; DB 12; Length 245;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
Db 26 GYSFTGY 32

RESULT 11  
US-10-207-655-13  
; Sequence 13, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 13  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1), (259)  
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD37 SCFV  
US-10-207-655-13

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Query Match      100.0%; Score 41; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      169 GYSFTGY 175
|||||

RESULT 12
US-09-813-659-30
; Sequence 30, Application US/09813659
; Patent No. US20020012989A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-30

Query Match      100.0%; Score 41; DB 10; Length 274;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      176 GYSFTGY 182
|||||

RESULT 13
US-09-813-659-18
; Sequence 18, Application US/09813659
; Patent No. US20020012989A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
```

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; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-18

Query Match      100.0%; Score 41; DB 10; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      176 GYSFTGY 182
|||||

RESULT 14
US-09-813-659-32
; Sequence 32, Application US/09813659
; Patent No. US20020012989A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-32

Query Match      100.0%; Score 41; DB 10; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      176 GYSFTGY 182
|||||

RESULT 15
US-10-207-655-348
; Sequence 348, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
```

```
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-348

Query Match      100.0%; Score 41; DB 15; Length 504;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
DB      174 GYSFTGY 180
      |||||

RESULT 16
US-09-480-236-1
; Sequence 1, Application US/09480236
; Patent No. US20020142000A1
; GENERAL INFORMATION:
; APPLICANT: Digan, Mary Ellen
; APPLICANT: Lake, Philip
; APPLICANT: Wright, Richard M.
; TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
; FILE REFERENCE: CGC 4-31157A/USN
; CURRENT APPLICATION NUMBER: US/09/480,236
; CURRENT FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: scfv(UCHT-1)-PE38 amino acid sequence
US-09-480-236-1

Query Match      100.0%; Score 41; DB 11; Length 601;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
DB      153 GYSFTGY 159
      |||||

RESULT 17
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US2003039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, PER
; APPLICANT: ANTONSSON, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188U0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)

; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match      100.0%; Score 41; DB 12; Length 672;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
DB      26 GYSFTGY 32
      |||||

RESULT 18
US-10-025-687-17
; Sequence 17, Application US/10025687
; Publication No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-025-687-17

Query Match      92.7%; Score 38; DB 15; Length 98;
Best Local Similarity 85.7%; Pred. No. 5.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
DB      26 GYTFTGY 32
      ||:||||

RESULT 19
US-10-194-975-1
; Sequence 1, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Roote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-194-975-1

Query Match      92.7%; Score 38; DB 15; Length 98;
Best Local Similarity 85.7%; Pred. No. 5.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
DB      26 GYTFTGY 32
      ||:||||

RESULT 20
US-10-125-687-17
; Sequence 17, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
```

; APPLICANT: Luo, Peter  
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY  
; FILE REFERENCE: 26050-705  
; CURRENT APPLICATION NUMBER: US/10/125,687  
; CURRENT FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-125-687-17

Query Match 92.7%; Score 38; DB 15; Length 98;  
Best Local Similarity 85.7%; Pred. No. 5.2;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 21

US-09-880-748-2008  
; Sequence 2008, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2008  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-880-748-2008

Query Match 92.7%; Score 38; DB 12; Length 241;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 22

US-09-880-748-2031  
; Sequence 2031, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2031  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2031

Query Match 92.7%; Score 38; DB 12; Length 241;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 23

US-09-880-748-2032  
; Sequence 2032, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2032  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-880-748-2032

Query Match 92.7%; Score 38; DB 12; Length 241;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 24

US-09-880-748-2021  
; Sequence 2021, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2021  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2021

Query Match 92.7%; Score 38; DB 12; Length 242;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 25

US-09-880-748-2046  
; Sequence 2046, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2046  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2046

Query Match 92.7%; Score 38; DB 12; Length 242;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 26

US-09-880-748-2106  
; Sequence 2106, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2106  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2106

Query Match 92.7%; Score 38; DB 12; Length 242;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 27

US-09-880-748-2009  
; Sequence 2009, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2009  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2009

Query Match 92.7%; Score 38; DB 12; Length 243;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 28

US-09-880-748-2012  
; Sequence 2012, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2012  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2012

Query Match 92.7%; Score 38; DB 12; Length 243;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 29

US-09-880-748-2014  
; Sequence 2014, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2014  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2014

Query Match 92.7%; Score 38; DB 12; Length 243;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 30

US-09-880-748-2063  
; Sequence 2063, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2063  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2063

Query Match 92.7%; Score 38; DB 12; Length 243;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 31

US-09-880-748-2107  
; Sequence 2107, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2107  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2107

Query Match 92.7%; Score 38; DB 12; Length 243;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

## RESULT 32

US-09-880-748-2109  
; Sequence 2109, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748

```
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2109
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2109

Query Match          92.7%; Score 38; DB 12; Length 243;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYTFTGY 32

RESULT 33
US-09-880-748-1908
; Sequence 1908, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1908
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1908

Query Match          92.7%; Score 38; DB 12; Length 244;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYTFTGY 32

RESULT 34
US-09-880-748-2011
; Sequence 2011, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
```

```
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2011
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2011
```

```
Query Match          92.7%; Score 38; DB 12; Length 244;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYTFTGY 32
```

```
RESULT 35
US-09-880-748-2026
; Sequence 2026, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2026
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2026
```

```
Query Match          92.7%; Score 38; DB 12; Length 244;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYTFTGY 32
```

```
RESULT 36
US-09-880-748-2037
; Sequence 2037, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
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; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2037  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2037

Query Match 92.7%; Score 38; DB 12; Length 244;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

RESULT 37  
US-09-880-748-1946  
; Sequence 1946, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1946  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1946

Query Match 92.7%; Score 38; DB 12; Length 245;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

RESULT 38  
US-09-880-748-2004  
; Sequence 2004, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2004  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2004

Query Match 92.7%; Score 38; DB 12; Length 245;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

RESULT 39  
US-09-880-748-2042  
; Sequence 2042, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2042  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2042

Query Match 92.7%; Score 38; DB 12; Length 245;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
||:||||  
Db 26 GYTFTGY 32

RESULT 40  
US-09-880-748-2116  
; Sequence 2116, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.

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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2116
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2116

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Query Match      92.7%; Score 38; DB 12; Length 245;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GYSFTGY 7
Db      26 GYFTGY 32

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Search completed: July 18, 2003, 15:35:51  
Job time : 19.06 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	41	100.0	63	2	S36383	Ig heavy chain V r
2	41	100.0	98	2	S17604	Ig heavy chain V r
3	41	100.0	102	2	B37263	Ig heavy chain V r
4	41	100.0	105	2	PH0978	Ig heavy chain V r
5	41	100.0	105	2	S67941	Ig heavy chain var
6	41	100.0	107	2	PH0971	Ig heavy chain V r
7	41	100.0	107	2	S26320	Ig heavy chain V r
8	41	100.0	108	2	PH0972	Ig heavy chain V r
9	41	100.0	108	2	PH0977	Ig heavy chain V r
10	41	100.0	114	2	S26319	Ig heavy chain V r
11	41	100.0	118	2	PL0084	Ig heavy chain V r
12	41	100.0	118	2	PL0200	anti-DNA autoantib
13	41	100.0	119	2	F30502	Ig heavy chain V r
14	41	100.0	119	2	B53285	Ig heavy chain V a
15	41	100.0	120	2	A49882	Ig heavy chain V r
16	41	100.0	122	2	F45722	Ig heavy chain V r
17	41	100.0	122	2	PH0887	anti-glycoprotein
18	41	100.0	125	2	PH0100	Ig heavy chain V r
19	41	100.0	135	2	PS0057	Ig heavy chain V r
20	41	100.0	137	2	H32513	Ig heavy chain pre
21	41	100.0	457	2	JC6551	Ig heavy chain pre
22	38	92.7	98	2	S26938	chitinase (EC 3.2.
23	38	92.7	98	2	S26912	Ig heavy chain V r
24	38	92.7	104	2	S69899	Ig heavy chain V r
25	38	92.7	109	2	PH1668	Ig heavy chain V r
26	38	92.7	110	2	PH1669	Ig heavy chain V r
27	38	92.7	117	1	HVHU35	Ig heavy chain pre
28	38	92.7	117	2	S18551	Ig heavy chain V r
29	38	92.7	118	2	S36265	Ig heavy chain V r

Query Match 100.0%; Score 41; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.76; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 19 GYSFTGY 25

RESULT 3  
B37263  
Ig heavy chain V region (IG3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 21-Jan-2000  
C;Accession: B37263  
R;Goshorn, S.C.; Retzel, E.; Jermerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A;Title: Common structural features among monoclonal antibodies binding the same antigen  
A;Reference number: A38601; MUID:91115823; PMID:1703527  
A;Accession: B37263  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-102 <GOS>  
A;Cross-references: GB:M57997; NID:g195426; PIDN:AAA63335.1; PID:g195427  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.79; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 18 GYSFTGY 24

RESULT 4  
PH0978  
Ig heavy chain V region (clone 17s.166) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH0978  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B cells  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH0978  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-105 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 25 GYSFTGY 31

RESULT 5  
S67941  
Ig heavy chain variable region, subgroup I (clone MH52) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 30-May-1997  
C;Accession: S67941  
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

Query Match 100.0%; Score 41; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.76; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 19 GYSFTGY 25

RESULT 3  
B37263  
Ig heavy chain V region (IG3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 21-Jan-2000  
C;Accession: B37263  
R;Goshorn, S.C.; Retzel, E.; Jermerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A;Title: Common structural features among monoclonal antibodies binding the same antigen  
A;Reference number: A38601; MUID:91115823; PMID:1703527  
A;Accession: B37263  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-102 <GOS>  
A;Cross-references: GB:M57997; NID:g195426; PIDN:AAA63335.1; PID:g195427  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.79; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 18 GYSFTGY 24

RESULT 4  
PH0978  
Ig heavy chain V region (clone 17s.166) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH0978  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B cells  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH0978  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-105 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 25 GYSFTGY 31

RESULT 5  
S67941  
Ig heavy chain variable region, subgroup I (clone MH52) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 30-May-1997  
C;Accession: S67941  
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.

Autoimmunity 12, 135-141, 1992  
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human antibody  
A;Reference number: S67940; MUID:92314301; PMID:1617110  
A;Accession: S67941  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-105 <HEX>  
A;Cross-references: EMBL:X73851  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 41; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 8 GYSFTGY 14

RESULT 6  
PH0971  
Ig heavy chain V region (clone 165.14) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH0971  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B cells  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH0971  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-107 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.83; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 22 GYSFTGY 28

RESULT 7  
S26320  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S26320  
R;Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A;Title: Antibodies that are specific for a single amino acid interchange in a protein elicit  
A;Reference number: S26309; MUID:91341421; PMID:1908510  
A;Accession: S26320  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <STA>  
A;Cross-references: EMBL:X59206  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.83; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0

QY 1 GYSFTGY 7  
|||||  
Db 14 GYSFTGY 20

## RESULT 8

PH0972  
Ig heavy chain V region (clone 17s.128) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH0972  
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B cells  
A:Reference number: PH0971, MUID:92381444; PMID:1512540  
A:Accession: PH0972

A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-108 <TIL>  
A:Experimental source: B cell, strain (NZB x NZW)F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.84; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||  
Db 25 GYSFTGY 31

## RESULT 9

PH0977  
Ig heavy chain V region (clone 10-cl) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH0977  
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B cells  
A:Reference number: PH0971, MUID:92381444; PMID:1512540  
A:Accession: PH0977

A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-108 <TIL>  
A:Experimental source: B cell, strain (NZB x NZW)F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.84; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||  
Db 26 GYSFTGY 32

## RESULT 10

PH0972  
Ig heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: S26319  
R:Stark, S.E.; Gaton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26319

A:Molecule type: mRNA  
A:Residues: 1-114 <STA>  
A:Cross-references: EMBL:X59172  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.89; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||  
Db 22 GYSFTGY 28

## RESULT 11

PH0084  
Ig heavy chain V region (E4) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PL0084  
J:Week, K.; Hasegawa, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Cai, J. Exp. Med. 169, 519-533, 1989  
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A:Reference number: PL0080; MUID:89094248; PMID:2492056  
A:Accession: PL0084

A:Molecule type: mRNA  
A:Residues: 1-118 <NEB>  
A:Cross-references: GB:X58595; GB:Y00794; NID:G51573; PIDN:CAA41470.1; PID:G938254  
A:Experimental source: strain BALB/c  
A:Note: 66-Gly is translated as "X" from the codon GGN  
A:Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal anti  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 0.92; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||  
Db 26 GYSFTGY 32

## RESULT 12

PL0200  
anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: PL0200  
R:Smith, R.G.; Voss Jr., E.W.  
Mol. Immunol. 27, 463-470, 1990  
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N

A:Reference number: PL0198; MUID:90309768; PMID:2114528  
A:Accession: PL0200  
A:Molecule type: mRNA  
A:Residues: 1-118 <SMI>  
A:Cross-references: GB:X53641; NID:G50193; PIDN:CAA37692.1; PID:G930139  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:50-66/Region: complementarity-determining 2  
F:99-110/Region: complementarity-determining 3  
F:99-106/Region: D region  
F:107-118/Region: JH region

Query Match 100.0%; Score 41; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 0.92; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
|||  
Db 26 GYSFTGY 32

## RESULT 13

F30502  
Ig heavy chain V region (A52) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Nov-1988 #sequence\_revision 03-Nov-1988 #text\_change 21-Jan-2000  
C:Accession: F30502  
R: Bilal, D.; Webster, D.M.; Rees, A.R.  
J. Immunol. 141, 1745-1753, 1988  
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice  
A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: F30502  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <EIL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.93; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 14

B53285  
Ig heavy chain V and J regions, monoclonal antibody OHP101.B11.1 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B53285  
R: Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
Mol. Immunol. 28, 1063-1072, 1991  
A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles.  
A:Reference number: A53285; MUID:92017897; PMID:1922102

A:Accession: B53285  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-119 <SAW>  
A:Note: sequence inconsistent with nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:63295, NCBIPI:63300)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.93; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 15

A49982  
Ig heavy chain V region (BA7.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: A49982  
R: Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.  
J. Biol. Chem. 269, 2805-2813, 1994  
A:Title: Topology of an amiloride-binding protein.

A:Reference number: A49982; MUID:94132051; PMID:8300613  
A:Accession: A49982  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <LIN>  
A:Cross-references: GB:124802; NID:G452096; PIDN:AAA98740.1; PID:G452097  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.94; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 16

F45722  
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: F45722

R: Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J.; Virol, J.; 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33)

A:Reference number: A45722; MUID:93100833; PMID:7677958  
A:Accession: F45722  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-120 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120594)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.94; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 17

PH0887  
Ig heavy chain V region (anti-CD3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
C:Accession: PH0887  
R: Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992  
A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes

A:Reference number: PH0885; MUID:92113462; PMID:1346155  
A:Accession: PH0887  
A:Molecule type: mRNA  
A:Residues: 1-122 <SHA>  
A:Note: the authors translated the codon TTC for residue 70 as Leu  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 0.95; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

## RESULT 18

PH0100  
Ig heavy chain V region (anti-cyclosporin E) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 21-Jan-2000  
C:Accession: PH0100

R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V  
 Mol. Immunol. 27, 1029-1038, 1990  
 A>Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
 A;Reference number: PH0087; MUID:91042649; PMID:2122240  
 A;Accession: PH0100  
 A;Molecule type: mRNA  
 A;Residues: 1-125 <SCH>  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 F;15-98/Domain: immunoglobulin homology <IMM>  
 F;31-35/Region: complementarity-determining 1  
 F;50-66/Region: complementarity-determining 2  
 F;99-112/Region: complementarity-determining 3

Query Match 100.0%; Score 41; DB 2; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 0.98;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 26 GYSFTGY 32

## RESULT 19

PS0057

Ig heavy chain precursor V region (PAR) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 20-Jun-2000  
 C;Accession: PS0057  
 R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.  
 J. Biochem. 104, 337-343, 1988  
 A>Title: Biased expression of variable region gene families of the immunoglobulin heavy  
 A;Reference number: PS0057; MUID:89197817; PMID:2467902  
 A;Accession: PS0057  
 A;Molecule type: DNA  
 A;Residues: 1-135 <YAO>  
 A;Cross-references: GB:D00307; NID:g220448; PIDN:BAA00213.1; PID:g220449  
 A;Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly  
 C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>  
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 45 GYSFTGY 51

## RESULT 20

H32513

Ig heavy chain precursor V region (BXW16) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
 C;Accession: H32513  
 R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
 J. Clin. Invest. 82, 852-860, 1988  
 A>Title: Immunoglobulin kappa light chain variable region gene complex organization and  
 A;Reference number: A94689; MUID:88331394; PMID:3138286  
 A;Accession: H32513  
 A;Molecule type: DNA  
 A;Residues: 1-137 <KOF>  
 A;Cross-references: GB:M20831; NID:gl196949; PIDN:AAA38848.1; PID:gl196950  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 45 GYSFTGY 51

Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 45 GYSFTGY 51

## RESULT 21

JC6551

chitinase (EC 3.2.1.14) precursor - Leishmania donovani  
 C;Species: Leishmania donovani  
 C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 07-May-1999  
 C;Accession: JC6551  
 R;Shakarian, A.M.; Dwyer, D.M.  
 Gene 208, 315-322, 1998  
 A>Title: The Ld Ch1 gene encodes the secretory chitinase of the human pathogen Leishmania  
 A;Reference number: JC6551; MUID:98201628; PMID:9524285  
 A;Accession: JC6551  
 A;Molecule type: DNA  
 A;Residues: 1-457 <SHA>  
 A;Cross-references: DDBJ:AF009354  
 C;Comment: This enzyme cleaves the beta-1-4 linkage between N-acetyl-glucosamine residues  
 C;Genetics:  
 A;Gene: chit1  
 C;Keywords: glycoprotein; glycosidase; glycosyltransferase; hexosyltransferase; hydrolase  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-457/Product: chitinase #status predicted <MAT>  
 F;384/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 41; DB 2; Length 457;  
 Best Local Similarity 100.0%; Pred. No. 3.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 364 GYSFTGY 370

## RESULT 22

S26938

Ig heavy chain V region (DP-75) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Nov-1993 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
 C;Accession: S26938  
 R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A>Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
 A;Reference number: S26885; MUID:93021117; PMID:1404388  
 A;Accession: S26938  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-98 <TOM>  
 A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970  
 A;Note: the nucleotide sequence was submitted to the EMBL data Library, July 1992  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 98;  
 Best Local Similarity 85.7%; Pred. No. 2.8;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
 |||||  
 Db 26 GYTFTGY 32

## RESULT 23

S26912

Ig heavy chain V region (DP-8) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S26912  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A:Reference number: S26885; MUID:93021117; PMID:1404388  
A:Accession: S26912  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <TM>  
A:Cross-references: EMBL:Z12310; NID:G32979; PIDN:CAA78180.1; PID:G32980  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 98;  
Best Local Similarity 85.7%; Pred. No. 2.8;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYTFTGY 32

RESULT 24  
S69899  
Ig heavy chain V region (clone RT57H), rheumatoid factor - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69899  
R:Randén, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J.  
Eur. J. Immunol. 23, 1220-1225, 1993  
A:Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune response  
A:Reference number: S69896; MUID:93272805; PMID:8500520  
A:Accession: S69899  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-104 <RAN>  
A:Cross-references: EMBL:Z34893; NID:G509803; PIDN:CAA84376.1; PID:G509804  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 104;  
Best Local Similarity 85.7%; Pred. No. 3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 26 GYTFTGY 32

RESULT 25  
PH1668  
Ig heavy chain V region (clone 3G5) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C:Accession: PH1668  
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococci  
A:Reference number: PH1642; MUID:93301610; PMID:8315388  
A:Accession: PH1668  
A:Molecule type: mRNA  
A:Residues: 1-109 <HIL>  
A:Experimental source: B cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 109;  
Best Local Similarity 85.7%; Pred. No. 3.1;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7

Db 18 GYTFTGY 24

## RESULT 26

PH1669  
Ig heavy chain V region (clone 3B2) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C:Accession: PH1669  
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococci  
A:Reference number: PH1642; MUID:93301610; PMID:8315388  
A:Accession: PH1669  
A:Molecule type: mRNA  
A:Residues: 1-110 <HIL>  
A:Experimental source: B cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 110;  
Best Local Similarity 85.7%; Pred. No. 3.1;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 18 GYTFTGY 24

RESULT 27  
HVHU35  
Ig heavy chain precursor V region (V35) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 21-Jul-2000  
C:Accession: S00476; S34013  
R:Matsumura, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuhara, J.  
EMBO J. 7, 1047-1051, 1988  
A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain locus  
A:Reference number: S00476; MUID:88296408; PMID:2841108  
A:Accession: S00476  
A:Molecule type: DNA  
A:Residues: 1-117 <MATS>  
A:Cross-references: EMBL:X07448; NID:G33104; PIDN:CA856703.1; PID:G6002173  
A>Note: the authors translated the codon AGT for residue 89 as Met  
R:Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A:Reference number: S34001; MUID:93209281; PMID:7681398  
A:Accession: S34013  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 20-116 <MAR>  
C:Genetics:  
A:Gene: GDB:IGHV@  
A:Cross-references: GDB:128528; OMIM:147070  
A:Map position: 14q32.33-14q32.33  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 1; Length 117;  
Best Local Similarity 85.7%; Pred. No. 3.3;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 45 GYTFTGY 51

```
RESULT 28
S18551
IG heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S23625
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:CROSS-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:CROSS-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 45 GYTFTGY 51

RESULT 29
S36265
IG heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>
A:CROSS-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 118;
Best Local Similarity 85.7%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYTFTGY 32

RESULT 30
I44151
IG heavy chain V region (BO) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999
```

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C:Accession: I44151
R:Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotien, R.H.; Graff, R.; DeGraw, J.; Pyat
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746; PMID:1373487
A:Accession: I44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-126 <ZEB>
A:CROSS-references: GB:M88309; NID:g183952; PIDN:AAA35967.1; PID:g183953
A:Note: nucleotide translation not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-99/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 126;
Best Local Similarity 85.7%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 27 GYTFTGY 33

RESULT 31
S46393
IG heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FIG>
A:CROSS-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 129;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYTFTGY 32

RESULT 32
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL data library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:CROSS-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 38; DB 2; Length 135;
Best Local Similarity 85.7%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Eur. J. Immunol. 23, 206-211, 1993
A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi
A:Reference number: S33391; MUID:93122092; PMID:8419173
A:Accession: S33404
A:Molecule type: mRNA
A:Residues: 1-40 <KET>
A:Cross-references: EMBL:X73024
A:Experimental source: strain BALB/c
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match      87.8%; Score 36; DB 2; Length 40;
Best Local Similarity 85.7%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      26 GYSFTGH 32

RESULT 36
PHI239
IG heavy chain V region (Clone CLL8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PHI239
R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VH5 gene in human B cell chroni
A:Reference number: PHI232; MUID:93018822; PMID:1402653
A:Accession: PHI239
A:Molecule type: mRNA
A:Residues: 1-102 <CAI>
A:Experimental source: B cell chronic lymphocytic leukemia
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match      87.8%; Score 36; DB 2; Length 102;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      30 GYSFAGY 36

RESULT 37
PH0099
IG heavy chain V region (anti-cyclosporin F) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C:Accession: PH0099
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; Va
Mol. Immunol. 27, 1029-1038, 1990
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A:Reference number: PH0087; MUID:91042649; PMID:2122240
A:Accession: PH0099
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2
F:99-106/Region: complementarity-determining 3

Query Match      87.8%; Score 36; DB 2; Length 119;
Best Local Similarity 85.7%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGY 7

```

```

QY      1 GYSFTGY 7
Db      45 GYTFTGY 51

RESULT 33
JQ1734
Genome polypeptide - shallot virus X
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: shallot virus X
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: JQ1734
R:Kanyuka, K.V.; Vishnichenko, V.K.; Levay, K.E.; Kondrikov, D.Y.; Ryabov, E.V.; Zavriv
J. Gen. Virol. 73, 2553-2560, 1992
A:Title: Nucleotide sequence of shallot virus X RNA reveals a 5'-proximal cistron closel
A:Reference number: JQ1734; MUID:93019008; PMID:1339468
A:Accession: JQ1734
A:Molecule type: genomic RNA
A:Residues: 1-1718 <KAN>
A:Cross-references: GB:M97264; NID:G295078; PID:AAA47787.1; PID:G295079
C:Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis; R
F:915-922/Region: nucleotide-binding motif A (P-loop)
F:978-983/Region: nucleotide-binding motif B
F:921/Binding site: ATP (Lys) #status predicted

Query Match      92.7%; Score 38; DB 1; Length 1718;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      623 GYSYTG 629

RESULT 34
S69468
hypothetical protein YPR150w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
C:Accession: S69468
R:Fulton, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of S. cerevisiae cosmid 9659.
A:Reference number: S69022
A:Accession: S69468
A:Molecule type: DNA
A:Residues: 1-173 <FUL>
A:Cross-references: EMBL:U40829; NID:gl066476; PID:g2347174; GSPDB:GN000016; MIPS:YPR150w
C:Genetics:
A:Gene: MIPS:YPR150w
A:Cross-references: SGD:S0006354
A:Map position: 16R
C:Superfamily: Saccharomyces hypothetical protein YPR150w

Query Match      90.2%; Score 37; DB 2; Length 173;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      135 GFSFTGY 141

RESULT 35
S33404
IG heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
C:Accession: S33404
R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

```

Db 26 GYSFAGY 32  
|||||

## RESULT 38

F75116

hypothetical protein PAB1881 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

C:Accession: F75116

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: F75116

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-862 &lt;KAW&gt;

A:Cross-references: GB:AJ248285; GB:AL096836; NID:G5458067; PIDN:CAB49647.1; PID:G545815

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1881

C:Superfamily: Pyrococcus abyssi hypothetical protein PAB1881

Query Match 87.8%; Score 36; DB 2; Length 862;

Best Local Similarity 85.7%; Pred. No. 61;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7

|||||

Db 369 GYSFVG 375

## RESULT 39

PH1429

Ig heavy chain V-region (clone VHS-2R1) - human (fragment)

N:Alternate names: Ig heavy chain V-III region (TD-Vn)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C:Accession: PH1429; PL0119

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of s dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1429

A:Molecule type: mRNA

A:Residues: 1-98 &lt;VAN&gt;

R:Bird, J.; Gallili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; MUID:88286083; PMID:2840480

A:Accession: PL0119

A:Molecule type: mRNA

A:Residues: 1-98 &lt;BIR&gt;

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL

A:Note: the sequence shows the V region (TD-Vn) from one of five DNA rearrangements from

C:Superfamily: immunoglobulin V region: immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology &lt;IMW&gt;

F;31-35/Region: complementarity-determining 1

F;49-65/Region: complementarity-determining 2

Query Match 85.4%; Score 35; DB 2; Length 98;

Best Local Similarity 85.7%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7

|||||

Db 26 GYSFTSY 32

## RESULT 40

PH1274

Ig heavy chain V region (clone PBL5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1274

R:Cai, J.; Humphries, C.; Richardson, A.; Tucker, P.W.

J. Exp. Med. 176, 1073-1081, 1992

A:Title: Extensive and selective mutation of a rearranged VHS gene in human B cell chroni

A:Reference number: PH1232; MUID:93018822; PMID:1402653

A:Accession: PH1274

A:Molecule type: DNA

A:Residues: 1-98 &lt;CAI&gt;

A:Experimental source: adult PBL

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 85.4%; Score 35; DB 2; Length 98;

Best Local Similarity 85.7%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7

|||||

Db 30 GYSFTSY 36

Search completed: July 18, 2003, 15:10:42

Job time : 10.1 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:20 ; Search time 4.34 Seconds  
(without alignments)  
66.897 Million cell updates/sec

Title: US-10-007-790-5  
Perfect score: 41  
Sequence: 1 GYSFTGY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	38	92.7	117	1	HV1G_HUMAN	P23083 homo sapien
2	38	92.7	1718	1	RRPO_SHVX	Q04575 shallot vir
3	34	82.9	117	1	HV03_CARAU	P19180 carassius a
4	34	82.9	353	1	ROD_RAT	Q9JJ54 rattus norv
5	34	82.9	355	1	ROD_HUMAN	Q14103 homo sapien
6	33	80.5	342	1	K6P1_STRCO	O08333 streptomyce
7	33	80.5	392	1	CAR1_DICDI	P13773 dictyosteli
8	33	80.5	426	1	Y057_METJA	Q60362 methanococc
9	33	80.5	427	1	CYB6_CHLIT	Q59297 chlorobium
10	33	80.5	427	1	CYB6_CHLTE	Q9F721 chlorobium
11	32	78.0	117	1	HV04_MOUSE	P01748 mus musculu
12	32	78.0	117	1	HV05_MOUSE	P01749 mus musculu
13	32	78.0	117	1	HV06_MOUSE	P01750 mus musculu
14	32	78.0	117	1	HV09_MOUSE	P01753 mus musculu
15	32	78.0	117	1	HV10_MOUSE	P01754 mus musculu
16	32	78.0	117	1	HV49_MOUSE	P06328 mus musculu
17	32	78.0	117	1	HV52_MOUSE	P06327 mus musculu
18	32	78.0	120	1	HV03_MOUSE	P01747 mus musculu
19	32	78.0	120	1	HV50_MOUSE	P06329 mus musculu
20	32	78.0	121	1	HV01_MOUSE	P01745 mus musculu
21	32	78.0	137	1	HV11_MOUSE	P01755 mus musculu
22	32	78.0	139	1	HV07_MOUSE	P01751 mus musculu
23	32	78.0	140	1	HV02_MOUSE	P01746 mus musculu
24	32	78.0	353	1	UL95_HSV6U	P24444 human herpe
25	32	78.0	391	1	CGAL_CARAU	Q92161 carassius a
26	32	78.0	435	1	HFEL_HAEIN	P45994 haemophilus
27	32	78.0	510	1	GARD_BACSU	P42240 bacillus su
28	32	78.0	523	1	GARD_ECOLI	P39829 escherichia
29	32	78.0	569	1	MANC_FIRSP	P55298 piromyces s
30	31	75.6	115	1	HV44_MOUSE	P01820 mus musculu
31	31	75.6	117	1	HV12_MOUSE	P01756 mus musculu
32	31	75.6	117	1	HV13_MOUSE	P01757 mus musculu
33	31	75.6	117	1	HV14_MOUSE	P01758 mus musculu

34	31	75.6	118	1	HV51_MOUSE	P06330 mus musculu
35	31	75.6	136	1	HV15_MOUSE	P01759 mus musculu
36	31	75.6	141	1	YEP5_YEAST	P32616 saccharomyc
37	31	75.6	144	1	HV43_MOUSE	P01819 mus musculu
38	31	75.6	210	1	CRB3_BOVIN	P19141 bos taurus
39	31	75.6	211	1	CRB3_HUMAN	P26998 homo sapien
40	31	75.6	211	1	CRB3_MOUSE	Q9JJU9 mus musculu
41	31	75.6	211	1	CRB3_RAT	P02524 rattus norv
42	31	75.6	254	1	YFEN_ECOLI	P45564 escherichia
43	31	75.6	375	1	YKUS_CAEEL	Q17778 caenorhabdi
44	31	75.6	477	1	GLGA_CLOAB	Q97GX6 clostridium
45	31	75.6	482	1	GLGA_CLOPE	Q8XPAL clostridium

ALIGNMENTS

RESULT 1						
HV1G_HUMAN						
ID	HV1G_HUMAN	STANDARD;	PRT;	117	AA.	
AC	P23083;					
DT	01-NOV-1991 (Rel. 20, Created)					
DT	01-NOV-1991 (Rel. 20, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Ig heavy chain V-I region V35 precursor.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]_TaxID=9606;					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=88296408; PubMed=2841108;					
RA	Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,					
RA	Ohno H., Fukuhara S., Honjo T.;					
RT	"Dispersed localization of D segments in the human immunoglobulin					
RT	heavy-chain locus.";					
RL	EMBO J. 7:1047-1051(1988).					
CC	-----					
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CC	-----					
DR	EMBL; X07448; -; NOT_ANNOTATED_CDS.					
DR	PIR; S00476; HVH35.					
DR	HSSP; P01772; 2FB4.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_v.					
DR	Pfam; PF00047; ig; 1.					
DR	SMART; SM00406; IGV; 1.					
KW	Immunoglobulin v region; Signal.					
FT	SIGNAL	1	19			
FT	CHAIN	20	117			
FT	NON_TER	117	117			
FT	SEQUENCE	117	AA;	13009	NW;	BE61CB63F8CE97BD CRC64;
Query Match 92.7%; Score 38; DB 1; Length 117;						
Best Local Similarity 85.7%; Pred. No. 2.1;						
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;						
QY	1	GYSFTGY	7			
Db	45	GITFTGY	51			
RESULT 2						
RRPO_SHVX						
ID	RRPO_SHVX	STANDARD;	PRT;	1718	AA.	
AC	Q04575;					
DT	01-JUN-1994 (Rel. 29, Created)					

```
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replication protein (194 kDa protein) (ORF 1) [Contains: RNA-
DE directed RNA polymerase (EC 2.7.7.48); Probable helicase].
OS Shalhot virus X (SHVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Allexivirus.
OX NCBI_TaxID=31770;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93019008; PubMed=1339468;
RA Kanyuka K.V., Vishnichenko V.K., Levay K.E., Kondrikov D.Y.,
RA Ryabov E.V., Zavrtev S.K.;
RT "Nucleotide sequence of shalhot virus X RNA reveals a 5'-proximal
RT cistron closely related to those of potexviruses and a unique
RT arrangement of the 3'-proximal cistrons.";
RL J. Gen. Virol. 73:2553-2560(1992).
CC -!- FUNCTION: RNA-replication. The central part of this protein
CC possibly functions as an ATP-binding helicase.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -----
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CC -----
DR EMBL; M97264; AAA47787.1; -
DR PIR; J01734;
DR InterPro; IPR005123; 2OG-PeII Oxy.
DR InterPro; IPR001788; RNA_dep_RNapol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNapol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR Pfam; PF03171; 2OG-PeII Oxy; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase.
FT NP_BIND 915 922 ATP (POTENTIAL).
SQ SEQUENCE 1718 AA; 194529 MW; 820FEAE1EB62415C CRC64;

Query Match 92.7%; Score 38; DB 1; Length 1718;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 623 GYSYTG 629

RESULT 3
ID HV03 CARAU STANDARD; PRT; 117 AA.
AC P19180;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
CC -----

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EMBL; J03616; AAA50807.1; -
PIR; A28966; A28966.
HSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13220 MW; 512B625003FA5ECB CRC64;

Query Match 82.9%; Score 34; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 45 GYTFSGY 51

RESULT 4
ID ROD RAT STANDARD; PRT; 353 AA.
AC Q9J54; Q9J53; Q9J52; Q9J51;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element
DE RNA-binding protein 1).
GN HNRPD OR AUFI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RA Arai Y., Kikuchi A.;
RT "Differential expression of AUFI isoforms in rat tissues.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS WITH HIGH AFFINITY TO RNA MOLECULES THAT CONTAIN
CC AU-RICH ELEMENTS (ARES) FOUND WITHIN THE 3-PRIME UNTRANSLATED
CC REGIONS OF MANY PROTOGENES AND CYTOKINE MRNAs (BY SIMILARITY);
CC -!- SUBCELLULAR LOCATION: Nuclear; component of ribonucleosomes (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1/P45 (SHOWN HERE), 2/P42, 3/P40
CC AND 4/P37; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
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DR EMBL; AB046615; BAB03465.1; -;  
DR EMBL; AB046616; BAB03466.1; -;  
DR EMBL; AB046617; BAB03467.1; -;  
DR EMBL; AB046618; BAB03468.1; -;  
DR HSSP; P09651; 1UPI.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rrm; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS00030; RRM RNP 1; 2.  
KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat;  
KW Alternative splicing.  
FT DOMAIN 11 45 ALA-RICH.  
FT DOMAIN 95 177 RNA-BINDING (RRM) 1.  
FT DOMAIN 180 259 RNA-BINDING (RRM) 2.  
FT DOMAIN 268 345 GLY-RICH.  
FT DOMAIN 292 330 TYR-RICH.  
FT VARSPLIC 77 95 MISSING (IN ISOFORM 2 AND ISOFORM 4).  
FT VARSPLIC 283 332 GPSQNWQGYNSYNGYSGYNSQGYGGYDYTGYN  
FT YGYGDYSN -> D (IN ISOFORM 3 AND ISOFORM 4).  
SQ SEQUENCE 353 AA; 38192 MW; 6190EE1006F07DCB CRC64;  
Query Match 82.9%; Score 34; DB 1; Length 353;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 315 GYDYGTY 321  
RESULT 5  
ROD\_HUMAN ID ROD\_HUMAN STANDARD; PRT; 355 AA.  
AC Q14103; Q14100; Q14101; Q14102;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1).  
GN HNRPD OR AUFI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 1;  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=95403404; PubMed=7673195;  
RA Kajita Y., Nakayama J., Aizawa M., Ishikawa F.;  
RT "The UUG-specific RNA binding protein, heterogeneous nuclear ribonucleoprotein D0. Common modular structure and binding properties of the 2xREP-Gly family.";  
RL J. Biol. Chem. 270:22167-22175 (1995).  
RN 2;  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=98277449; PubMed=9615222;  
RA Dempsey L.A., Li M.-J., DePace A., Bray-Ward P., Maizels N.;  
RT "The human HNRPD locus maps to 4q21 and encodes a highly conserved protein.";  
RL Genomics 49:378-384 (1998).  
RN 3;  
RP SEQUENCE OF 9-355 FROM N.A. (ISOFORM 3).  
RC TISSUE=Blood;  
RA Tolnay M., Tsokos G.C.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: BINDS WITH HIGH AFFINITY TO RNA MOLECULES THAT CONTAIN AU-RICH ELEMENTS (ARES) FOUND WITHIN THE 3-PRIME UNTRANSLATED REGIONS OF MANY PROTOONCOGENES AND CYTOKINE MRNAs.  
CC -1- SUBCELLULAR LOCATION: Nuclear; component of ribonucleosomes.  
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (SHOWN HERE), 2, 3 AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).

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DR EMBL; D55674; BAA09525.1; -;  
DR EMBL; D55671; BAA09522.1; -;  
DR EMBL; D55672; BAA09523.1; -;  
DR EMBL; D55673; BAA09524.1; -;  
DR EMBL; AF026126; AAC23474.1; -;  
DR EMBL; AF026126; AAC23475.1; -;  
DR EMBL; AF026126; AAC23476.1; -;  
DR EMBL; AF039575; AAB96683.1; -;  
DR HSSP; P09651; 1UPI.  
DR Genew; HGNC:5036; HNRPD.  
DR MIM; 601324; -;  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rrm; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS00102; RRM; 2.  
DR PROSITE; PS00030; RRM RNP 1; 2.  
KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat;  
KW Alternative splicing.  
FT DOMAIN 11 45 ALA-RICH.  
FT DOMAIN 97 179 RNA-BINDING (RRM) 1.  
FT DOMAIN 182 261 RNA-BINDING (RRM) 2.  
FT DOMAIN 270 347 GLY-RICH.  
FT DOMAIN 294 332 TYR-RICH.  
FT VARSPLIC 79 97 MISSING (IN ISOFORM 2 AND ISOFORM 4).  
FT VARSPLIC 285 334 GPSQNWQGYNSYNGYSGYNSQGYGGYDYTGYN  
FT YGYGDYSN -> D (IN ISOFORM 3 AND ISOFORM 4).  
SQ SEQUENCE 355 AA; 38434 MW; D0B6EAL77BEF789E CRC64;  
Query Match 82.9%; Score 34; DB 1; Length 355;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 317 GYDYGTY 323  
RESULT 6  
K6P1\_STRCO ID K6P1\_STRCO STANDARD; PRT; 342 AA.  
AC O08333;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 6-phosphofructokinase 1 (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase 1) (ATP-PFK).  
GN PFK1 OR PFK1 OR PFK1 OR SCO2119 OR SC6E10.13C.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN 1;  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=A3(2) / 1109;  
RX MEDLINE=97208211; PubMed=9055413;  
RA Alves A.M.C.R., Euvrink G.J.W., Bibb M.J., Dijkhuizen L.;  
RT "Identification of ATP-dependent phosphofructokinase as a regulatory step in the glycolytic pathway of the actinomycete Streptomyces coelicolor A3(2)";  
RL Appl. Environ. Microbiol. 63:956-961 (1997).  
RN 2;  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;

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EMBL; AB046615; BAB03465.1; -  
EMBL; AB046616; BAB03466.1; -  
EMBL; AB046617; BAB03467.1; -  
EMBL; AB046618; BAB03468.1; -  
HSP; P09651; IUP1.  
InterPro: IPR000504; RNA\_rec\_mot.  
Pfam; PF00076; rrm; 2.  
SMART; SM00360; RRM; 2.  
PROSITE; PS00030; RRM\_RNP\_1; 2.  
Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat;  
KW Alternative splicing.  
FT DOMAIN 11 45  
FT DOMAIN 95 177  
FT DOMAIN 180 259  
FT DOMAIN 268 345  
FT DOMAIN 292 330  
FT TVR-RICH.  
FT VARSPLIC 77 95  
FT VARSPLIC 283 332  
MISSING (IN ISOFORM 2 AND ISOFORM 4).  
GPSQNWQGSYNNMQGYSYGSGYNSQGSGGYDGTGYNM  
YYGYGDYSN -> D (IN ISOFORM 3 AND ISOFORM 4).  
SQ SEQUENCE 353 AA; 38192 MW; 6190EE1006F07DCB CRC64;

Query Match 82.9%; Score 34; DB 1; Length 353;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGY 7  
|||:  
Db 315 GYDYTG 321

RESULT 5  
ROD\_HUMAN ID ROD\_HUMAN STANDARD; PRT; 355 AA.  
AC Q14103; Q14100; Q14101; Q14102;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element  
DE RNA-binding protein 1).  
GN HNRPD OR AUF1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=95403404; PubMed=7673195;  
RA Kajita Y., Nakayama J., Aizawa M., Ishikawa F.;  
RT "The UUG-specific RNA binding protein, heterogeneous nuclear  
ribonucleoprotein D0. Common modular structure and binding properties  
of the xREP-Gly family.";  
RL J. Biol. Chem. 270:22167-22175(1995).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=98277449; PubMed=9615222;  
RA Dempsey L.A., Li M.-J., DePace A., Bray-Ward P., Maizels N.;  
RT "The human HNRPD locus maps to 4q21 and encodes a highly conserved  
protein.";  
RL Genomics 49:378-384(1998).  
RN [3]  
RP SEQUENCE OF 9-355 FROM N.A. (ISOFORM 3).  
RC TISSUE=Blood;  
RA Tolnay M., Tsokos G.C.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: BINDS WITH HIGH AFFINITY TO RNA MOLECULES THAT CONTAIN  
AU-RICH ELEMENTS (ARES) FOUND WITHIN THE 3-PRIME UNTRANSLATED  
REGIONS OF MANY PROTOONCOGENES AND CYTOKINE MRNAS  
CC -!- SUBCELLULAR LOCATION: Nuclear; component of ribonucleosomes.  
CC -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (SHOWN HERE), 2, 3 AND 4; ARE  
PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).

EMBL; D55674; BAA09525.1; -  
EMBL; D55671; BAA09522.1; -  
EMBL; D55672; BAA09523.1; -  
EMBL; D55673; BAA09524.1; -  
EMBL; AF026126; AAC23474.1; -  
EMBL; AF026126; AAC23475.1; -  
EMBL; AF026126; AAC23476.1; -  
EMBL; AF039575; AAB96683.1; -  
HSP; P09651; IUP1.  
Genew; HGNC:5036; HNRPD.  
MIM; 601324; -  
InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rrm; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS00102; RRM; 2.  
DR PROSITE; PS00030; RRM\_RNP\_1; 2.  
KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat;  
KW Alternative splicing.  
FT DOMAIN 11 45  
FT DOMAIN 97 179  
FT DOMAIN 182 261  
FT DOMAIN 270 347  
FT TYR-RICH.  
FT VARSPLIC 79 97  
FT VARSPLIC 285 334  
MISSING (IN ISOFORM 2 AND ISOFORM 4).  
GPSQNWQGSYNNMQGYSYGSGYNSQGSGGYDGTGYNM  
YYGYGDYSN -> D (IN ISOFORM 3 AND ISOFORM 4).  
SQ SEQUENCE 355 AA; 38434 MW; D0B6EAL77BEF789E CRC64;

Query Match 82.9%; Score 34; DB 1; Length 355;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGY 7  
|||:  
Db 317 GYDYTG 323

RESULT 6  
K6P1\_STRCO ID K6P1\_STRCO STANDARD; PRT; 342 AA.  
AC O08333;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 6-phosphofructokinase 1 (EC 2.7.1.11) (Phosphofructokinase 1)  
DE (Phosphohexokinase 1) (ATP-PFK).  
GN PFK1 OR PKA OR PFKI OR SCO2119 OR SC6E10.13C.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=A3(2)/1109;  
RX MEDLINE=97208211; PubMed=9055413;  
RA Alves A.M.C.R., Everink G.J.W., Bibb M.J., Dijkhuizen L.;  
RT "Identification of ATP-dependent phosphofructokinase as a regulatory  
step in the glycolytic pathway of the actinomycete Streptomyces  
coelicolor A3(2).";  
RL Appl. Environ. Microbiol. 63:956-961(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2)/M145;

RX MEDLINE=21996410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,  
RA Warren T., Wierozorek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-  
CC fructose 1,6-bisphosphate.  
CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY  
CC PHOSPHOENOLPYRUVATE.  
CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.  
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U51728; AAC45135.1; -;  
DR EMBL; AL109661; CAB51967.1; -;  
DR HSSP; P00512; 3PFK.  
DR InterPro; IPR000023; Ppfckinase.  
DR Pfam; PF00365; PFK; 1.  
DR PRINTS; PD0476; PHFRCTKINASE.  
DR ProDom; PD00707; Ppfckinase; 1.  
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.  
KW Kinase; Transferase; Glycolysis; Multigene family; Allosteric enzyme;  
KW Complete proteome.  
SQ SEQUENCE 342 AA; 36664 MW; CEEFC7B74092AB34 CRC64;  
  
Query Match 80.5%; Score 33; DB 1; Length 342;  
Best Local Similarity 71.4%; Pred. No. 47;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
DB 31 GYDFTGF 37  
  
RESULT 7  
ID CARL\_DICDI STANDARD; PRT; 392 AA.  
AC P13773;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cyclic AMP receptor 1.  
GN CARA OR CAR1.  
OS Dictyostelium discoideum (slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44699;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88336877; PubMed=3047871;  
RA Klein P.S., Sun T.J., Saxe C.L. III, Kimmel A.R., Johnson R.L.,  
RA Devrotes P.N.;  
RT "A chemotactant receptor controls development in Dictyostelium  
RT discoideum.";  
RL Science 241:1467-1472(1988).  
CC -1- FUNCTION: RECEPTOR FOR CAMP. COORDINATES THE AGGREGATION  
CC OF INDIVIDUAL CELLS INTO A MULTICELLULAR ORGANISM AND REGULATES

CC THE EXPRESSION OF A LARGE NUMBER OF DEVELOPMENTALLY REGULATED  
CC GENES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PREDOMINANTLY DURING EARLY  
CC AGGREGATION AND AT LOW LEVELS DURING LATER STAGE.  
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.  
CC -1- SIMILARITY: BELONGS TO FAMILY 5 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M21824; AAA33177.1; -;  
DR EMBL; A41238; A41238.  
DR DictyDB; DD02012; carA.  
DR InterPro; IPR000848; GPCR\_CAMP.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR Pfam; PF00002; 7tm\_2; 1.  
DR PRINTS; PR00247; GPCR\_CAMP.  
DR PROSITE; PS0261; G-PROTEIN RECEPTOR; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Phosphorylation; Multigene family.  
FT DOMAIN 1 13 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 14 33 1 (POTENTIAL).  
FT DOMAIN 34 47 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 48 68 2 (POTENTIAL).  
FT DOMAIN 69 83 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 84 109 3 (POTENTIAL).  
FT DOMAIN 110 120 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 121 139 4 (POTENTIAL).  
FT DOMAIN 140 162 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 163 181 5 (POTENTIAL).  
FT DOMAIN 182 205 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 206 224 6 (POTENTIAL).  
FT DOMAIN 225 235 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 236 260 7 (POTENTIAL).  
FT DOMAIN 261 392 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 10 10 N-LINKED (GLCNAC...) (POTENTIAL).  
FT DOMAIN 337 356 ASN-RICH.  
FT DOMAIN 360 368 SER-RICH.  
FT MOD\_RES 299 299 PHOSPHORYLATION (POTENTIAL).  
FT MOD\_RES 304 304 PHOSPHORYLATION (POTENTIAL).  
SQ SEQUENCE 392 AA; 44312 MW; 38C4561EE1CC9A69 CRC64;  
  
Query Match 80.5%; Score 33; DB 1; Length 392;  
Best Local Similarity 85.7%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
DB 153 GVSFTGY 159  
  
RESULT 8  
ID Y057\_METJA STANDARD; PRT; 426 AA.  
AC Q60362;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Putative Na(+)/H(+) exchanger MJ0057.  
GN MJ0057.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanocaldococcaceae; Methanocaldococcus.  
OX NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RA MEDLINE=96337999; PubMed=8688087;  
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glödek A.,  
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
RT jannaschii.";  
RL Science 273:1058-1073(1996).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: BELONGS TO THE NA(4+)/H(+) EXCHANGER FAMILY. STRONG, TO  
CC M.JANNASCHII Mj1521.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U67463; AAB98037.1; -;  
CC TIGR; M00057; -;  
DR InterPro; IPR000676; NaH\_Exchange.  
DR Pfam; PF00999; Na\_H\_Exchange; 1.  
KW Hypothetical protein; Transmembrane; Transport; Antiport;  
KW Sodium transport; Complete proteome.  
FT TRANSMEM 1 21 POTENTIAL.  
FT TRANSMEM 29 49 POTENTIAL.  
FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 95 115 POTENTIAL.  
FT TRANSMEM 120 140 POTENTIAL.  
FT TRANSMEM 158 178 POTENTIAL.  
FT TRANSMEM 184 204 POTENTIAL.  
FT TRANSMEM 208 228 POTENTIAL.  
FT TRANSMEM 236 256 POTENTIAL.  
FT TRANSMEM 286 306 POTENTIAL.  
FT TRANSMEM 309 329 POTENTIAL.  
FT TRANSMEM 382 402 POTENTIAL.  
SQ SEQUENCE 426 AA; 45966 MW; 9679A3E60949A1D CRC64;  
  
Query Match 80.5%; Score 33; DB 1; Length 426;  
Best Local Similarity 71.4%; Pred. No. 58;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
DB 242 GYGFGY 248  
  
RESULT 9  
CYB6\_CHLLT STANDARD; PRT; 427 AA.  
AC Q59237;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cytochrome B-C complex cytochrome B subunit.  
GN PETB.  
OS Chlorobium limicola f.sp. thiosulfatophilum.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium.  
OX NCBI\_TaxID=115852;  
RN [1]  
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 1-24.  
RA Schuetz M., Ziringibl S., le Coutre J., Buettner M., Xie D.-L.,  
RA Nelson N., Deutzmann R., Hauska G.;  
RT "A transcription unit for the Rieske FeS-protein and cytochrome b in  
RT Chlorobium limicola.";  
RL Photosyn. Res. 39:163-174(1994).

CC -1- FUNCTION: COMPONENT OF THE GREEN S-BACTERIA BC-COMPLEX WHICH  
CC CONSISTS OF THE RIESKE PROTEIN AND CYTOCHROME B SUBUNIT AND  
CC WHICH, APPEARS TO LACK A CYTOCHROME C1-EQUIVALENT. THIS  
CC COMPLEX HAS A COMPARATIVELY LOW REDOX POTENTIAL.  
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
CC BOUND TO THE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X73628; CAA52008.1; -;  
CC InterPro; IPR000179; Cyt\_b\_b6.  
CC Pfam; PF00033; cytochrome\_b\_5; 1.  
DR PROSITE; PS00192; CYTOCHROME B\_HEME; 1.  
DR PROSITE; PS00193; CYTOCHROME B\_QO; FALSE NEG.  
KW Electron transport; Respiratory chain; Transmembrane; Heme.  
FT INIT MET 0  
FT TRANSMEM 109 129 POTENTIAL.  
FT TRANSMEM 161 181 POTENTIAL.  
FT TRANSMEM 192 212 POTENTIAL.  
FT TRANSMEM 259 279 POTENTIAL.  
FT TRANSMEM 311 330 POTENTIAL.  
FT TRANSMEM 368 388 POTENTIAL.  
FT TRANSMEM 400 420 POTENTIAL.  
FT METAL 160 160 IRON 1 (HEME B562 AXIAL LIGAND) (BY  
FT METAL 174 174 IRON 2 (HEME B566 AXIAL LIGAND) (BY  
FT METAL 260 260 IRON 2 (HEME B562 AXIAL LIGAND) (BY  
FT METAL 275 275 IRON 1 (HEME B566 AXIAL LIGAND) (BY  
FT SEQUENCE 427 AA; 47346 MW; CEE6FOAE1BC757D4 CRC64;  
  
Query Match 80.5%; Score 33; DB 1; Length 427;  
Best Local Similarity 71.4%; Pred. No. 58;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
DB 204 GYGFTGY 210  
  
RESULT 10  
CYB6\_CHLTE STANDARD; PRT; 427 AA.  
AC Q9F721;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cytochrome B-C complex cytochrome B subunit.  
GN PETB.  
OS Chlorobium tepidum.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium.  
OX NCBI\_TaxID=1097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-TLS / ATCC 49652 / DSM 12025;  
RX MEDLINE=20433268; PubMed=10976061;  
RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;  
RT "Molecular evidence for the early evolution of photosynthesis.";  
RL Science 289:1724-1730(2000).  
CC -1- FUNCTION: COMPONENT OF THE GREEN S-BACTERIA BC-COMPLEX WHICH  
CC CONSISTS OF THE RIESKE PROTEIN AND CYTOCHROME B SUBUNIT AND  
CC WHICH, APPEARS TO LACK A CYTOCHROME C1-EQUIVALENT. THIS  
CC COMPLEX HAS A COMPARATIVELY LOW REDOX POTENTIAL (BY SIMILARITY).

--1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY  
BOUND TO THE PROTEIN  
--1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
-----  
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-----  
EMBL: AF287480; AAC12195.1; --  
InterPro: IPR000179; Cyt\_b\_b6.  
Pfam: PF00033; Cytochrome\_B\_N; 1.  
DR PROSITE: PS00192; CYTOCHROME\_B\_HEME; 1.  
DR PROSITE: PS00193; CYTOCHROME\_B\_QO; FALSE NEG.  
KW Electron transport; Respiratory chain; Heme; Transmembrane.  
FT INIT MET 0  
FT TRANSMEM 107 127  
FT TRANSMEM 159 179  
FT TRANSMEM 190 210  
FT TRANSMEM 257 277  
FT TRANSMEM 309 328  
FT TRANSMEM 366 386  
FT TRANSMEM 398 418  
FT METAL 158 158  
FT METAL 172 172  
FT METAL 258 258  
FT METAL 273 273  
SQ SEQUENCE 427 AA; 47364 MW; 87736B20F89167E3 CRC64;  
  
Query Match 80.5%; Score 33; DB 1; Length 427;  
Best Local Similarity 71.4%; Pred. No. 58;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
| : ||||  
Db 202 GFGFTGY 208  
  
RESULT 11  
HV04 MOUSE STANDARD; PRT; 117 AA.  
AC P01748;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 23 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
Baltimore D.;  
RT "Heavy chain variable region contribution to the Npb family of  
antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY  
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL: J00536; AAA38605.1; --  
DR PIR: A02031; HVMS3.  
DR HSSP: P01810; 2FBJ  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;  
  
Query Match 78.0%; Score 32; DB 1; Length 117;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
| : ||||  
Db 45 GYTFTSY 51  
  
RESULT 12  
HV05 MOUSE STANDARD; PRT; 117 AA.  
AC P01749;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 3 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
Baltimore D.;  
RT "Heavy chain variable region contribution to the Npb family of  
antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY  
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
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-----  
EMBL: J00536; AAA38605.1; --  
DR PIR: A02031; HVMS3.  
DR HSSP: P01810; 2FBJ  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;



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DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543B996 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 45 GYTFTSY 51

RESULT 16
HV49 MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DE 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
CC EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 78.0%; Score 32; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 45 GYTFTSY 51

RESULT 17
HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DE 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
CC EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 78.0%; Score 32; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 45 GYTFTSY 51

RESULT 18
HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RN  SEQUENCE FROM N.A.
RX  MEDLINE=83131846; PubMed=6186498;
RA  Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA  Marshak-Rothstein A.; antibody production: the dominant anti-arsenate
RT  idotype response of the strain A mouse."
RL  Eur. J. Immunol. 12:1023-1032(1982).
CC  -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC  DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC  CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC  SEGMENT, JH2.
DR  PIR; A02028; HWSG7.
DR  HSSP; P01789; IMCP.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region; Antiarsenate antibody; Hybridoma.
FT  NON TER 120
SQ  SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 78.0%; Score 32; DB 1; Length 120;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 25 GYFTSY 31

RESULT 19
HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes."
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 105
FT DOMAIN 106 120
FT DISULFID 22 96
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 120;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYFTSY 32

RESULT 20
HV01 MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11."
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 78.0%; Score 32; DB 1; Length 121;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 26 GYFTNY 32

RESULT 21
HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----  
DR EMBL; J00539; AAA38172.1; -;  
DR PIR; A02038; G2MS43.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 122 D SEGMENT.  
FT DOMAIN 123 137 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448EC9 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 137;  
Best Local Similarity 71.4%; Pred. No. 29;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 45 GYTFTSY 51

RESULT 22  
HV07 MOUSE  
ID HV07 MOUSE STANDARD; PRT; 139 AA.  
AC P01751; P01752;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region B1-8/186-2 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82134548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;  
RA "Heavy chain variable region contribution to the NPB family of antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).  
CC -----  
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CC EMBL; J00529; AAA38170.1; -;  
DR PIR; A02034; MHMS18.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19  
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 124 D SEGMENT.  
FT DOMAIN 125 139 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 139 139  
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 139;  
Best Local Similarity 71.4%; Pred. No. 30;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 45 GYTFTSY 51

RESULT 23  
HV02 MOUSE  
ID HV02 MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 93G7 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W., Capra J.D.;  
RA "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).  
CC -----  
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CC EMBL; J00493; AAA38128.1; -;  
DR PIR; A02028; HVMSG7.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.  
FT NON\_TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 140;  
Best Local Similarity 71.4%; Pred. No. 30;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 45 GYTFTSY 51

```
RESULT 24
UL95_HSV6U          STANDARD;          PRT;   353 AA.
ID  UL95_HSV6U
AC  P24444;
DT  01-MAR-1992 (Rel. 21, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Protein U67.
GN  U67 OR 13R.
OS  Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC  Betaherpesvirinae; Roseolovirus.
OX  NCBI_TaxID=10370;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90080132; PubMed=2152817;
RA  Lawrence G.B., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
RA  Barrell B.G.;
RT  "Human herpesvirus 6 is closely related to human cytomegalovirus.";
RL  J. Virol. 64:287-299(1990).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=95266321; PubMed=7747482;
RA  Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA  Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT  "The DNA sequence of human herpesvirus-6: structure, coding content,
RT  and genome evolution.";
RL  Virology 209:29-51(1995).
CC  -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BGLF3,
CC  HVS-1 34, HSV-6 U67, AND HCMV UL95.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M69963; AAA65575.1; -;
DR  EMBL; X83413; CAA56359.1; -;
DR  PIR; C36769; C36769.
DR  InterPro; IPR004280; UL95.
DR  Pfam; PF03038; UL95; 1.
SQ  SEQUENCE 353 AA; 39531 MW; E30E73D5D0ACEBA7 CRC64;

Query Match      78.0%; Score 32; DB 1; Length 353;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GYSFTGY 7
Db  191 GYSKTYG 197

RESULT 25
CGAL_CARAU          STANDARD;          PRT;   391 AA.
ID  CGAL_CARAU
AC  Q92161;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Cyclin A1 (Cyclin A).
GN  CCNA1 OR CCNA.
OS  Carassius auratus (Goldfish).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Carassius.
OX  NCBI_TaxID=7957;
RN  [1]
RP  SEQUENCE FROM N.A.

TISSUE=Ovary;
RX  MEDLINE=95377548; PubMed=7649388;
RA  Katsu Y., Yamashita M., Hirai T., Tokumoto T., Kajiuura H.,
RA  Nagahama Y.;
RT  "Molecular cloning and immunological analysis of goldfish cyclin A
RT  during oocyte maturation.";
RL  Dev. Biol. 170:616-625(1995).
CC  -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF THE CELL CYCLE AT THE
CC  G1/S (START) AND G2/M (MITOSIS) TRANSITIONS (BY SIMILARITY).
CC  -1- SUBUNIT: INTERACTS WITH THE CDK2 AND THE CDK2 PROTEIN KINASES TO
CC  FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN
CC  SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX (BY
CC  SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN A1 SUBFAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; S79215; AAB35103.1; -;
DR  HSSP; P20248; LJSU.
DR  InterPro; IPR004366; Cyclin.
DR  InterPro; IPR004367; Cyclin_Cterm.
DR  Pfam; PF00134; cyclin; 1.
DR  Pfam; PF02984; cyclin_C; 1.
DR  SMART; SM00385; CYCLIN; 2.
DR  PROSITE; PS00292; CYCLINS; 1.
KW  Cyclin; Cell cycle; Cell division; Mitosis.
SQ  SEQUENCE 391 AA; 43594 MW; 00402E02AFCB45F3 CRC64;

Query Match      78.0%; Score 32; DB 1; Length 391;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  2 YSFTGY 7
Db  335 YAFYGY 340

RESULT 26
HFEL_HAEIN          STANDARD;          PRT;   435 AA.
ID  HFEL_HAEIN
AC  P45954;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  Minor fimbrial subunit hife precursor.
GN  HIFE.
OS  Haemophilus influenzae.
OC  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC  Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=Eagan / Serotype B;
RX  MEDLINE=95012708; PubMed=7927773;
RA  McCrea K.W., Watson W.J., Gileford J.R., Marrs C.F.;
RT  "Identification of hife and hife in the pilus gene cluster of
RT  Haemophilus influenzae type b strain Eagan.";
RL  Infect. Immun. 62:4922-4928(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  STRAIN=AM30 (770235) / Serotype B;
RX  MEDLINE=95089703; PubMed=799179;
RA  van Ham M.S., van Alphen L., Mooi F.R., van Putten J.P.M.;
RT  "The fimbrial gene cluster of Haemophilus influenzae type b.";
RL  Mol. Microbiol. 13:673-684(1994).
CC  -1- FUNCTION: MAY BE A MINOR STRUCTURAL PROTEIN REQUIRED FOR PILUS
CC  BIOGENESIS. MAY BE THE ADHESIVE COMPONENT IN THE PILI.
```

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CC -!- SIMILARITY: TO B.PERTUSSIS FIMD AND E.COLI FIMH
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CC -----
CC EMBL; U13254; AAA61542.1; -
CC EMBL; Z33502; CAA83904.1; -
CC InterPro; IPR000259; Fimbril.
CC Pfam; PF00419; Fimbril; 1.
CC Fimbril; Signal.
CC FT SIGNAL 1 31 POTENTIAL.
CC FT CHAIN 32 435 MINOR FIMBRIAL SUBUNIT HIFE.
CC SQ SEQUENCE 435 AA; 48851 MW; 420C733661DE7D67 CRC64;
CC -----
CC Query Match 78.0%; Score 32; DB 1; Length 435;
CC Best Local Similarity 71.4%; Pred. No. 89;
CC Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 GYSFTGY 7
CC |||||
CC Db 107 GYSFAGF 113
CC -----
CC RESULT 27
CC GARD_BACSU STANDARD; PRT; 510 AA.
CC ID_GARD_BACSU STANDARD; PRT; 510 AA.
CC AC P42240; P42241;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Probable D-galactarate dehydratase (EC 4.2.1.42) (GalCD)
CC GN GARD.
CC OS Bacillus subtilis.
CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC OX NCBI_TaxID=1423;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=168;
CC RX MEDLINE=95219079; PubMed=7704254;
CC RA Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
CC RT "Determination of a 21548 bp nucleotide sequence around the 24
CC RL Microbiology 141:269-275(1995).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=168;
CC RX MEDLINE=98044033; PubMed=9384377;
CC RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
CC RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
CC RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
CC RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
CC RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
CC RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
CC RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
CC RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
CC RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
CC RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
CC RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
CC RA Joris B., Karamata D., Kaahara Y., Klaerr-Blanchard M., Klein C.,
CC RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
CC RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
CC RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
CC RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
CC RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudaga B., Park S.H.,
CC RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
CC RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
CC RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
CC RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
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RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Solido B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandendol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yamamoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: D-galactarate = 5-dehydro-4-deoxy-D-glucarate
CC + H(2)O.
CC -!- PATHWAY: FIRST STEP IN THE METABOLISM OF D-GALACTARATE.
CC -!- SIMILARITY: BELONGS TO THE UXAA FAMILY.
CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
CC FRAMESHIFTS.
CC -----
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CC -----
CC EMBL; D30808; BAA06472.1; ALT_FRAME.
CC EMBL; D30808; BAA06473.1; ALT_FRAME.
CC EMBL; Z99105; CABI2045.1; -
CC Subtilist; BG1163; gard.
CC Lyase; Complete proteome.
CC SQ SEQUENCE 510 AA; 54792 MW; C7283A007174CDE3 CRC64;
CC -----
CC Query Match 78.0%; Score 32; DB 1; Length 510;
CC Best Local Similarity 71.4%; Pred. No. 18+02;
CC Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 GYSFTGY 7
CC |||||
CC Db 115 GYTFEGY 121
CC -----
CC RESULT 28
CC GARD_ECOLI STANDARD; PRT; 523 AA.
CC ID_GARD_ECOLI STANDARD; PRT; 523 AA.
CC AC P39829;
CC DT 01-FEB-1995 (Rel. 31, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE D-galactarate dehydratase (EC 4.2.1.42) (GalCD)
CC GN GARD OR B3128.
CC OS Escherichia coli.
CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC OC Escherichia.
CC OX NCBI_TaxID=562;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=K12 / MG1655;
CC RX MEDLINE=97426617; PubMed=9278503;
CC RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
CC RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
CC RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
CC RA Mau B., Shao Y.;
CC RT "The complete genome sequence of Escherichia coli K-12.";
CC RL Science 277:1453-1474(1997).
CC [2]
CC SEQUENCE OF 449-523 FROM N.A.
CC RP MEDLINE=90170878; PubMed=2407727;
CC RX Baird L., Georgopoulos C.;
CC RA "Identification, cloning, and characterization of the Escherichia
CC RT coli sodA gene, a suppressor of the hcrA (desp) null phenotype.";
CC RL J. Bacteriol. 172:1587-1594(1990).
CC [3]
CC RN IDENTIFICATION.
```

RA Rudd K.E.;  
RL Unpublished observations (DEC-1994).  
RN [4]  
RX CHARACTERIZATION.  
RA MEDLINE=98447507; PubMed=9772162;  
RA Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;  
RT "Evolution of enzymatic activities in the enolase superfamily:  
RT characterization of the (D)-glucarate/galactarate catabolic pathway  
RT in *Escherichia coli*.";  
RL Biochemistry 37:14369-14375(1998).  
RN [5]  
RP GENE NAME.  
RX MEDLINE=2025875; PubMed=10762278;  
RA Monterrubio R., Baldona L., Obradors N., Aguilar J., Badia J.;  
RT "A common regulator for the operons encoding the enzymes involved in  
RT D-galactarate, D-glucarate, and D-glycerate utilization in  
RT *Escherichia coli*.";  
RL J. Bacteriol. 182:2672-2674(2000).  
CC -!- CATALYTIC ACTIVITY: D-galactarate = 5-dehydro-4-deoxy-D-glucarate  
CC + H(2)O.  
CC -!- PATHWAY: FIRST STEP IN THE METABOLISM OF D-GALACTARATE.  
CC -!- SIMILARITY: BELONGS TO THE UKAA FAMILY.  
CC  
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CC  
CC EMBL; U18997; AAA57931.1; -  
DR EMBL; AE000394; AAC76162.1; -  
DR EMBL; M30178; -; NOT ANNOTATED\_CDS.  
DR EcoGene; EG12522; garD.  
KW Lyase; Complete proteome.  
SQ SEQUENCE 523 AA; 56401 MW; 919BC8B49411BB0 CRC64;  
  
Query Match 78.0%; Score 32; DB 1; Length 523;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
Db 117 GYTFEGY 123  
  
RESULT 29  
MANC\_PIRSP STANDARD; PRT; 569 AA.  
AC P55238;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Mannan endo-1,4-beta-mannosidase C precursor (EC 3.2.1.78) (Beta-  
DE mannanase C) (1,4-beta-D-mannan mannanohydrolase C).  
GN MANC.  
OS Piromyces sp.  
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;  
OC Neocallimastixaceae; Piromyces.  
OX NCBI\_TaxID=45796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96313314; PubMed=8768520;  
RA Millward-Sadler S.J., Hall J., Black G.W., Hazlewood G.P.,  
RA Gilbert H.J.;  
RT "Evidence that the Piromyces gene family encoding endo-1,4-mannanases  
RT arose through gene duplication.";  
RL FEMS Microbiol. Lett. 141:183-188(1996).  
CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic  
CC linkages in mannans, galactomannans, glucomannans, and  
CC galactoglucomannans.  
CC -!- SIMILARITY: THE 39 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANC

CC AND XYNA; AND TO THOSE OF N.PATRICIARUM XYNA.  
CC -!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.  
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CC  
CC EMBL; X97520; CAA66134.1; -  
DR InterPro; IPR002883; CBD 5.  
DR InterPro; IPR000805; Glyco\_hydro 26.  
DR InterPro; IPR001230; Prenyl\_site.  
DR Pfam; PF02013; CBM 10; 2.  
DR Pfam; PF02156; Glyco\_hydro 26; 1.  
DR PRINTS; PR00739; GLYDRLASE26.  
KW Hydrolase; Glycosidase; Signal; Multigene family; Repeat.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 569 MANNAN ENDO-1,4-BETA-MANNOSIDASE C.  
FT DOMAIN 490 569 2 X 39 AA APPROXIMATE REPEATS.  
FT REPEAT 488 525 1.  
FT REPEAT 531 569 2.  
FT DOMAIN 473 477 POLY-ASN.  
FT DOMAIN 480 486 POLY-ASN.  
SQ SEQUENCE 569 AA; 64115 MW; 1927764E18328B5 CRC64;  
  
Query Match 78.0%; Score 32; DB 1; Length 569;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYSFTGY 7  
Db 41 GISGTCY 47  
  
RESULT 30  
HV44\_MOUSE STANDARD; PRT; 115 AA.  
ID HV44\_MOUSE  
AC P01820;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region PJ14 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81012133; PubMed=6774258;  
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;  
RT "Two types of somatic recombination are necessary for the generation  
RT of complete immunoglobulin heavy-chain genes.";  
RL Nature 286:676-683(1980).  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; V00767; CAA24148.1; -  
DR PIR; A02095; HVMS14.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.

```
FT SIGNAL 1 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION P014.
FT NON TER 115
SQ SEQUENCE 115 AA; 12447 MW; 7569DDA4A843D500 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 115;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 45 GFSLTGY 51

RESULT 31
HV12_MOUSE STANDARD; PRT; 117 AA.
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424 (1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON TER 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYTFTDY 32

RESULT 32
HV13_MOUSE STANDARD; PRT; 117 AA.
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=80078170; PubMed=6765983;
RX SEQUENCE.

RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RA "Amino acid sequence of homogeneous antibodies to dextran and DNA
RA rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40 (1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON TER 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYTFTDY 32

RESULT 33
HV14_MOUSE STANDARD; PRT; 117 AA.
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430 (1981).
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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CC or send an email to license@isb-sib.ch).
DR PIR; A02041; HVMS8A.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON TER 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 117;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
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Db 45 GYFTDY 51
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RESULT 34
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MEMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
FT SEQUENCE 118 AA; 12934 MW; 94FTBEE4C762A018 CRC64;
Query Match 75.6%; Score 31; DB 1; Length 118;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYSFTGY 7
Db 26 GYFTDY 32
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Query Match 75.6%; Score 31; DB 1; Length 118;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYSFTGY 7
Db 26 GYFTDY 32
-----
RESULT 35
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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-----
EMBL; U18779; AAB64997.1; -
PIR; S30832; S30832.
SGD; S0000771; YEL045C.
KW Hypothetical protein; ATP-binding; Transmembrane.
FT NP BIND 15 22 ATP (POTENTIAL).
FT TRANSMEM 38 58 POTENTIAL.
FT TRANSMEM 67 87 POTENTIAL.
FT SEQUENCE 141 AA; 16468 MW; F6604AC5343ASD5C CRC64;
Query Match 75.6%; Score 31; DB 1; Length 141;
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EMBL; J00494; AAA38130.1; -
DR PIR; A02042; HVMSB1.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
FT SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
Query Match 75.6%; Score 31; DB 1; Length 136;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYSFTGY 7
Db 45 GYFTDY 51
-----
RESULT 36
YEF5_YEAST
ID YEF5_YEAST STANDARD; PRT; 141 AA.
AC P32616;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 16.5 kDa protein in GLY1-GDA1 intergenic region.
GN YEL045C OR SYGP-ORF33.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
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-----
EMBL; U18779; AAB64997.1; -
PIR; S30832; S30832.
SGD; S0000771; YEL045C.
KW Hypothetical protein; ATP-binding; Transmembrane.
FT NP BIND 15 22 ATP (POTENTIAL).
FT TRANSMEM 38 58 POTENTIAL.
FT TRANSMEM 67 87 POTENTIAL.
FT SEQUENCE 141 AA; 16468 MW; F6604AC5343ASD5C CRC64;
Query Match 75.6%; Score 31; DB 1; Length 141;
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Best Local Similarity 83.3%; Pred. No. 46;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSFTGY 7  
Db 62 YSFTGF 67

RESULT 37  
HV43\_MOUSE STANDARD; PRT; 144 AA.  
AC P01819;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE IG heavy chain V region MOPC 141 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81012133; PubMed=6774258;  
RA Sakano H., Maki R., Kuroawa Y., Roeder W., Tonegawa S.;  
RT "Two types of somatic recombination are necessary for the generation  
of complete immunoglobulin heavy-chain genes.";  
RL Nature 286:676-683 (1980).  
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A  
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.  
CC  
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CC  
CC EMBL; V00768; CAA24149.1; --  
DR PIR; A02094; G2MS14.  
DR HSP; P01825; 7FAB.  
DR InterPro; IPR0031006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.  
FT NON TER 144 144  
FT SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;  
SQ

Query Match 75.6%; Score 31; DB 1; Length 144;  
Best Local Similarity 71.4%; Pred. No. 47;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 45 GFSLTGY 51

RESULT 38  
CRB3\_BOVIN STANDARD; PRT; 210 AA.  
AC P19141; O18790;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Beta crystallin B3 (Beta-B3-crystallin).  
GN CRYBB3.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shih M., Lampi K.J., Shearer T.R., David L.L.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Lens cortex;  
RX MEDLINE=84132067; PubMed=6698025;  
RA Berbers G.A.M., Hoekman W.A., Bloemendal H., de Jong W.W.,  
RA Kleinschmidt T., Braunitzer G.;  
RT "Homology between the primary structures of the major bovine beta-  
crystallin chains.";  
RL Eur. J. Biochem. 139:467-479 (1984)  
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS  
OF THE VERTEBRATE EYE LENS.  
CC -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE  
STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED  
THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).  
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR  
VERY SIMILAR GREEK KEY MOTIFS.  
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.  
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CC  
CC EMBL; AF013259; AAB67120.1; --  
DR PIR; B27898; B27898.  
DR HSP; P02522; 2BB2.  
DR InterPro; IPR001064; Crystallin.  
DR Pfam; PF00030; Crystall; 2.  
DR PRINTS; PR01367; BGCYSTALLIN.  
DR SMART; SM00247; XTALbg; 2.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 4.  
KW Eye lens protein; Repeat.  
FT INIT MET 0 0  
FT MOD RES 1 1 BLOCKED.  
FT DOMAIN 1 22 N-TERMINAL ARM.  
FT DOMAIN 23 62 MOTIF 1.  
FT DOMAIN 63 108 MOTIF 2.  
FT DOMAIN 109 112 CONNECTING PEPTIDE.  
FT DOMAIN 113 154 MOTIF 3.  
FT DOMAIN 155 198 MOTIF 4.  
FT DOMAIN 199 210 C-TERMINAL ARM.  
FT CONFLICT 21 21 G -> GG (IN REF. 2).  
FT CONFLICT 25 26 VI -> IV (IN REF. 2).  
FT CONFLICT 38 38 C -> S (IN REF. 2).  
FT CONFLICT 50 50 S -> A (IN REF. 2).  
FT CONFLICT 70 70 R -> Q (IN REF. 2).  
FT CONFLICT 92 93 SN -> NG (IN REF. 2).  
FT CONFLICT 97 101 SDSLL -> QDNLS (IN REF. 2).  
FT CONFLICT 106 107 LH -> IK (IN REF. 2).  
FT CONFLICT 110 110 G -> GH (IN REF. 2).  
FT CONFLICT 116 116 H -> G (IN REF. 2).  
FT CONFLICT 120 124 NPAPG -> HPNPA (IN REF. 2).  
FT CONFLICT 181 182 NE -> DD (IN REF. 2).  
FT CONFLICT 186 186 N -> Q (IN REF. 2).  
FT CONFLICT 208 208 L -> LG (IN REF. 2).  
SQ SEQUENCE 210 AA; 24197 MW; 9D1C68B93C9966EC CRC64;

Query Match 75.6%; Score 31; DB 1; Length 210;  
Best Local Similarity 71.4%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
Db 159 GYFPGY 165

Query Match	75.6%	Score 31;	DB 1;	Length 211;
Best Local Similarity	71.4%;	Pred. No. 67;		
Matches	5;	Conservative	0;	Mismatches
			2;	Indels
				Gaps
				0;

```

RN [1]
RP SEQUENCE FROM N.A.
RA Graw J.;
RT "Sequence analysis of beta-A2-, beta-A4- and beta-B3-crystallin cDNA
RT completes the identification of the members of this gene family in the
RT mouse."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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CC -----
CC EMBL; AJ272229; CAB75587.1; -
CC HSP; P02522; 2BB2
CC MGD; MGI102717; Crybb3.
CC InterPro; IPR001064; Crystallin.
CC Pfam; PFO030; crystall; 2.
CC PRINTS; PR01367; BGCYSTALLIN.
CC SMART; SM00247; XTALbg; 2.
CC PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 4.
KW Eye lens protein; Repeat; Acetylation.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 1 23 N-TERMINAL ARM.
FT DOMAIN 24 63 MOTIF 1.
FT DOMAIN 64 109 MOTIF 2.
FT DOMAIN 110 113 CONNECTING PEPTIDE.
FT DOMAIN 114 155 MOTIF 3.
FT DOMAIN 156 199 MOTIF 4.
FT DOMAIN 200 211 C-TERMINAL ARM.
SQ SEQUENCE 211 AA; 24291 MW; 2F23F47987102196 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 211;
Best Local Similarity 71.4%; Pred.No. 67;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 160 GYEFGY 166

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Search completed: July 18, 2003, 15:07:15  
 Job time : 6.34 secs

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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:40 ; Search time 18.06 Seconds  
(without alignments)  
79.863 Million cell updates/sec

Title: US-10-007-790-5

Perfect score: 41 GYSFTGY 7

Sequence: 1 GYSFTGY 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	120	11	Q920E8	Q920E8 mus musculus
2	41	100.0	123	11	Q8VIJ1	Q8VIJ1 mus musculus
3	41	100.0	457	5	O60994	O60994 leishmania
4	38	92.7	119	4	Q9UL94	Q9UL94 homo sapien
5	38	92.7	119	5	Q9GVZ2	Q9GVZ2 schistosoma
6	38	92.7	125	4	Q9UL95	Q9UL95 homo sapien
7	38	92.7	463	11	Q9SLC4	Q9SLC4 mus musculus
8	37	90.2	173	3	O13572	O13572 saccharomyc
9	37	90.2	239	2	Q9ANJ6	Q9ANJ6 brachyrihizob
10	36	87.8	246	17	Q979R4	Q979R4 thermoplasm
11	36	87.8	862	17	Q9V0Q6	Q9V0Q6 pyrococcus
12	35	85.4	114	11	Q9JL81	Q9JL81 mus musculus
13	35	85.4	117	11	Q9Z1C6	Q9Z1C6 mus musculus
14	34	82.9	122	10	Q9M0D5	Q9M0D5 arabidopsis
15	34	82.9	122	10	O82209	O82209 arabidopsis
16	34	82.9	122	10	Q9STR3	Q9STR3 arabidopsis

17	34	82.9	128	17	Q96X81	Q96X81 sulfolobus
18	34	82.9	257	11	Q9IX94	Q9IX94 mus musculus
19	34	82.9	301	4	Q96IM0	Q96IM0 homo sapien
20	34	82.9	301	11	Q9Z130	Q9Z130 mus musculus
21	34	82.9	403	2	Q9F750	Q9F750 bacteroides
22	34	82.9	420	4	O14979	O14979 homo sapien
23	34	82.9	446	16	Q9S115	Q9S115 streptococc
24	34	82.9	2183	12	Q64962	Q64962 apple stem
25	34	82.9	2185	12	Q9E948	Q9E948 apple stem
26	33	80.5	460	16	Q8VED0	Q8VED0 bruceella me
27	33	80.5	505	16	Q92F18	Q92F18 listeria in
28	33	80.5	548	2	Q9EXF6	Q9EXF6 listeria mo
29	33	80.5	548	2	O33931	O33931 listeria mo
30	33	80.5	548	16	Q9ZEY1	Q9ZEY1 listeria mo
31	33	80.5	567	2	O33932	O33932 listeria in
32	33	80.5	596	16	Q92E00	Q92E00 mycobacteri
33	33	80.5	678	16	P71707	P71707 mycobacteri
34	33	80.5	797	5	Q9XUI7	Q9XUI7 caenorhabdi
35	33	80.5	812	3	O60159	O60159 schizosacch
36	33	80.5	820	16	Q8VKSS	Q8VKSS mycobacteri
37	33	80.5	1023	5	Q95Z93	Q95Z93 leishmania
38	33	80.5	1031	5	O09489	O09489 leishmania
39	33	80.5	1645	16	Q97MX7	Q97MX7 clostridium
40	32	78.0	61	16	Q8R8E7	Q8R8E7 thermoanaer
41	32	78.0	109	11	Q9UL75	Q9UL75 mus musculus
42	32	78.0	137	11	Q924R6	Q924R6 mus musculus
43	32	78.0	139	11	Q924R5	Q924R5 mus musculus
44	32	78.0	140	11	Q924R2	Q924R2 mus musculus
45	32	78.0	140	11	Q924P8	Q924P8 mus musculus

#### ALIGNMENTS

##### RESULT 1

Q920E8 ID Q920E8 PRELIMINARY; PRT; 120 AA.  
AC Q920E8;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-WAR-2002 (Tremblrel. 20, Last annotation update)  
DE Pterin-mimicking anti-idiotope heavy chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307936; AAL09420.1; -;  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; ig; 1.  
FT NON\_TER 1  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;

Query Match 100.0%; Score 41; DB.11; Length 120;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7  
DB 26 GYSFTGY 32

##### RESULT 2

Q8VIJ1 PRELIMINARY; PRT; 123 AA.  
ID Q8VIJ1  
AC Q8VIJ1;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Anti-DNA heavy chain (Fragment).  
 GN J558.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/HEJ-LPR/LPR;  
 RX MEDLINE=96409289; PubMed=8814271;  
 RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;  
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among  
 RL anti-DNA from C3H-lpr mice and lupus mice with nephritis.";  
 DR Eur. J. Immunol. 26:2225-2233(1996).  
 DR EMBL; U59154; AAB02916.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003599; Ig.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 FT NON\_TER 1  
 FT NON\_TER 123  
 SQ SEQUENCE 123 AA; 13806 MW; CC0037A806F9911E CRC64;

Query Match 100.0%; Score 41; DB 11; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 DB 26 GYSFTGY 32

RESULT 3  
 ID O60994 PRELIMINARY; PRT; 457 AA.  
 AC O60994;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Chitinase.  
 GN Chi-1.  
 OS Leishmania donovani.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5661;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shakarian A.M., Dwyer D.M.;  
 RT "Characterization and expression of a gene encoding the chitinase of  
 RL Leishmania donovani";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF009354; AAC17944.1; -.  
 DR InterPro; IPR001579; Chitinase\_18/2.  
 DR InterPro; IPR001223; Glyco\_hydro\_18.  
 DR Pfam; PF00704; Glyco\_hydro\_18; 1.  
 DR ProDom; PD000471; Glyco\_hydro\_18; 1.  
 DR PROSITE; PS01095; CHITINASE\_18; UNKNOWN 1.  
 SQ SEQUENCE 457 AA; 50454 MW; EC68AE4329AD9D45 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 457;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 DB 364 GYSFTGY 370

RESULT 4

Q9UL94  
 ID Q9UL94 PRELIMINARY; PRT; 119 AA.  
 AC Q9UL94;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035020; AAD58256.1; -.  
 DR HSSP; P01810; 2FBU.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 FT NON\_TER 1  
 FT NON\_TER 119  
 SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345F4A16E CRC64;

Query Match 92.7%; Score 38; DB 4; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 6.4;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 DB 26 GYSFTGY 32

RESULT 5  
 ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.  
 AC Q9GYZ2;  
 DT 01-WAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region  
 DE (Fragment).  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Song X.T., Feng Z.Q., Guan X.H.;  
 RT "Amplification, cloning and sequence analysis of the heavy chain  
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
 RL Schistosoma japonicum";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF282622; AAG01452.1; -.  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003600; Ig\_like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR PRINTS; PR01573; SUPERTUBBY.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR SMART; SM00410; IG\_like; 1.  
 FT NON\_TER 1  
 FT NON\_TER 119  
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

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Query Match          92.7%; Score 38; DB 5; Length 119;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYTFTGY 32

RESULT 6
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 125 125
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match          92.7%; Score 38; DB 4; Length 125;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYTFTGY 32

RESULT 7
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; IGH-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00407; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match          92.7%; Score 38; DB 11; Length 463;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 45 GYTFTGY 51

RESULT 8
O13572 PRELIMINARY; PRT; 173 AA.
AC O13572;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE YPR150WP.
GN YPR150W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoerge W.,
RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
RA Follis H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,
RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
RA Heumann K., Hilbert H., Hillier L., Hunkle-Smith S., Hyman R.,
RA Johnston M., Kalman S., Kleene K., Komp C., Kurdi O., Lashkari D.,
RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
RA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,
RA Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.
RA Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,
RA Schroeder M., Sdicu A.M., Tettelin H., Urrestazu L.A., Ushinsky S.,
RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
RA Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Fulton L.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Halloworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
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RA Jia Y., Cherry J.M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00829; AAB68295.1; -.
DR SGD; S0006354; YPR150W.
SQ SEQUENCE 173 AA; 19321 MW; DB830B5335F22DB1 CRC64;

Query Match          90.2%; Score 37; DB 3; Length 173;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 135 GFSFTGY 141

RESULT 9
Q9ANJ6 PRELIMINARY; PRT; 239 AA.
AC Q9ANJ6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ID170.
GN ID170.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL; AF322012; AAG60774.1; -.
SQ SEQUENCE 239 AA; 27386 MW; 719BB59C815165F4 CRC64;

Query Match          90.2%; Score 37; DB 2; Length 239;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 182 GFSFTGY 188

RESULT 10
Q979R4 PRELIMINARY; PRT; 246 AA.
AC Q979R4
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pseudouridylylate synthase 1.
GN TV1096 OR TVG1128771.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Anano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000995; BAB60238.1; -.

Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
EMBL; U00829; AAB68295.1; -.
SGD; S0006354; YPR150W.
SEQUENCE 173 AA; 19321 MW; DB830B5335F22DB1 CRC64;

Query Match          90.2%; Score 37; DB 3; Length 173;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 135 GFSFTGY 141

RESULT 9
Q9ANJ6 PRELIMINARY; PRT; 239 AA.
AC Q9ANJ6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ID170.
GN ID170.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL; AF322012; AAG60774.1; -.
SQ SEQUENCE 239 AA; 27386 MW; 719BB59C815165F4 CRC64;

Query Match          90.2%; Score 37; DB 2; Length 239;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 182 GFSFTGY 188

RESULT 10
Q979R4 PRELIMINARY; PRT; 246 AA.
AC Q979R4
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pseudouridylylate synthase 1.
GN TV1096 OR TVG1128771.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Anano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000995; BAB60238.1; -.

DR InterPro; IPR001406; PseudoU synth 1.
DR Pfam; PF01416; PseudoU synth_1; 1.
DR Complete proteome.
SQ SEQUENCE 246 AA; 28352 MW; 124AECE9BBED1218 CRC64;

Query Match          87.8%; Score 36; DB 17; Length 246;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 13 GYMFTGY 19

RESULT 11
Q9V0Q6 PRELIMINARY; PRT; 862 AA.
AC Q9V0Q6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAB1881.
GN PAB1881.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence; insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248285; CAB49647.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 862 AA; 98273 MW; 722D1DBE2148603D CRC64;

Query Match          87.8%; Score 36; DB 17; Length 862;
Best Local Similarity 85.7%; Pred. No. 14e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 369 GYSFVG 375

RESULT 12
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
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DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match      85.4%; Score 35; DB 11; Length 114;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 18 GYSFTSY 24

RESULT 13
Q921C6 PRELIMINARY; PRT; 117 AA.
AC Q921C6;
DC Q921C6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-porcine VCAM mab 2A2 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT endothelial cells";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78799; AAD00291.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77B5B CRC64;

Query Match      85.4%; Score 35; DB 11; Length 117;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 26 GYSFTSY 32

RESULT 14
Q9M0D5 PRELIMINARY; PRT; 122 AA.
AC Q9M0D5;
DC Q9M0D5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 13.9 kDa protein (AT4G29480/F17A13_300).
GN AT4G29480.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eusoids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
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RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene F17A13_300/AT4G29480 (GI:7269847).";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene F17A13_300/AT4G29480 (GI:7269847).";
RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RN Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RN Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
* DR EMBL; AL161575; CAB79706.1; -.
DR EMBL; AF326889; AAG41471.1; -.
DR EMBL; AF339706; AAK00388.1; -.
DR EMBL; AY054144; AAL06805.1; -.
DR EMBL; AY039587; AAK62642.1; -.
KW Hypothetical protein.
SQ SEQUENCE 122 AA; 13940 MW; D0AA4E25852207B5 CRC64;

Query Match      82.9%; Score 34; DB 10; Length 122;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 114 GFTFTGY 120

RESULT 15
O82209 PRELIMINARY; PRT; 122 AA.
ID O82209;
AC O82209;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Copia-like retroelement pol polyprotein.
GN AT2G19680 OR AT2G19680, F6F22.29.
OS Arabidopsis thaliana (Mouse-ear cross).
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhaver G.P., Preuss D., Nieman W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Frazer C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 402:761-768 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RA Lin X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC005169; AAC62147.1; -;  
 DR EMBL; AF370542; AAK48969.1; -;  
 DR EMBL; AY072517; AAL66932.1; -;  
 KW Polyprotein.  
 SQ SEQUENCE 122 AA; 13847 MW; 09E6355930E82A51 CRC64;  
 Query Match 82.9%; Score 34; DB 10; Length 122;  
 Best Local Similarity 71.4%; Pred. No. 38;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 Db 114 GFTFTGY 120  
 RESULT 16  
 ID Q9STR3 PRELIMINARY; PRT; 122 AA.  
 AC Q9STR3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical 13.9 KDa protein.  
 GN T25K17.20 OR AT4G26210.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Koettler P., Hempel S., Entian K.-D., Bancroft I.,

RA Mewes H.W., Mayer K.F.X., Schueller C.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G.,  
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,  
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,  
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,  
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 RL "Full Length cDNA of gene AT4G26210.";  
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Lee J.M., Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wu H.C.,  
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,  
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,  
 RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RT "Full Length cDNA of gene AT4G26210.";  
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL049171; CAB38950.1; -;  
 DR EMBL; AL161564; CAB79476.1; -;  
 DR EMBL; AF370342; AAK44157.1; -;  
 DR EMBL; AY063002; AAL34176.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 122 AA; 13869 MW; DF854368DD4AF6AF CRC64;  
 Query Match 82.9%; Score 34; DB 10; Length 122;  
 Best Local Similarity 71.4%; Pred. No. 38;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYSFTGY 7  
 Db 114 GFTFTGY 120  
 RESULT 17  
 ID Q96X81 PRELIMINARY; PRT; 128 AA.  
 AC Q96X81;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical protein ST2629.  
 GN ST2629.  
 OS Sulfolobus tokodaii.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxID=111955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JCM 10545 / 7;  
 RX PubMed=11572479;  
 RA Kawarayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
 RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,  
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

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RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yanagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000390; BAB67747.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 128 AA; 15109 MW; 9D81AA58DA521885 CRC64;

Query Match      82.9%; Score 34; DB 17; Length 128;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
   ||:||||
Db 2 GYGVTGY 8

RESULT 18
Q91X94 PRELIMINARY; PRT; 257 AA.
AC Q91X94;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to heterogeneous nuclear ribonucleoprotein D (AU-rich
DE element RNA-binding protein 1, 37kD).
GN HNRPD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011172; AAH11172.1; -.
DR MGD; MGI:101947; Hnrpd.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 2.
DR PROSITE; PS0102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2.
KW Nucleocapsid; Ribonucleoprotein.
SQ SEQUENCE 257 AA; 29283 MW; 043CC8A52329ACD CRC64;

Query Match      82.9%; Score 34; DB 11; Length 257;
Best Local Similarity 71.4%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
   ||:||||
Db 219 GYDTGY 225

RESULT 19
Q96IMO PRELIMINARY; PRT; 301 AA.
AC Q96IMO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein D-like.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC007392; AAH07392.1; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 2.
DR PROSITE; PS0102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2.
KW Nucleocapsid; Ribonucleoprotein.
SQ SEQUENCE 301 AA; 33589 MW; 6BF76C3AEB682BAD CRC64;

Query Match      82.9%; Score 34; DB 4; Length 301;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
   ||:||||
Db 257 GYDTGY 263

RESULT 20
Q92I30 PRELIMINARY; PRT; 301 AA.
AC Q92I30;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE JKTBP (Heterogeneous nuclear ribonucleoprotein D-like).
GN HNRPD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183688; PubMed=10717477;
RA Akagi T., Kamei D., Tsuchiya N., Nishina Y., Horiguchi H., Matsui M.,
RA Kamma H., Yamada M.;
RT "Molecular characterization of a mouse heterogeneous nuclear
RT ribonucleoprotein D-like protein JKTBP and its tissue-specific
RT expression.";
RL Gene 245:267-273(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207031; PubMed=9538234;
RA Tsuchiya N., Kamei D., Takano A., Matsui T., Yamada M.;
RT "Cloning and Characterization of a cDNA Encoding a Novel Heterogeneous
RT Nuclear Ribonucleoprotein-Like Protein and Its Expression in Myeloid
RT Leukemia Cells.";
RL J. Biochem. 123:499-507(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017020; BAA75479.1; -.
DR EMBL; BC021374; AAH21374.1; -.
DR HSSP; P09651; IUP1.
DR MGD; MGI:1355299; Hnrpd.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS0102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2.
KW Nucleocapsid; Ribonucleoprotein.
SQ SEQUENCE 301 AA; 33559 MW; 8AB2787FEB73311C CRC64;

Query Match      82.9%; Score 34; DB 11; Length 301;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
   ||:||||
Db 257 GYDTGY 263

RESULT 21
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Q9F750 Q9F750 PRELIMINARY; PRT; 403 AA.
AC Q9F750;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative glycosyltransferase.
GN WGV.
OS Bacteroides fragilis.
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
OC Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIC 9343;
RX MEDLINE=20490546; PubMed=11035722;
RA Coyne M.J., Kalka-Moll W., Trianabos A.O., Kasper D.L., Comstock L.E.;
RT "Bacteroides fragilis NCTC9343 Produces at Least Three Distinct
RT Capsular Polysaccharides: Cloning, Characterization, and Reassignment
RT of Polysaccharide B and C Biosynthesis Loci.";
RL Infect. Immun. 68:6176-6181(2000).
DR EMBL; AF285774; AAG26480.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase.
SQ SEQUENCE 403 AA; 46120 MW; E722DC52275FBC13 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 403;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 48 GYSFWGY 54

RESULT 22
O14979 O14979 PRELIMINARY; PRT; 420 AA.
AC O14979;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE JKTBP2 (HnRNP JKTBP) (A+U-rich element RNA binding factor) (Similar to
DE heterogeneous nuclear ribonucleoprotein D-like).
GN JKTBP OR HnRNP JKTBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamei D., Tsuchiya N., Yamazaki M., Meguro H., Yamada M.;
RT "Two forms of expression and genomic structure of the human
RT heterogeneous nuclear ribonucleoprotein D-like JKTBP gene (HNRPDL).";
RL Gene 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207031; PubMed=9538234;
RA Tsuchiya N., Kamei D., Takano A., Matsui T., Yamada M.;
RT "Cloning and characterization of a cDNA encoding a novel heterogeneous
RT nuclear ribonucleoprotein-like protein and its expression in myeloid
RT leukemia cells.";
RL J. Biochem. 123:499-507(1998).
RN [3]
RP SEQUENCE OF 120-420 FROM N.A.
RA Tsuchiya N., Kamei D., Takano A., Matsui T., Yamada M.;
RL J. Biochem. 0:0-0(1998).
RN [4]
RP SEQUENCE OF 150-420 FROM N.A.
RA Doi A., Takaoka Y., Yanagisawa K., Shiosaka T., Fujita S.;
RL Biochim. Biophys. Acta 0:0-0(1997).
RN [5]
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RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017019; BAA75241.1; -.
DR EMBL; AB017018; BAA75239.1; -.
DR EMBL; D89092; BAA24361.1; -.
DR EMBL; D89678; BAA22860.1; -.
DR EMBL; AB017018; BAA75240.1; -.
DR EMBL; BC011714; AAH11714.1; -.
DR HSSP; P09651; IUP1.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; xtm; 2.
DR SMART; SM00360; REM; 2.
DR PROSITE; PS0102; REM; 3.
DR PROSITE; PS00030; REM_RNP_1; 2.
KW Nucleocapsid; Ribonucleoprotein.
SQ SEQUENCE 420 AA; 46437 MW; 00F631863859D0CA CRC64;

Query Match 82.9%; Score 34; DB 4; Length 420;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 376 GYDTGY 382

RESULT 23
Q9S115 Q9S115 PRELIMINARY; PRT; 446 AA.
ID Q9S115;
AC Q9S115;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Histidine kinase (BLPH protein) (Sensor histidine kinase BLPH,
DE putative).
GN HK13 OR IH OR BLPH OR SP0527.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99453779; PubMed=10524254;
RA Lange R., Wagner C., de Saizieu A.B., Flint N., Molinos J., Stieger M.,
RA Caspers P., Kamber M., Keck W., Amrein K.;
RT "Domain organization and molecular characterization of 13 two-
RT component systems identified by genome sequencing of S. pneumoniae.";
RL Gene 237:223-234(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KNR7/87;
RA Reichmann P., Hakenbeck R.;
RT "A Peptide Inducible Signal Transduction System in Streptococcus
RT pneumoniae: Evidence for Bacteriocin Production.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA de Saizieu A., Gardes C., Flint N., Wagner C., Kamber M.,
RA Mitchell T.J., Keck W., Amrein K.E., Lange R.;
RT "Microarray based identification of a novel Streptococcus pneumoniae
RT regulon controlled by an autoinduced peptide.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Unayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
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RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR ENBL; AJ006401; CAB54587.1; -.
DR ENBL; AJ278419; CAB18581.1; -.
DR ENBL; AJ276410; CAC03516.1; -.
DR ENBL; AE007364; AAK74685.1; -.
DR TIGR; SP0527; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF02518; HATPase_C; 1.
DR DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KW Kinase; Complete proteome.
SQ SEQUENCE 446 AA; 51824 MW; D8CBDCD28F5DF274C CRC64;

Query Match 82.9%; Score 34; DB 16; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTG 6
Db 119 GYSFTG 124

RESULT 24
Q64962
ID Q64962 PRELIMINARY; PRT; 2183 AA.
AC Q64962;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Viral RNA-dependent RNA polymerase.
OS Apple stem pitting virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.
OX NCBI_TaxID=35350;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ASPV;
RX MEDLINE=94292903; PubMed=8021584;
RA Jalkmann W.;
RT "Nucleotide sequences of apple stem pitting virus and of the coat
RT protein gene of a similar virus from pear associated with vein yellows
RT disease and their relationship with potex- and carlaviruses.";
RL J. Gen. Virol. 75:1535-1542(1994).
DR ENBL; D21829; BAA04853.1; -.
DR MEROPS; C23.001; -.
DR InterPro; IPR005123; 2OG-Fell_Oxy.
DR InterPro; IPR003323; OTU.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF03171; 2OG-Fell_Oxy; 1.
DR Pfam; PF02338; OTU; 1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR PROSITE; PS50802; OTU; 1.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 2183 AA; 247359 MW; 2156D7A75A548CC5 CRC64;

Query Match 82.9%; Score 34; DB 12; Length 2183;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTG 7
Db 732 GYSYTG 738

RESULT 25
Q9E948
ID Q9E948 PRELIMINARY; PRT; 2185 AA.
AC Q9E948;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RNA polymerase.
OS Apple stem pitting virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.
OX NCBI_TaxID=35350;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP38;
RA Yoshikawa N., Matsuda H., Oda Y., Isogai M., Takahashi T., Ito T.,
RA Yoshida K.;
RT "Genome heterogeneity of apple stem pitting virus in apple trees.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB045371; BAB15950.1; -.
DR MEROPS; C23.001; -.
DR InterPro; IPR005123; 2OG-Fell_Oxy.
DR InterPro; IPR003323; OTU.
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF03171; 2OG-Fell_Oxy; 1.
DR Pfam; PF02338; OTU; 1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR PROSITE; PS50802; OTU; 1.
SQ SEQUENCE 2185 AA; 247591 MW; 76DB4BB6FC202029 CRC64;

Query Match 82.9%; Score 34; DB 12; Length 2185;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTG 7
Db 732 GYSYTG 738

RESULT 26
Q8YED0
ID Q8YED0 PRELIMINARY; PRT; 460 AA.
AC Q8YED0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytosol aminopeptidase (EC 3.4.11.1).
GN BMEI1948.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L6M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Resnik G.,
RA Jablonov L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kypides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR ENBL; AE009628; AAL53129.1; -.
DR InterPro; IPR000819; Peptidase_M17.
DR Pfam; PF00883; Peptidase_M17; 1.
DR PRINTS; PR00481; LAMNOPPTDASE.
DR DR PROSITE; PS00631; CYTOSOL_AP; 1.
KW Hydrolase; Aminopeptidase; Complete proteome.
SQ SEQUENCE 460 AA; 48742 MW; B7559FB05F185412 CRC64;

Query Match 80.5%; Score 33; DB 16; Length 460;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR ENBL; AJ006401; CAB54587.1; -.
DR ENBL; AJ278419; CAB18581.1; -.
DR ENBL; AJ276410; CAC03516.1; -.
DR ENBL; AE007364; AAK74685.1; -.
DR TIGR; SP0527; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF02518; HATPase_C; 1.
DR DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KW Kinase; Complete proteome.
SQ SEQUENCE 446 AA; 51824 MW; D8CBDCD28F5DF274C CRC64;
```

Query Match 82.9%; Score 34; DB 16; Length 446;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTG 6  
Db 119 GYSFTG 124

RESULT 24  
Q64962  
ID Q64962 PRELIMINARY; PRT; 2183 AA.  
AC Q64962;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Viral RNA-dependent RNA polymerase.  
OS Apple stem pitting virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.  
OX NCBI\_TaxID=35350;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ASPV;  
RX MEDLINE=94292903; PubMed=8021584;  
RA Jalkmann W.;

RT "Nucleotide sequences of apple stem pitting virus and of the coat  
RT protein gene of a similar virus from pear associated with vein yellows  
RT disease and their relationship with potex- and carlaviruses.";

RL J. Gen. Virol. 75:1535-1542(1994).  
DR ENBL; D21829; BAA04853.1; -.  
DR MEROPS; C23.001; -.  
DR InterPro; IPR005123; 2OG-Fell\_Oxy.  
DR InterPro; IPR003323; OTU.  
DR InterPro; IPR001788; RNA\_dep\_RNAPol2.  
DR InterPro; IPR000606; Viral\_helicase1.  
DR Pfam; PF03171; 2OG-Fell\_Oxy; 1.  
DR Pfam; PF02338; OTU; 1.  
DR Pfam; PF00978; RNA\_dep\_RNAPol2; 1.  
DR Pfam; PF01443; Viral\_helicase1; 1.  
DR PROSITE; PS50802; OTU; 1.  
KW RNA-directed RNA polymerase.  
SQ SEQUENCE 2183 AA; 247359 MW; 2156D7A75A548CC5 CRC64;

Query Match 82.9%; Score 34; DB 12; Length 2183;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTG 7  
Db 732 GYSYTG 738

RESULT 25  
Q9E948  
ID Q9E948 PRELIMINARY; PRT; 2185 AA.

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RT monocytes EGD: characterization of the gene products InlF, InlD,
RT and InlJ and arrangement of the corresponding genes."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ012385; CAC20635.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 7.
DR SMART; SM00370; LRR; 5.
DR SMART; SM00369; LRR_TYP; 4.
SQ SEQUENCE 548 AA; 58552 MW; B0A192B18A414AEF CRC64;

Query Match 80.5%; Score 33; DB 2; Length 548;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 376 GYTFTGW 382

RESULT 29
O33931 PRELIMINARY; PRT; 548 AA.
ID O33931
AC O33931
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Internalin.
GN INLC2.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD;
RX MEDLINE=97270455; PubMed=9125538;
RA Dramai S., Dehoux P., Lebrun M., Goossens P.L., Cossart P.;
RT "Identification of four new members of the internalin multigene family
RL of Listeria monocytogenes EGD."
RL Infect. Immun. 65:1615-1625(1997).
DR EMBL; U77368; AAB67969.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR; 7.
DR SMART; SM00370; LRR; 2.
DR SMART; SM00370; LRR; 2.
SQ SEQUENCE 548 AA; 58631 MW; 4A36A8112C564872 CRC64;

Query Match 80.5%; Score 33; DB 2; Length 548;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
Db 376 GYTFTGW 382

RESULT 30
O9ZEY1 PRELIMINARY; PRT; 548 AA.
ID O9ZEY1
AC O9ZEY1
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Internalin H.
GN INLH OR LMO0263.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=EGD;
RX MEDLINE=99077282; PubMed=9862466;
RA Rafelsbauer D., Bubert A., Engelbrecht F., Scheinplug J., Simm A.,
RA Hess J., Kaufmann S.H.E., Goebel W.;
RT "The gene cluster inlC2DE of Listeria monocytogenes contains
RT additional new internalin genes and is important for virulence in
RT mice.";
RL Mol. Gen. Genet. 260:144-158 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-E / SEROVAR 1/2A;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species";
RL Science 294:849-852 (2001).
DR EMBL; AJ007319; CAA07457.1; -.
DR EMBL; AL591974; CAD00790.1; -.
DR Listlist; LMO00263; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR; 7.
DR SMART; SM00370; LRR; 2.
KW Complete proteome.
SQ SEQUENCE 548 AA; 58681 MW; 3EE34A05CAA1B88F CRC64;

Query Match 80.5%; Score 33; DB 16; Length 548;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 376 GYFTGW 382

RESULT 31
O33932 PRELIMINARY; PRT; 567 AA.
AC O33932
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE InlD protein.
GN InlD
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD;
RX MEDLINE=97270455; PubMed=9125538;
RA Dramsi S., Dehoux P., Lebrun M., Goossens P.L., Cossart P.;
RT "Identification of four new members of the internalin multigene family
RT of Listeria monocytogenes EGD.";
RL Infect. Immun. 65:1615-1625 (1997).
DR EMBL; U77368; AAB67970.1; -.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 7.
SQ SEQUENCE 567 AA; 61326 MW; F52C836CE8F3C4BE CRC64;

Query Match 80.5%; Score 33; DB 2; Length 567;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GYSFTGY 7
DB 395 GYFTGW 401

RESULT 32
Q92E00 PRELIMINARY; PRT; 596 AA.
ID Q92E00
AC Q92E00;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Internalin like protein (LPXTG motif).
GN InlN0661.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species";
RL Science 294:849-852 (2001).
DR EMBL; AL596165; CAC95893.1; -.
DR Listlist; LINO00661; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 10.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 596 AA; 66183 MW; 03AD790E5E069F1E CRC64;

Query Match 80.5%; Score 33; DB 16; Length 596;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGY 7
DB 490 GYFTGW 496

RESULT 33
P71707 PRELIMINARY; PRT; 678 AA.
ID P71707
AC P71707;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable penicillin-binding proteins 1A/1B (PBPI).
GN PONA OR RV0050 OR MTCY21.13.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

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RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Horneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence.";  
RL Nature 393:537-544 (1998).  
CC -1- FUNCTION: CELL WALL FORMATION.  
CC -1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.  
CC -1- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).  
CC -1- SIMILARITY: TO OTHER BACTERIAL CLASS 1A PENICILLIN-BINDING  
CC PROTEINS.  
DR EMBL; Z80775; CAB02529.1; -;  
DR Tuberculin; RV0050; -;  
DR InterPro; IPR001264; GT 51.  
DR InterPro; IPR001460; Transpeptidase.  
DR Pfam; PF00912; Transglycosyl; 1.  
DR Pfam; PF00905; Transpeptidase; 1.  
DR ProDom; PD001895; GT\_51; 1.  
KW Peptidoglycan synthesis; Cell wall; Transmembrane; Complete proteome.  
FT ACT SITE 347 347 ACYLATED BY PENICILLIN (BY SIMILARITY).  
FT DOMAIN 625 631 POLY-PRO.  
FT DOMAIN 664 670 POLY-PRO.  
SQ SEQUENCE 678 AA; 71150 MW; 01040BAC347B0E2 CRC64;  
Query Match 80.5%; Score 33; DB 16; Length 678;  
Best Local Similarity 71.4%; Pred. No. 4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 80 GFSFTGF 86  
RESULT 34  
Q9XUI7 PRELIMINARY; PRT; 797 AA.  
AC Q9XUI7;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ZC334.5 protein.  
GN ZC334.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McLaughlin K.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018 (1998).  
DR EMBL; Z82082; CAB04966.1; -;  
DR HSP; P37687; IFOV.  
DR InterPro; IPR002109; Glutaredoxin.  
DR PRINTS; PR00160; GUTAREDOXIN.  
SQ SEQUENCE 797 AA; 90812 MW; 43C58B2B64394698 CRC64;  
Query Match 80.5%; Score 33; DB 5; Length 797;  
Best Local Similarity 71.4%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 80 GFSFTGF 86

Db 689 GYSYVGY 695  
RESULT 35  
O60159 PRELIMINARY; PRT; 812 AA.  
AC O60159;  
DT 01-AUG-1998 (TReMBLrel. 07, Created)  
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Chloride channel.  
GN SPBCL19C7.11.  
OS Schizosaccharomyces pombe (Fission Yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972H-;  
RA Lyne M., Rajandream M.A., Barrell B.G., Lucas M., Gaillardin C.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL023859; CAAL19579.1; -;  
DR InterPro; IPR000644; CBS domain.  
DR InterPro; IPR001807; Cl-channel\_volt.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF00854; voltage CLC; 1.  
DR PRINTS; PR00762; CLCHANNEL.  
DR SMART; SM00116; CBS; 1.  
SQ SEQUENCE 812 AA; 90562 MW; B0BAA8CDB9F672D CRC64;  
Query Match 80.5%; Score 33; DB 3; Length 812;  
Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYSFTGY 7  
DB 649 GYDFSGY 655  
RESULT 36  
Q8VKSS PRELIMINARY; PRT; 820 AA.  
AC Q8VKSS;  
DT 01-MAR-2002 (TReMBLrel. 20, Created)  
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Penicillin-binding protein.  
GN MT0056.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / OSHKOSH;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB006918; AAK44278.1; -;  
DR TIGR; MT0056; -;  
DR InterPro; IPR001264; GT 51.  
DR InterPro; IPR001460; Transpeptidase.  
DR Pfam; PF00912; Transglycosyl; 1.  
DR Pfam; PF00905; Transpeptidase; 1.  
DR ProDom; PD001895; GT\_51; 1.  
SQ SEQUENCE 820 AA; 85977 MW; CA94D5D830332B1C CRC64;

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Query Match      80.5%; Score 33; DB 16; Length 820;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      222 GFSFTGF 228
      |:|||||:
      |:|||||:

RESULT 37
Q95293      Q95293      PRELIMINARY;      PRT; 1023 AA.
AC      Q95293;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Probable organelle-type calcium ATPase.
GN      Lt. 01.
OS      Leishmania major.
OC      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX      NCBI_TaxID=5664;
RN      [1]
RC      STRAIN=FRIEDLIN;
RA      Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D.,
RA      Rajandream M.A., Barrell B.G.;
RA      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=FRIEDLIN;
RX      MEDLINE=98146435; PubMed=9477341;
RA      Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA      Smith D.F.;
RT      "A physical map of the Leishmania major Friedlin genome.";
RL      Genome Res. 8:135-145 (1998).
DR      EMBL: AL389894; CAC44909.1;
DR      InterPro: IPR001757; ATPase_E1-E2.
DR      InterPro: IPR004014; Cation ATPase.
DR      InterPro: IPR000661; H/K Na/K ATPase.
DR      InterPro: IPR001454; Hlgase/hydrilase.
DR      Pfam: PF00689; Cation ATPase C; 1.
DR      Pfam: PF00690; Cation ATPase N; 1.
DR      Pfam: PF00122; El-E2 ATPase; 1.
DR      Pfam: PF00702; Hydrolase; 1.
DR      PROSITE: PS00154; ATPASE_E1_E2; UNKNOWN 1.
SQ      SEQUENCE 1023 AA; 111719 MW; DOB451CECAF3F67E CRC64;

Query Match      80.5%; Score 33; DB 5; Length 1023;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      651 GLSFTGY 657
      |:|||||:
      |:|||||:

RESULT 38
O09489      O09489      PRELIMINARY;      PRT; 1031 AA.
ID      O09489;
AC      O09489;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DT      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Organelle-type Ca2+-ATPase.
OS      Leishmania amazonensis.
OC      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX      NCBI_TaxID=5659;
RN      [1]
RC      STRAIN=RAT/BA/LV78;
RC      SEQUENCE FROM N.A.
RX      MEDLINE=97238888; PubMed=9083086;
RA      Lu H.G., Zhong L., Chang K.P., Docampo R.;
RA      "Intracellular Ca2+ pool content and signaling and expression of a
```

```
RT      calcium pump are linked to virulence in Leishmania mexicana amazonensis
RT      amastigotes.";
RL      J. Biol. Chem. 272:9464-9473 (1997).
DR      EMBL: U70540; AAC47505.1;
DR      HSSP: P04191; LEUL.
DR      InterPro: IPR001757; ATPase_E1-E2.
DR      InterPro: IPR004014; Cation ATPase.
DR      InterPro: IPR000661; H/K Na/K ATPase.
DR      InterPro: IPR001454; Hlgase/hydrilase.
DR      Pfam: PF00689; Cation ATPase C; 1.
DR      Pfam: PF00690; Cation ATPase N; 1.
DR      Pfam: PF00122; El-E2 ATPase; 1.
DR      Pfam: PF00702; Hydrolase; 1.
DR      PRINTS: PR00119; CATATPASE.
DR      PROSITE: PS00154; ATPASE_E1_E2; UNKNOWN 1.
SQ      SEQUENCE 1031 AA; 113097 MW; 07B51CE3C51B142B CRC64;

Query Match      80.5%; Score 33; DB 5; Length 1031;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      657 GLSFTGY 663
      |:|||||:
      |:|||||:

RESULT 39
Q97MX7      Q97MX7      PRELIMINARY;      PRT; 1645 AA.
ID      Q97MX7;
AC      Q97MX7;
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE      Phage-related protein.
DE      CAC0063.
GN      Clostridium acetobutylicum.
OS      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC      Clostridiales; Clostridiaceae; Clostridium.
OX      NCBI_TaxID=1488;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX      MEDLINE=21359325; PubMed=11466286;
RA      Noelling J., Berton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA      Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA      Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA      Bennett G.N., Koonin E.V., Smith D.R.;
RT      "Genome sequence and comparative analysis of the solvent-producing
RT      bacterium Clostridium acetobutylicum.";
RL      J. Bacteriol. 183:4823-4838 (2001).
DR      EMBL: AB007519; AAK78049.1;
KW      Complete proteome.
SQ      SEQUENCE 1645 AA; 185238 MW; B6312D7AF0BCF50A CRC64;

Query Match      80.5%; Score 33; DB 16; Length 1645;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGY 7
Db      1181 GYSSTGY 1187
      |:|||||:
      |:|||||:

RESULT 40
Q8R8E7      Q8R8E7      PRELIMINARY;      PRT; 61 AA.
ID      Q8R8E7;
AC      Q8R8E7;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Hypothetical protein TTE2057.
GN      TTE2057.
OS      Thermoanaerobacter tengcongensis.
```

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.  
 OX NCBI\_TaxID=119072;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4T / JCM11007;  
 RX MEDLINE=21992816; PubMed=11997336;  
 RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RT "A complete sequence of T. tengcongensis genome."  
 RL Genome Res. 12:689-700(2002).  
 DR EMBL: AE013155; AM25231.1; --  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 61 AA; 7109 MW; D646EDAB651451FE CRC64;

Query Match 78.0%; Score 32; DB 16; Length 61;  
 Best Local Similarity 71.4%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYSFTGY 7  
 Db 33 GYSYMGY 39  
 |||: ||

Search completed: July 18, 2003, 15:09:41  
 Job time : 29.06 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:01:44 ; Search time 16.9 Seconds  
(without alignments)  
39.423 Million cell updates/sec

Title: US-10-007-790-6

Perfect score: 30

Sequence: 1 SCVNA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	21	Murine PIP3 recogn
2	30	100.0	124	21	Murine PIP3 recogn
3	30	100.0	137	22	Novel human diagno
4	30	100.0	346	20	Polypeptide with t
5	30	100.0	346	21	Human PRO1007 prot
6	30	100.0	346	21	Membrane-bound pro
7	30	100.0	346	21	Albumin fusion pro
8	30	100.0	346	22	Human PRO1007 poly
9	30	100.0	346	22	Human secreted pro
10	30	100.0	346	22	Human metastasis-a

11	30	100.0	346	22	Human PRO1007 (UNQ
12	30	100.0	346	22	Human PRO1007 prot
13	30	100.0	346	23	Human albumin fusi
14	30	100.0	346	23	Human angiogenesis
15	30	100.0	346	23	Human PRO1007 prot
16	30	100.0	346	22	Novel human diagno
17	27	90.0	20	22	Peptide #11607 enc
18	27	90.0	20	22	Protein #8990 enco
19	27	90.0	20	22	Human brain expres
20	27	90.0	20	22	Peptide #8167 enco
21	27	90.0	20	23	Human peptide enco
22	27	90.0	30	21	Human secreted pro
23	27	90.0	54	22	Peptide #7834 enco
24	27	90.0	54	22	Protein #6723 enco
25	27	90.0	54	22	Human brain expres
26	27	90.0	54	22	Human bone marrow
27	27	90.0	54	22	Peptide #6557 enco
28	27	90.0	54	22	Peptide #8060 enco
29	27	90.0	54	23	Human peptide enco
30	27	90.0	83	22	Novel central nerv
31	27	90.0	83	22	Novel human enzyme
32	27	90.0	83	22	Cone snail O-supe
33	27	90.0	84	22	Cone snail O-supe
34	27	90.0	88	21	SEN virus protein
35	27	90.0	90	21	Human secreted pro
36	27	90.0	94	22	Human polypeptide
37	27	90.0	94	22	Human foetal prote
38	27	90.0	190	21	Arabidopsis thalia
39	27	90.0	194	21	Arabidopsis thalia
40	27	90.0	227	21	Arabidopsis thalia
41	27	90.0	238	22	Novel central nerv
42	27	90.0	238	22	Novel human enzyme
43	27	90.0	249	22	Novel central nerv
44	27	90.0	292	21	K. aestuarii carbo
45	27	90.0	296	21	K. aestuarii carbo

ALIGNMENTS

RESULT 1  
AA1987658  
ID AAY87658 standard; Protein; 5 AA.  
XX AAY87658;  
XX AC  
XX AC  
XX AC  
DT 11-AUG-2000 (first entry)  
XX  
DE Murine PIP3 recognizing Mab variable region heavy chain CDR2 region.  
XX  
KW PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR2;  
KW immunogen; antibody; heavy chain; complementarity determining region.  
XX  
OS Mus sp.  
XX  
PN JF2000083664-A.  
XX  
PD 28-MAR-2000.  
XX  
PF 07-SEP-1998; 98JP-0252921.  
XX  
PR 07-SEP-1998; 98JP-0252921.  
XX  
(FUKU/) FUKUI Y.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
XX  
DR WPI; 2000-353334/31.  
XX  
PT A monoclonal antibody recognizing  
PT phosphatidylinositol-3,4,5-triphosphate  
XX  
PS Claim 8; Page 13; 15pp; Japanese.  
XX

CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain complementarity determining region, CDR2 described in the method of  
 CC the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 30; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 |||||  
 Db 1 SCYNA 5

RESULT 2  
 AAY87655  
 ID AAY87655 standard; Protein; 124 AA.

AC AAY87655;

XX 11-AUG-2000 (first entry)

DE Murine PIP3 recognizing Mab variable region heavy chain protein.

XX PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;  
 KW immunogen; antibody; heavy chain.

XX Mus sp.

PN JP2000083664-A.

PD 28-MAR-2000.

XX 07-SEP-1998; 98JP-0252921.

XX 07-SEP-1998; 98JP-0252921.

PA (FUKU)/ FUKUI Y.

PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.

DR N-PSDB; AAA12202.

XX A monoclonal antibody recognizing  
 PT phosphatidylinositol-3,4,5-triphosphate -

XX Claim 5; Page 11; 15pp; Japanese.

CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain described in the method of the invention.

XX Sequence 124 AA;

Query Match 100.0%; Score 30; DB 21; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 |||||  
 Db 52 SCYNA 56

RESULT 3

ABG15138  
 ID ABG15138 standard; Protein; 197 AA.

XX AC ABG15138;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #15129.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS79325.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

XX Claim 20; SEQ ID No 45497; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 197 AA;

Query Match 100.0%; Score 30; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

Db	158 SCYNA 162		160 SCYNA 164
RESULT 4	RESULT 5		
AAW85739	AAW85739	AAW85739	AAW85739
ID AAW85739 standard; Protein; 346 AA.	ID AAW85739 standard; Protein; 346 AA.	ID AAB33441 standard; Protein; 346 AA.	ID AAB33441 standard; Protein; 346 AA.
XX	XX	XX	XX
AC AAW85739;	AC AAW85739;	AC AAB33441;	AC AAB33441;
XX	XX	XX	XX
DT 01-OCT-1999 (first entry)	DT 01-OCT-1999 (first entry)	DT 29-JAN-2001 (first entry)	DT 29-JAN-2001 (first entry)
XX	XX	XX	XX
DE Polypeptide with transmembrane domain.	DE Polypeptide with transmembrane domain.	DE Human PRO1007 protein UNQ491 SEQ ID NO:146.	DE Human PRO1007 protein UNQ491 SEQ ID NO:146.
XX	XX	XX	XX
KW Transmembrane protein; transmembrane domain; translocation protein;	KW Transmembrane protein; transmembrane domain; translocation protein;	KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;	KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW endoplasmic reticulum; sec61 alpha subunit; research; probe;	KW endoplasmic reticulum; sec61 alpha subunit; research; probe;	KW dermatological; antiarthritic; antirheumatic; immunosuppressive;	KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW diagnosis; gene therapy; nutritional supplement;	KW diagnosis; gene therapy; nutritional supplement;	KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;	KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW cytokine proliferation; cell proliferation; cell differentiation;	KW cytokine proliferation; cell proliferation; cell differentiation;	KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;	KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW haematopoiesis regulation; tissue growth; activin; inhibin;	KW haematopoiesis regulation; tissue growth; activin; inhibin;	KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;	KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW chemotactic activity; chemokinesis; haemostasis; thrombolysis;	KW chemotactic activity; chemokinesis; haemostasis; thrombolysis;	KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;	KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW receptor; ligand; anti-inflammatory; tumour inhibition;	KW receptor; ligand; anti-inflammatory; tumour inhibition;	KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;	KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW antibody production.	KW antibody production.	KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;	KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
XX	XX	KW autoimmune thrombocytopaenia; immune-mediated renal disease;	KW autoimmune thrombocytopaenia; immune-mediated renal disease;
OS Homo sapiens.	OS Homo sapiens.	KW demyelinating disease; hepatobiliary disease; Whipple's disease;	KW demyelinating disease; hepatobiliary disease; Whipple's disease;
XX	XX	KW inflammatory bowel disease; gluten-sensitive enteropathy;	KW inflammatory bowel disease; gluten-sensitive enteropathy;
PN WO9918202-A2.	PN WO9918202-A2.	KW autoimmune disease; immune-mediated skin disease; allergic disease;	KW autoimmune disease; immune-mediated skin disease; allergic disease;
XX	XX	KW immunological disease; transplantation associated disease;	KW immunological disease; transplantation associated disease;
PD 15-APR-1999.	PD 15-APR-1999.	KW graft rejection; graft-versus-host-disease.	KW graft rejection; graft-versus-host-disease.
XX	XX	XX	XX
PF 05-OCT-1998; 98WO-JP04474.	PF 05-OCT-1998; 98WO-JP04474.	OS Homo sapiens.	OS Homo sapiens.
XX	XX	XX	XX
PR 08-OCT-1997; 97JP-0276269.	PR 08-OCT-1997; 97JP-0276269.	XX	XX
XX	XX	XX	XX
PA (PROT-) PROTEGENE INC.	PA (PROT-) PROTEGENE INC.	XX	XX
PA (SAGA ) SAGAMI CHEM RES CENT.	PA (SAGA ) SAGAMI CHEM RES CENT.	XX	XX
XX	XX	XX	XX
PI Kato S, Sekine S;	PI Kato S, Sekine S;	XX	XX
XX	XX	XX	XX
DR WPI; 1999-277267/23.	DR WPI; 1999-277267/23.	XX	XX
DR N-PSDB; AAX08740, AAX08746.	DR N-PSDB; AAX08740, AAX08746.	XX	XX
XX	XX	XX	XX
PT Human transmembrane proteins and nucleotide sequences	PT Human transmembrane proteins and nucleotide sequences	XX	XX
XX	XX	XX	XX
PS Claim 1; Page 73-75; 96pp; English.	PS Claim 1; Page 73-75; 96pp; English.	XX	XX
XX	XX	XX	XX
CC A novel method of cloning cDNAs from the human full-length cDNA	CC A novel method of cloning cDNAs from the human full-length cDNA	XX	XX
CC bank is described. The protein is identified by the presence of a	CC bank is described. The protein is identified by the presence of a	XX	XX
CC hydrophobic N-terminal secretory signal region, knowledge of the	CC hydrophobic N-terminal secretory signal region, knowledge of the	XX	XX
CC protein function is not required, as in e.g. methods of expression	CC protein function is not required, as in e.g. methods of expression	XX	XX
CC cloning. The cDNAs encode proteins comprising transmembrane domains	CC cloning. The cDNAs encode proteins comprising transmembrane domains	XX	XX
CC and can be used as probes for gene diagnosis and gene sources for	CC and can be used as probes for gene diagnosis and gene sources for	XX	XX
CC gene therapy. Abnormalities of membrane proteins are associated	CC gene therapy. Abnormalities of membrane proteins are associated	XX	XX
CC with a number of hitherto-cryptogenic diseases. e.g. cystic	CC with a number of hitherto-cryptogenic diseases. e.g. cystic	XX	XX
CC fibrosis. Polynucleotides and proteins of the invention can be used	CC fibrosis. Polynucleotides and proteins of the invention can be used	XX	XX
CC in research; as nutritional supplements; for cell proliferation;	CC in research; as nutritional supplements; for cell proliferation;	XX	XX
CC cell differentiation or cytokine activity or to induce the	CC cell differentiation or cytokine activity or to induce the	XX	XX
CC production of cytokines; for immune stimulating or suppressing	CC production of cytokines; for immune stimulating or suppressing	XX	XX
CC activity i.e generation of antibodies; for haematopoiesis regulating	CC activity i.e generation of antibodies; for haematopoiesis regulating	XX	XX
CC for chemotactic/chemokinetic activity; for activin/inhibin activity;	CC for chemotactic/chemokinetic activity; for activin/inhibin activity;	XX	XX
CC thrombolytic activity; for receptor/ligand activity; for	CC thrombolytic activity; for receptor/ligand activity; for	XX	XX
CC anti-inflammatory activity or for tumour inhibition activity.	CC anti-inflammatory activity or for tumour inhibition activity.	XX	XX
CC A search of a protein database revealed no proteins having an	CC A search of a protein database revealed no proteins having an	XX	XX
CC analogy with this sequence.	CC analogy with this sequence.	XX	XX
XX	XX	XX	XX
SQ Sequence 346 AA;	SQ Sequence 346 AA;	XX	XX
Query Match	Query Match	XX	XX
Best Local Similarity 100.0%; Score 30; DB 20; Length 346;	Best Local Similarity 100.0%; Score 30; DB 20; Length 346;	XX	XX
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;	XX	XX
OY 1 SCYNA 5	OY 1 SCYNA 5	XX	XX
		XX	XX

PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04114.  
 XX (GETH ) GENENTECH INC.  
 XX Aahkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX WPI; 2000-572271/53.  
 DR N-PSDB; AAC58606.  
 XX  
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 33; Fig 56; 309pp; English.  
 PS  
 XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 XX Sequence 346 AA;  
 SQ  
 Query Match 100.0%; Score 30; DB 21; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SCYNA 5  
 Db 160 SCYNA 164  
 RESULT 6  
 AAY66679  
 ID AAY66679 standard; protein; 346 AA.  
 XX  
 AC AAY66679;  
 AC  
 DT 05-APR-2000 (first entry)  
 XX  
 XX Membrane-bound protein PRO1007.  
 DE  
 XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 KW pharmaceutical; receptor immunoadhesin; gene mapping.  
 KW  
 XX Homo sapiens.  
 XX  
 XX WO9963088-A2.  
 XX  
 XX 09-DEC-1999.  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 XX  
 XX 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 02-JUN-1998; 98US-0087759.  
 PR

PR 03-JUN-1998; 98US-0087827.  
 PR 04-JUN-1998; 98US-0088021.  
 PR 04-JUN-1998; 98US-0088025.  
 PR 04-JUN-1998; 98US-0088028.  
 PR 04-JUN-1998; 98US-0088029.  
 PR 04-JUN-1998; 98US-0088030.  
 PR 04-JUN-1998; 98US-0088033.  
 PR 04-JUN-1998; 98US-0088326.  
 PR 05-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088202.  
 PR 05-JUN-1998; 98US-0088212.  
 PR 05-JUN-1998; 98US-0088217.  
 PR 09-JUN-1998; 98US-0088655.  
 PR 10-JUN-1998; 98US-0088722.  
 PR 10-JUN-1998; 98US-0088730.  
 PR 10-JUN-1998; 98US-0088734.  
 PR 10-JUN-1998; 98US-0088738.  
 PR 10-JUN-1998; 98US-0088740.  
 PR 10-JUN-1998; 98US-0088741.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-JUN-1998; 98US-0088810.  
 PR 10-JUN-1998; 98US-0088811.  
 PR 10-JUN-1998; 98US-0088824.  
 PR 10-JUN-1998; 98US-0088825.  
 PR 10-JUN-1998; 98US-0088826.  
 PR 11-JUN-1998; 98US-0088858.  
 PR 11-JUN-1998; 98US-0088861.  
 PR 11-JUN-1998; 98US-0088863.  
 PR 11-JUN-1998; 98US-0088876.  
 PR 12-JUN-1998; 98US-0089090.  
 PR 12-JUN-1998; 98US-0089105.  
 PR 12-JUN-1998; 98US-0089108.  
 PR 16-JUN-1998; 98US-0089440.  
 PR 16-JUN-1998; 98US-0089512.  
 PR 16-JUN-1998; 98US-0089514.  
 PR 17-JUN-1998; 98US-0089532.  
 PR 17-JUN-1998; 98US-0089538.  
 PR 17-JUN-1998; 98US-0089598.  
 PR 17-JUN-1998; 98US-0089599.  
 PR 17-JUN-1998; 98US-0089600.  
 PR 17-JUN-1998; 98US-0089653.  
 PR 18-JUN-1998; 98US-0089801.  
 PR 18-JUN-1998; 98US-0089907.  
 PR 18-JUN-1998; 98US-0089908.  
 PR 19-JUN-1998; 98US-0089947.  
 PR 19-JUN-1998; 98US-0089948.  
 PR 19-JUN-1998; 98US-0089952.  
 PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090576.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090595.  
 PR 25-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090862.  
 PR 26-JUN-1998; 98US-0090863.  
 PR 01-JUL-1998; 98US-0091358.

PR	01-JUL-1998;	98US-0091360.
PR	01-JUL-1998;	98US-0091544.
PR	02-JUL-1998;	98US-0091478.
PR	02-JUL-1998;	98US-0091486.
PR	02-JUL-1998;	98US-0091519.
PR	02-JUL-1998;	98US-0091626.
PR	02-JUL-1998;	98US-0091628.
PR	02-JUL-1998;	98US-0091633.
PR	02-JUL-1998;	98US-0091646.
PR	02-JUL-1998;	98US-0091673.
PR	07-JUL-1998;	98US-0091978.
PR	07-JUL-1998;	98US-0091982.
PR	09-JUL-1998;	98US-0092182.
PR	10-JUL-1998;	98US-0092472.
PR	20-JUL-1998;	98US-0093339.
PR	30-JUL-1998;	98US-0094651.
PR	04-AUG-1998;	98US-0095282.
PR	04-AUG-1998;	98US-0095285.
PR	04-AUG-1998;	98US-0095301.
PR	04-AUG-1998;	98US-0095302.
PR	04-AUG-1998;	98US-0095318.
PR	04-AUG-1998;	98US-0095321.
PR	04-AUG-1998;	98US-0095325.
PR	10-AUG-1998;	98US-0095916.
PR	10-AUG-1998;	98US-0095929.
PR	10-AUG-1998;	98US-0096012.
PR	11-AUG-1998;	98US-0096143.
PR	11-AUG-1998;	98US-0096146.
PR	12-AUG-1998;	98US-0096323.
PR	17-AUG-1998;	98US-0096757.
PR	17-AUG-1998;	98US-0096766.
PR	17-AUG-1998;	98US-0096768.
PR	17-AUG-1998;	98US-0096773.
PR	17-AUG-1998;	98US-0096791.
PR	17-AUG-1998;	98US-0096867.
PR	17-AUG-1998;	98US-0096891.
PR	17-AUG-1998;	98US-0096894.
PR	17-AUG-1998;	98US-0096895.
PR	17-AUG-1998;	98US-0096897.
PR	18-AUG-1998;	98US-0096949.
PR	18-AUG-1998;	98US-0096950.
PR	18-AUG-1998;	98US-0096959.
PR	18-AUG-1998;	98US-0096960.
PR	18-AUG-1998;	98US-0097022.
PR	19-AUG-1998;	98US-0097141.
PR	20-AUG-1998;	98US-0097218.
PR	24-AUG-1998;	98US-0097661.
PR	26-AUG-1998;	98US-0097951.
PR	26-AUG-1998;	98US-0097952.
PR	26-AUG-1998;	98US-0097954.
PR	26-AUG-1998;	98US-0097955.
PR	26-AUG-1998;	98US-0097971.
PR	26-AUG-1998;	98US-0097974.
PR	26-AUG-1998;	98US-0097978.
PR	26-AUG-1998;	98US-0097979.
PR	26-AUG-1998;	98US-0097986.
PR	26-AUG-1998;	98US-0098014.
PR	31-AUG-1998;	98US-0098525.
PR	16-SEP-1998;	98US-0100634.
PR	12-JAN-1999;	99US-0115565.
XX		XX
PA	(GETH ) GENENTECH INC.	
PI	Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;	
PI	Wood WI, Yuan J;	
XX		XX
DR	WPI; 2000-072883/06.	
DR	N-PSDB; AA265016.	
XX		XX
PT	Membrane-bound proteins and related nucleotide sequences	
XX	claim 12; Fig 125; 822pp; English.	
PS		XX
XX		XX

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

Query Match 100.0%; Score 30; DB 21; Length 346;  
Best Local Similarity 100.0%; Pred. No. 46+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVNA 5  
|||  
DB 160 SCVNA 164

RESULT 7  
AAE12413  
ID AAE12413 standard; Protein; 346 AA.  
AC AAE12413;  
XX  
XX 18-DEC-2001 (first entry)  
DT  
XX  
DE Albumin fusion protein related human protein #4.  
KW Human; albumin; HA; immune system disorder; transplant rejection;  
KW blood related disorder; myocardial infarction; glomerulonephritis;  
KW hyperproliferative disorder; childhood acute myeloid leukaemia;  
KW renal cell carcinoma; cardiovascular disorder; vulnary; melanoma;  
KW arthralgia; respiratory disorder; non-allergic rhinitis; antileukaemic;  
KW neurological disease; Alzheimer's disease; endocrine disorder; measles;  
KW pheochromocytoma; reproductive system disorder; neuroprotective; syphilis;  
KW infectious disease; gastrointestinal disorder; wound healing; nootropic;  
KW irritable bowel syndrome; HIV; human immunodeficiency virus infection;  
KW cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant;  
KW antiarthritic; antirheumatic; renal disorder; antimicrobial.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200179480-A1.  
XX  
XX 25-OCT-2001.  
XX  
XX 12-APR-2001; 2001WO-US11991.  
XX  
XX 12-APR-2000; 2000US-229358P.  
XX  
XX 25-APR-2000; 2000US-199384P.  
XX  
XX 21-DEC-2000; 2000US-256931P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX  
XX Rosen CA, Haseltine WA;  
XX  
XX WPI; 2001-616756/71.  
XX  
XX Albumin fusion proteins comprising a therapeutic protein and albumin,  
XX useful in the treating metastatic renal cell carcinoma, metastatic  
PT melanoma, malignant melanoma, renal cell carcinoma, HIV (human  
PT immunodeficiency virus) or infection -  
XX  
XX Disclosure; Page 388-389; 394pp; English.  
XX

CC The invention relates to human albumin (HA) fusion proteins and their  
 CC corresponding nucleic acid sequences. Therapeutic proteins fused to  
 CC albumin or its fragments have an extended shelf-life. The albumin  
 CC fusion proteins are useful in the treatment, prevention, diagnosis,  
 CC and/or detection of diseases, disorders such as immune system  
 CC disorders (e.g. transplant rejection), blood related disorders (e.g.  
 CC myocardial infarction), hyperproliferative disorders (e.g. childhood  
 CC acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic  
 CC melanoma, malignant melanoma, renal cell carcinoma), renal disorders  
 CC (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),  
 CC respiratory disorders (e.g. non-allergic rhinitis), neurological  
 CC diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.  
 CC pheochromocytoma), reproductive system disorders (e.g. syphilis),  
 CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.  
 CC irritable bowel syndrome), HIV (human immunodeficiency virus) infection  
 CC and wound healing. Nucleic acids encoding albumin fusion protein is  
 CC used in gene therapy. The present sequence is a human protein related  
 CC to albumin fusion proteins.

XX Sequence 346 AA;

Query Match 100.0%; Score 30; DB 22; Length 346;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 160 SCYNA 164

RESULT 8

AAU12387  
 ID AAU12387 standard; Protein; 346 AA.

XX AC AAU12387;

DT 24-OCT-2001 (first entry)

DE Human PR01007 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX OS Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28564.

XX 02-DEC-1999; 99WO-US28565.

XX 09-DEC-1999; 99US-0170262.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 30-DEC-1999; 99WO-US31243.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04594.

XX 01-MAR-2000; 2000WO-US05004.

XX 20-MAR-2000; 2000WO-US05601.

XX 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.

XX (GETH ) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.

DR N-PSDB; AAS21459.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing

PT PRO polypeptides, and detect the presence of mammalian tumours e.g.

PT lung, breast, prostate, cervical

XX Claim 12; Fig 432; 813pp; English.

PS AAU12172-AAU12446 represent novel human secretory and transmembrane

XX PRO polypeptides. The PRO polypeptides are useful to detect other

CC PRO polypeptides, to link bioactive molecules to cells expressing

CC PRO polypeptides, to modulate biological activities of cells expressing

CC PRO polypeptides, and to detect the presence of mammalian lung, colon,

CC breast, prostate, rectal, cervical or liver tumours by comparing PRO

CC polypeptide expression in a cell sample to that in a control sample.

CC Some of the 275 sequences are also useful to stimulate the release of

CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the

CC proliferation or differentiation of chondrocytes, the proliferation or

CC gene expression in pericyte cells, the release of proteoglycans from

CC cartilage, the proliferation of inner ear utricular supporting cells or

CC of T-lymphocytes, the release of a cytokine from peripheral blood

CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of

CC the PRO polypeptides may modulate glucose or free fatty acid uptake by

CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide

CC to factor VIIA. The PRO polypeptides can be used in assays to identify

CC molecules involved in binding interactions. The polynucleotides encoding

CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,

CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 346 AA;

Qy 1 SCYNA 5

Db 160 SCYNA 164

Query Match 100.0%; Score 30; DB 22; Length 346;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 160 SCYNA 164

RESULT 9

AAU12387

ID AAB74735 standard; Protein; 346 AA.

XX AAB74735;

XX 12-JUN-2001 (first entry)

XX Human secreted protein sequence encoded by gene 3 SEQ ID NO:44.

XX Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;

XX dermatological; immunosuppressive; antiinflammatory; anti-HIV;

XX immunostimulant; cytostatic; cardiac; vascular; anti-angiogenic;

XX ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine;

XX antitumor; antiparkinsonian; antimicrobial; vulnerary; gene therapy;

XX immune disorder; hyperproliferative disorder; cardiovascular disease;

XX cancer; angiogenic disorder; neurological disorder; infectious disease;

XX

KW wound healing; regeneration; chemotaxis; chromosome 19.  
 OS Homo sapiens.  
 XX  
 XX WO200112775-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 16-AUG-2000; 2000WO-US22325.  
 XX  
 XX 17-AUG-1999; 99US-0149182.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ni J, Florence KA, Fiscella M, Wei P, Baker KP;  
 XX Birse CE, Young PE, Komatsoulis GA, Moore PA, Soppet DR;  
 XX WPI; 2001-147550/15.  
 XX  
 XX N-PSDB; AAF81789.  
 XX  
 XX Nucleic acids encoding 25 human secreted polypeptides, useful for  
 XX preventing, diagnosing and/or treating e.g. cancers, Parkinson's  
 XX disease and diabetic retinopathy -  
 XX  
 XX Claim 11; Page 462-463; 485pp; English.  
 XX  
 XX AAF81787 to AAF81817 encode the human secreted proteins given in AAB74733  
 XX to AAB74772. Human secreted proteins can have activities based on the  
 XX tissues and cells they are expressed in. Example of activities include:  
 XX immunomodulatory; antisclerotic; dermatological; immunosuppressive;  
 XX antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant;  
 XX vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic;  
 XX anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; and  
 XX vulnery. Human secreted proteins can be used in gene therapy and  
 XX vaccine. Human secreted protein nucleotide sequences (NAM1) and proteins  
 XX (PEP1) may be used in the prevention, diagnosis and treatment of diseases  
 XX associated with inappropriate polypeptide expression. For example, NAM1  
 XX and PEP1 may be used to treat disorders associated with decreased  
 XX expression by rectifying mutations or deletions in a patients genome  
 XX that affect the activity of proteins by expressing inactive proteins or  
 XX to supplement the patients own production of polypeptides. Disorders that  
 XX may be prevented, diagnosed and/or treated include immune disorders,  
 XX hyperproliferative disorders (e.g. cancers), cardiovascular diseases,  
 XX angiogenic disorders, neurological disorders, infectious diseases and/or  
 XX for promoting wound healing, regeneration and /or chemotaxis. AAF81778 to  
 XX AAF81786 and AAB74732 represent sequences used in the exemplification of  
 XX the present invention.  
 XX  
 XX SQ Sequence 346 AA;  
 XX  
 XX Query Match 100.0%; Score 30; DB 22; Length 346;  
 XX Best Local Similarity 100.0%; Pred. No. 4e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 DB 160 SCYNA 164  
 RESULT 10  
 AAB35462  
 ID AAB35462 standard; Protein; 346 AA.  
 XX  
 XX AAB35462;  
 XX  
 XX 06-JUN-2001 (first entry)  
 XX  
 XX Human metastasis-associated antigen C4-4A.  
 XX  
 XX Rat; human; metastasis-associated antigen; C4.4A; cancer.  
 XX  
 XX Homo sapiens.  
 XX  
 XX  
 PN WO200123553-A2.  
 XX  
 XX 05-APR-2001.  
 XX  
 XX 29-SEP-2000; 2000WO-EP09567.  
 XX  
 XX 29-SEP-1999; 99US-0407784.  
 XX  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 XX Zoeller M, Roesel M, Wuerfel J;  
 XX WPI; 2001-358133/26.  
 XX  
 XX N-PSDB; AAF58882.  
 XX  
 XX New nucleic acid encoding rat or human metastasis-associated antigen  
 XX C4.4A for treating cell proliferative disorder associated with a  
 XX metastasizing tumor -  
 XX  
 XX Claim 1; Fig 2; 63pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences of the  
 XX human and rat metastasis-associated antigen C4.4A. The protein is  
 XX expressed rarely in the adult, except on metastasizing cancer cells.  
 XX Because of this, the sequences are useful in cancer diagnosis and  
 XX treatment of cell proliferation diseases. The present sequence is the  
 XX human C4.4A antigen.  
 XX  
 XX SQ Sequence 346 AA;  
 XX  
 XX Query Match 100.0%; Score 30; DB 22; Length 346;  
 XX Best Local Similarity 100.0%; Pred. No. 4e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 DB 160 SCYNA 164  
 RESULT 11  
 AAB65202  
 ID AAB65202 standard; Protein; 346 AA.  
 XX  
 XX AAB65202;  
 XX  
 XX 02-APR-2001 (first entry)  
 XX  
 XX Human PRO1007 (UNQ491) protein sequence SEQ ID NO:197.  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cytostatic;  
 XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 XX diagnostic assay.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200073454-A1.  
 XX  
 XX 07-DEC-2000.  
 XX  
 XX 30-MAR-2000; 2000WO-US08439.  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 XX  
 XX 23-JUN-1999; 99US-0141037.  
 XX  
 XX 07-JUL-1999; 99US-0143048.  
 XX  
 XX 20-JUL-1999; 99US-0144758.  
 XX  
 XX 26-JUL-1999; 99US-0145698.  
 XX  
 XX 28-JUL-1999; 99US-0146222.  
 XX  
 XX 17-AUG-1999; 99US-0149396.  
 XX  
 XX 15-SEP-1999; 99WO-US21090.  
 XX  
 XX 15-SEP-1999; 99WO-US21547.  
 XX  
 XX 08-OCT-1999; 99US-0158663.  
 XX  
 XX 30-NOV-1999; 99WO-US28313.  
 XX  
 XX 01-DEC-1999; 99WO-US28301.



XX Alumin fusion protein; therapeutic protein X; human albumin; HA;  
KW human serum albumin; HSA; cancer; reproductive disorder;  
KW digestive disorder; immune disorder; endocrine disorder;  
KW haematopoietic disorder; neural disorder; connective disorder;  
KW cytotatic; antiinfectility; antiinflammatory; antitumor;  
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neuroleptic;  
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
KW osteopathic; antiarthritic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200177137-A1.  
XX  
XX 18-OCT-2001.  
XX  
XX 12-APR-2001; 2001WO-US11988.  
XX  
PR 12-APR-2000; 2000US-229358P.  
PR 25-APR-2000; 2000US-199384P.  
PR 21-DEC-2000; 2000US-256931P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Haseltine WA;  
XX  
XX WPI; 2002-010886/01.  
XX  
PT New fusion protein for treating disease e.g. diabetes comprises an  
PT albumin fused to a therapeutic protein -  
XX  
XX Claim 1; Page 1914-1915; 2102pp; English.  
XX  
XX The present invention relates to albumin fusion proteins comprising a  
CC therapeutic protein X and human albumin (HA, also known as human serum  
CC albumin, HSA). The proteins are useful for treating a disease or  
CC disorder that may be modulated by therapeutic protein X. The albumin  
CC extends the shelf-life of protein X, and may increase its biological  
CC in vitro/in vivo activity. The protein is useful for treating and  
CC diagnosing disorders such as cancer, reproductive disorders, digestive  
CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
CC (e.g. diabetes), haematopoietic disorders, neural disorders  
CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
CC fusion proteins of the invention.  
XX  
SQ Sequence 346 AA;  
Query Match 100.0%; Score 30; DB 23; Length 346;  
Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SCYNA 5  
Db 160 SCYNA 164  
RESULT 14  
AB95487  
ID ABB95487 standard; Protein; 346 AA.  
XX  
AC ABB95487;  
XX  
XX 19-JUL-2002 (first entry)  
XX  
DE Human angiogenesis related protein PRO1007 SEQ ID NO: 130.  
XX  
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;

KW antiarteriosclerotic.  
XX  
XX Homo sapiens.  
XX  
XX WO200208284-A2.  
XX  
PD 31-JAN-2002.  
XX  
XX 09-JUL-2001; 2001WO-US21735.  
XX  
XX 20-JUL-2000; 2000US-219556P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 02-AUG-2000; 2000US-222695P.  
XX 17-AUG-2000; 2000US-0643657.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 07-SEP-2000; 2000US-230978P.  
XX 15-SEP-2000; 2000US-000000P.  
XX 18-SEP-2000; 2000US-0664610.  
XX 18-SEP-2000; 2000US-0665350.  
XX 24-OCT-2000; 2000US-242322P.  
XX 08-NOV-2000; 2000US-0709238.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000WO-US34956.  
XX 22-JAN-2001; 2001US-0767609.  
XX 28-FEB-2001; 2001US-0796498.  
XX 01-MAR-2001; 2001WO-US06666.  
XX 09-MAR-2001; 2001US-0802706.  
XX 14-MAR-2001; 2001US-0808689.  
XX 22-MAR-2001; 2001US-0816744.  
XX 05-APR-2001; 2001US-0828366.  
XX 10-MAY-2001; 2001US-0854208.  
XX 10-MAY-2001; 2001US-0854280.  
XX 25-MAY-2001; 2001US-0866028.  
XX 25-MAY-2001; 2001US-0866034.  
XX 25-MAY-2001; 2001WO-US17092.  
XX 30-MAY-2001; 2001US-0870574.  
XX 30-MAY-2001; 2001WO-US17443.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 28-JUN-2001; 2001WO-US00000.  
XX  
XX (GETH ) GENENTECH INC.  
XX (BAKE/) BAKER K P.  
XX (FERR/) FERRARA N.  
XX (GERB/) GERBER H.  
XX (GERR/) GERRITSEN M E.  
XX (GODD/) GODDARD A.  
XX (GODO/) GODOWSKI P J.  
XX (GURN/) GURNEY A L.  
XX (HILL/) HILLAN K J.  
XX (MARS/) MARSTERS S A.  
XX (PANJ/) PAN J.  
XX (PAON/) PAONI N F.  
XX (STEP/) STEPHAN J F.  
XX (WATA/) WATANABE C K.  
XX (WILL/) WILLIAMS P M.  
XX (WOOD/) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-171999/22.  
XX N-PSDB; ABL95625.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11; Fig 130; 567pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.  
 XX  
 SQ Sequence 346 AA;

Query Match 100.0%; Score 30; DB 23; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 160 SCYNA 164

RESULT 15  
 ABB84881  
 ID ABB84881 standard; Protein; 346 AA.

AC ABB84881;  
 XX  
 XX 16-MAY-2002 (first entry)  
 DT  
 DE Human PRO1007 protein sequence SEQ ID NO:130.  
 XX  
 XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200200690-A2.

XX 03-JAN-2002.  
 PD  
 XX  
 XX 20-JUN-2001; 2001WO-US19692.  
 XX  
 PR 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0843657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.

PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
 XX  
 DR WPI; 2002-090516/12.  
 DR N-PSDB; ABL88136.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 130; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.

XX Sequence 346 AA;

Query Match 100.0%; Score 30; DB 23; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 Db 160 SCYNA 164

RESULT 16  
 ABB815137  
 ID ABB815137 standard; Protein; 366 AA.

XX  
 AC ABB815137;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #15128.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 OS Homo sapiens.  
 XX  
 XX WO200175067-A2.  
 PN  
 XX

PD 11-OCT-2001.  
 XX 30-MAR-2001; 2001WO-US08631.  
 PF 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Dmanac RT, Liu C, Tang YT;  
 XX WPI; 2001-639362/73.  
 XX N-PSDB; AAS79324.  
 DR New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX Claim 20; SEQ ID NO 45496; 103pp; English.  
 PS The invention relates to isolated polynucleotide (I) and  
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 366 AA;  
 Query Match 100.0%; Score 30; DB 22; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 180 SCYNA 184  
 RESULT 17  
 ABB44101  
 ID ABB44101 standard; Peptide; 20 AA.  
 XX AC ABB44101;  
 XX DT 04-FEB-2002 (first entry)  
 XX Peptide #11607 encoded by human foetal liver single exon probe.  
 DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
 XX Homo sapiens.  
 KW WO200157277-A2.  
 XX 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00669.  
 PF

XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-483447/52.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human foetal liver -  
 XX Claim 27; SEQ ID NO 36736; 639pp + sequence listing; English.  
 PS The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC foetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 20 AA;  
 Query Match 90.0%; Score 27; DB 22; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 4 SCYNS 8  
 RESULT 18  
 ABB26991  
 ID ABB26991 standard; Protein; 20 AA.  
 XX AC ABB26991;  
 XX DT 23-JAN-2002 (first entry)  
 XX Protein #8990 encoded by probe for measuring heart cell gene expression.  
 DE Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.  
 XX Homo sapiens.  
 OS WO200157274-A2.  
 XX PN 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00666.  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PA

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-48899/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX  
PS Claim 15; SEQ ID No 28761; 530pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 20 AA;  
Query Match 90.0%; Score 27; DB 22; Length 20;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SCYNA 5  
Db ||||:  
4 SCVNS 8  
RESULT 19  
AAM65123  
ID AAM65123 standard; Protein; 20 AA.  
XX  
AC AAM65123;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37228.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe;  
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
KW epilepsy; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00667.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483446/52.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains -  
XX  
PS Example 4; SEQ ID NO: 37228; 650pp + Sequence Listing; English.

XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention.  
XX  
SQ Sequence 20 AA;  
Query Match 90.0%; Score 27; DB 22; Length 20;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SCYNA 5  
Db ||||:  
4 SCVNS 8  
RESULT 20  
AAM21733  
ID AAM21733 standard; Protein; 20 AA.  
XX  
AC AAM21733;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Peptide #8167 encoded by probe for measuring cervical gene expression.  
XX  
KW Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200157278-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00670.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488901/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human cervical epithelial cells -  
XX  
PS Claim 27; SEQ ID No 26559; 487pp; English.  
XX  
CC The present invention relates to human single exon nucleic acid probes  
CC (SENPs: see AAT10068-AA128459). The present sequence is a peptide encoded  
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 20 AA;

Query Match 90.0%; Score 27; DB 22; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 Db 4 SCYNS 8  
 |||||

RESULT 21  
 ABG46861  
 ID ABG46861 standard; Peptide; 20 AA.  
 AC ABG46861;  
 DT 19-AUG-2002 (first entry)  
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 36526.  
 DE Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX Homo sapiens.  
 XX WO200186003-A2.  
 XX 15-NOV-2001.  
 XX 30-JAN-2001; 2001WO-US000665.  
 XX 04-FEB-2000; 2000US-180312P.  
 XX 26-MAY-2000; 2000US-207456P.  
 XX 30-JUN-2000; 2000US-0608408.  
 XX 03-AUG-2000; 2000US-0632366.  
 XX 21-SEP-2000; 2000US-234687P.  
 XX 27-SEP-2000; 2000US-236359P.  
 XX 04-OCT-2000; 2000GB-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2002-114183/15.  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -  
 XX Claim 27; SEQ ID No 36526; 634bp; English.  
 XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 90.0%; Score 27; DB 23; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 Db 4 SCYNS 8  
 |||||

RESULT 22  
 AAB39403  
 ID AAB39403 standard; Protein; 30 AA.  
 AC AAB39403;  
 DT 02-FEB-2001 (first entry)  
 XX Human secreted protein sequence encoded by gene 2 SEQ ID NO:62.  
 XX Homo sapiens.  
 XX WO2000058340-A2.  
 XX 05-OCT-2000.  
 XX 23-MAR-2000; 2000WO-US07724.  
 XX 26-MAR-1999; 99US-0126510.  
 XX 07-JAN-2000; 2000US-0174850.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM, Komatsoulis G;  
 XX WPI; 2000-594638/56.  
 XX N-PSDB; AAC74338.

PT Fifty nucleic acid molecules encoding human secreted proteins, useful  
PT in the prevention, treatment and diagnosis of cancer, immune disorders,  
PT cardiovascular disorders and neurological diseases -  
XX  
XX  
XX Claim 11; Page 357; 391pp; English.  
PS  
XX The polynucleotide sequences given in AAC74337 to AAC74386 encode the  
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to  
CC AAB39484 represent human secreted polypeptide sequences and proteins  
CC homologous to them, which are given in the exemplification of the present  
CC invention. Human secreted proteins have activities based on the tissues  
CC and cells the genes are expressed in. Example of activities include:  
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
CC anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
CC vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and  
CC treating or ameliorating a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides  
CC can also be used as a food additive or preservative to increase or  
CC decrease storage capabilities. The polynucleotide are useful for  
CC chromosome identification. They are also useful as probes for diagnosing  
CC a disorder related to the female reproductive system, particularly breast  
CC and/or ovary cancer. They are also useful in the gene therapy of breast  
CC and ovarian cancer. Secreted protein nucleic acids, proteins,  
CC antibodies, agonists and antagonists are useful in the diagnosis,  
CC treatment and prevention of: (a) cancer; (b) immune disorders; (c)  
CC cardiovascular disorders; (d) wound healing; (e) neurological diseases;  
CC and (f) infectious diseases such as viral, bacterial, fungal and  
CC parasitic infections. AAC74328 to AAC74336 and AAB39401 represent  
CC sequences used in the exemplification of the present invention.  
XX  
XX SQ Sequence 30 AA;

Query Match 90.0%; Score 27; DB 21; Length 30;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCVNA 5  
Db 19 NCVNA 23

RESULT 23  
ABB40328  
ID ABB40328 standard; Peptide; 54 AA.  
XX  
XX AC ABB40328;  
XX  
XX DT 04-FEB-2002 (first entry)  
XX  
XX DE Peptide #7834 encoded by human foetal liver single exon probe.  
XX  
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200157277-A2.  
XX  
XX PD 09-AUG-2001.  
XX  
XX PF 30-JAN-2001; 2001WO-US00669.  
XX  
XX PR 04-FEB-2000; 2000US-0180312.  
XX  
XX PR 26-MAY-2000; 2000US-0207456.  
XX  
XX PR 30-JUN-2000; 2000US-0608408.  
XX  
XX PR 03-AUG-2000; 2000US-0632366.  
XX  
XX PR 21-SEP-2000; 2000US-0234687.  
XX  
XX PR 27-SEP-2000; 2000US-0236359.  
XX  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX DR WPI; 2001-488899/53.  
XX  
XX PT Single exon nucleic acid probes for analyzing gene expression in human  
XX hearts -  
XX  
XX PS Claim 15; SEQ ID No 26494; 530pp; English.  
XX  
XX CC The present invention relates to single exon nucleic acid probes for  
XX measuring human gene expression in a sample derived from human heart (see  
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

XX  
XX WPI; 2001-483447/52.  
XX  
XX PT Human genome-derived single exon nucleic acid probes useful for  
XX PT analyzing gene expression in human fetal liver -  
XX  
XX PS Claim 27; SEQ ID NO 32963; 639pp + sequence listing; English.  
XX  
XX CC The invention relates to a single exon nucleic acid probe for  
XX measuring human gene expression in a sample derived from human foetal  
XX liver. The single exon nucleic acid probes may be used for predicting,  
XX measuring and displaying gene expression in samples derived from human  
XX fetal liver. The present sequence is a peptide encoded by a single exon  
XX nucleic acid probe of the invention.  
XX  
XX CC Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 54 AA;  
XX  
XX Query Match 90.0%; Score 27; DB 22; Length 54;  
XX Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX OY 1 SCVNA 5  
XX Db 5 SCVNS 9  
XX  
XX RESULT 24  
XX ABB24724  
XX ID ABB24724 standard; Protein; 54 AA.  
XX  
XX AC ABB24724;  
XX  
XX XX 23-JAN-2002 (first entry)  
XX  
XX DE Protein #6723 encoded by probe for measuring heart cell gene expression.  
XX  
XX KW Human; gene expression; heart; microarray; vascular system;  
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;  
XX KW congenital heart disease.  
XX  
XX OS Homo sapiens.  
XX  
XX XX WO200157274-A2.  
XX  
XX PD 09-AUG-2001.  
XX  
XX PF 30-JAN-2001; 2001WO-US00666.  
XX  
XX PR 04-FEB-2000; 2000US-0180312.  
XX  
XX PR 26-MAY-2000; 2000US-0207456.  
XX  
XX PR 30-JUN-2000; 2000US-0608408.  
XX  
XX PR 03-AUG-2000; 2000US-0632366.  
XX  
XX PR 21-SEP-2000; 2000US-0234687.  
XX  
XX PR 27-SEP-2000; 2000US-0236359.  
XX  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX DR WPI; 2001-488899/53.  
XX  
XX PT Single exon nucleic acid probes for analyzing gene expression in human  
XX hearts -  
XX  
XX PS Claim 15; SEQ ID No 26494; 530pp; English.  
XX  
XX CC The present invention relates to single exon nucleic acid probes for  
XX measuring human gene expression in a sample derived from human heart (see  
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 54 AA;

Query Match 90.0%; Score 27; DB 22; Length 54;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db |||||:  
5 SCYNS 9

RESULT 25

AAM61129  
ID AAM61129 standard; Protein; 54 AA.

XX AC AAM61129;

XX 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33234.

XX Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

XX Homo sapiens.

XX WO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00667.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains -

XX Example 4; SEQ ID NO: 33234; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is a protein encoded by one of

XX the probes of the invention.

XX SQ Sequence 54 AA;

Query Match 90.0%; Score 27; DB 22; Length 54;

Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

Db |||||:  
5 SCYNS 9

RESULT 26

AAM73838  
ID AAM73838 standard; Protein; 54 AA.

XX AC AAM73838;

XX 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34144.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 34144; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which may enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukaemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention.

XX SQ Sequence 54 AA;

Query Match 90.0%; Score 27; DB 22; Length 54;

Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

Db |||||:  
5 SCYNS 9

RESULT 27

AAM20123  
ID AAM20123 standard; Protein; 54 AA.

XX AC AAM20123;

XX 12-OCT-2001 (first entry)

XX Peptide #6557 encoded by probe for measuring cervical gene expression.  
DE Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer.  
KW Homo sapiens.  
OS  
XX WO200157278-A2.  
PN  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US006670.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488901/53.  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human cervical epithelial cells -  
XX  
XX Claim 27; SEQ ID No 24949; 487pp; English.  
XX  
XX The present invention relates to human single exon nucleic acid probes  
CC (SENPs; see AAI10068-AAI28459). The present sequence is a peptide encoded  
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 54 AA;  
SQ  
Query Match 90.0%; Score 27; DB 22; Length 54;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SCVNA 5  
Db 5 SCVNS 9  
RESULT 28  
AAM34023  
ID AAM34023 standard; Protein; 54 AA.  
AC AAM34023;  
XX  
XX 17-OCT-2001 (first entry)  
XX  
XX Peptide #8060 encoded by probe for measuring placental gene expression.  
DE Probe; microarray; human; placenta; antenatal diagnosis;  
XX genetic disorder.  
KW  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
PN  
XX

PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US006663.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488997/53.  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human placenta -  
XX  
XX Claim 27; SEQ ID No 34292; 654pp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes (SENPs;  
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders.  
XX  
XX Sequence 54 AA;  
SQ  
Query Match 90.0%; Score 27; DB 22; Length 54;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SCVNA 5  
Db 5 SCVNS 9  
RESULT 29  
ABG43727  
ID ABG43727 standard; Peptide; 54 AA.  
XX  
XX ABG43727;  
XX  
XX 19-AUG-2002 (first entry)  
XX  
XX Human peptide encoded by genome-derived single exon probe SEQ ID 33392.  
DE  
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.  
XX  
XX Homo sapiens.  
OS  
XX WO200186003-A2.  
PN  
XX 15-NOV-2001.  
PD  
XX 30-JAN-2001; 2001WO-US006665.  
XX  
XX 04-FEB-2000; 2000US-180312P.  
PR 26-MAY-2000; 2000US-207456P.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR

PR 21-SEP-2000; 2000US-234687P.  
PR 27-SEP-2000; 2000US-236359P.  
PR 04-OCT-2000; 2000GB-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2002-114183/15.  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
XX measure gene expression in human lung samples -  
XX Claim 27; SEQ ID No 33392; 634pp; English.  
XX The invention relates to a spatially-addressable set of single exon  
XX nucleic acid probes for measuring gene expression in a sample derived  
XX from human lung comprising single exon nucleic acid probes having one of  
XX 12614 nucleic acid sequences mentioned in the specification, or their  
XX complements or the 12387 open reading frames derived from the 12614  
XX probes. Also included are a microarray comprising the novel set of  
XX probes; the novel set of probes which hybridise at high stringency to a  
XX nucleic acid expressed in the human lung; measuring gene expression in a  
XX sample derived from human lung, comprising (a) contacting the array with  
XX a collection of detectably labeled nucleic acids derived from human lung  
XX mRNA, and (b) measuring the label detectably bound to each probe of  
XX the array; identifying exons in a eukaryotic genome, comprising  
XX (a) algorithmically predicting at least one exon from genomic sequences  
XX of the eukaryote; and (b) detecting specific hybridisation of detectably  
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
XX having a fragment identical to the predicted exon, the probe is included  
XX in the above mentioned microarray; assigning exons to a single gene,  
XX comprising (a) identifying exons from genomic sequence by the method  
XX above and (b) measuring the expression of each of the exons in several  
XX tissues and/or cell types using hybridisation to a single exon  
XX microarrays having a probe with the exon, where a common pattern of  
XX expression of the exons in the tissues and/or cell types indicates that  
XX the exons should be assigned to a single gene; a peptide comprising one  
XX of 12011 sequences, mentioned in the specification, or encoded by the  
XX probes/open reading frames (ORF). The probes are used for gene  
XX expression analysis, and for identifying exons in a gene, particularly  
XX using human lung derived mRNA and for the study of lung diseases  
XX such as asthma, lung cancer, chronic obstructive pulmonary disease  
XX (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
XX fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
XX Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
XX haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
XX pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
XX and hyaline membrane disease. The present sequence is a peptide/protein  
XX encoded by a single exon probe of the invention.  
XX Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic  
XX format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 90.0%; Score 27; DB 23; Length 54;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SCYNA 5  
Db 5 SCYNS 9  
|||||  
RESULT 30  
AAU87496  
ID AAU87496 standard; Protein; 83 AA.  
XX  
AC AAU87496;  
XX

DT 05-JUN-2002 (first entry)  
XX Novel central nervous system protein #406.  
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200155318-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01332.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 07-JUN-2000; 2000US-0205515.  
PR 19-MAY-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226686.  
PR 23-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.



KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;  
XX nephrotropic; anticoagulant.  
OS Homo sapiens.  
XX  
PN WO20015301-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01239.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216847.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 08-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-02334223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236602.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 01-NOV-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 05-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 06-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-465566/50.  
 DR N-PSDB; AAS41142.  
 XX  
 PT Novel polypeptides and polynucleotides useful for diagnosing,  
 PT preventing, treating neural, immune system, muscular, reproductive,  
 PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous  
 PT diseases  
 XX  
 PS Claim 11; SEQ ID No 1268; 1180pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human enzyme  
 CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders  
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),  
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders  
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),  
 CC blood-related disorders (e.g. haemophilia), reproductive disorders  
 CC (e.g. infertility) and infectious disorders (e.g. Influenza). The  
 CC polynucleotides of the invention can also be used in gene therapy.  
 CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the  
 CC invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 83 AA;  
 Query Match 90.0%; Score 27; DB 22; Length 83;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCVNA 5  
 Db :|||||  
 37 NCYNA 41  
 RESULT 32  
 AAU05900  
 ID AAU05900 standard; Peptide; 83 AA.  
 XX  
 AC AAU05900;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Cone snail O-superfamily conotoxin propeptide, M6.8.  
 XX  
 KW Cone snail; O-superfamily conotoxin; sodium channel;  
 KW demyelinating disease; multiple sclerosis; Huntington's disease;  
 KW neuropathy; carpal tunnel syndrome; cardiovascular disorder;  
 KW congestive heart failure; cancer; immunosuppression; epilepsy;  
 KW asthma; ischaemia; stroke; pain.  
 XX  
 OS Conus magus.  
 XX  
 PN WO200149312-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US35431.  
 XX  
 XX 30-DEC-1999; 99US-0173754.

PR 26-JUN-2000; 2000US-0214263.  
 PR 20-JUL-2000; 2000US-0219440.  
 PR 27-OCT-2000; 2000US-0243412.  
 XX  
 PA (UTAH) UNIV UTAH RES FOUND.  
 XX (COGN-) COGNETIX INC.  
 PI Olivera BM, Cartier GE, Watkins M, Hillyard DR, McIntosh JM;  
 PI Layer RT, Jones RM;  
 XX  
 DR WPI; 2001-418352/44.  
 DR N-PSDB; AAS10938.  
 XX  
 PT New O-superfamily polypeptides useful for treating voltage gated ion  
 PT channel disorders, including demyelinating diseases i.e. multiple  
 PT sclerosis  
 XX  
 PS Claim 15; Page 53; 277pp; English.  
 XX  
 CC The sequence is a cone snail O-superfamily conotoxin propeptide.  
 CC The peptides are useful for regulating the flow of sodium through of  
 CC sodium channels in an individual and the treatment or prevention of  
 CC disorders associated with voltage gated ion channel disorders,  
 CC including demyelinating diseases i.e. multiple sclerosis, optic  
 CC neuromyelitis, disseminated encephalomyelitis, adrenoleukodystrophy,  
 CC acute transverse myelitis, progressive multifocal leukoencephalopathy,  
 CC sub acute sclerosing panencephalomyelitis (SSPE), metachromatic  
 CC leukodystrophy, Pellizaeus-Merzbacher disease, spinal cord injury,  
 CC botulinum toxin poisoning, Huntington's, compression, entrapment  
 CC neuropathies i.e. ulnar nerve palsy, and carpal tunnel syndrome,  
 CC cardiovascular disorders, i.e. cardiac arrhythmias and congestive heart  
 CC failure, reactive gliosis, hyperglycaemia, immunosuppression, cocaine  
 CC addiction, cancer, cognitive dysfunction, neurotransmitter disorders  
 CC (i.e. Eaton-Lambert syndrome) and reversal of curare and other  
 CC neuromuscular blocking drugs. The neurological disorder is a seizure,  
 CC preferably one associated with epilepsy. The neurological disorder is a  
 CC neurotoxic injury associated with hypoxia, anoxia or ischaemia. The  
 CC neurotoxic injury is associated with stroke, cerebrovascular accident,  
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,  
 CC drownings, suffocation, perinatal asphyxia or hypoglycaemic events. The  
 CC disorder is pain i.e. migraine, acute pain, persistent pain,  
 CC neuropathic pain, nociceptive pain. The disorder is inflammation or a  
 CC cardiovascular disorder. A conotoxin peptide of is useful to  
 CC alleviate pain in a mammal in pain or about to be subjected to a pain  
 CC causing event, and to treat disorders associated with radical  
 CC depolarisation of excitable membranes by activating a KATP channel, the  
 CC disorders include cardiac, ocular and cerebral ischaemia and asthma.  
 XX  
 SQ Sequence 83 AA;  
 Query Match 90.0%; Score 27; DB 22; Length 83;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCVNA 5  
 Db :|||||  
 53 ACVNA 57  
 RESULT 33  
 AAU05898  
 ID AAU05898 standard; Peptide; 84 AA.  
 XX  
 AC AAU05898;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Cone snail O-superfamily conotoxin propeptide, M6.7.  
 XX  
 KW Cone snail; O-superfamily conotoxin; sodium channel;  
 KW demyelinating disease; multiple sclerosis; Huntington's disease;  
 KW neuropathy; carpal tunnel syndrome; cardiovascular disorder;  
 KW congestive heart failure; cancer; immunosuppression; epilepsy;



XX PD 06-SEP-2000.  
 XX PF 21-FEB-2000; 2000EP-0200610.  
 XX PR 26-FEB-1999; 99US-0122487.  
 XX PA (GEST ) GENSET.  
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX DR WPI; 2000-500381/45.  
 XX DR N-PSDB; AAC01511.  
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX PT  
 XX PS Claim 13; SEQ ID 5586; 71pp + CD-ROM; English.  
 XX CC The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
 CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer cDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length cDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.  
 XX SQ Sequence 90 AA;  
 Query Match 90.0%; Score 27; DB 21; Length 90;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 84 SCYNS 88  
 RESULT 36  
 AAO13404  
 ID AAO13404 standard; Protein; 94 AA.  
 AC AAO13404;  
 DT 06-NOV-2001 (first entry)  
 XX Human polypeptide SEQ ID NO 27296.  
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX Homo sapiens.  
 OS WO200164835-A2.  
 PN 07-SEP-2001.  
 XX 26-FEB-2001; 2001WO-US04927.  
 PF 28-FEB-2000; 2000US-0515126.  
 PR 18-MAY-2000; 2000US-0577409.  
 XX (HYSE-) HYSEQ INC.  
 PA Yeung G, Ford JE, Boyle BJ, Arterburn MC, Drmanac RA, Tang YT;  
 PI Liu C, Asundi V, Zhou P, Werhman T;  
 DR WPI; 2001-465571/50.  
 DR N-PSDB; AAH94156.  
 XX

PI Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-514838/56.  
 DR N-PSDB; AA193335.  
 XX Isolated nucleic acids and polypeptides, useful for preventing  
 PT diagnosing and treating e.g. leukaemia, inflammation and immune  
 PT disorders -  
 XX PS Claim 20; SEQ ID NO 27296; 1399pp + Sequence Listing; English.  
 XX CC The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 94 AA;  
 Query Match 90.0%; Score 27; DB 22; Length 94;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 71 ACYNA 75  
 RESULT 37  
 AAM06481  
 ID AAM06481 standard; Protein; 96 AA.  
 AC AAM06481;  
 DT 05-OCT-2001 (first entry)  
 XX Human foetal protein, SEQ ID NO: 212.  
 DE Human; foetal protein; cytostatic; immunosuppressive; immunostimulant;  
 XX neurotropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory;  
 KW gene therapy; antisense therapy; cancer; immune disorder;  
 KW growth disorder; osteoporosis; thrombolytic disorder;  
 KW nervous system disorder; inflammation.  
 XX Homo sapiens.  
 OS WO200155339-A2.  
 PN 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-US02723.  
 PF 25-JAN-2000; 2000US-0491404.  
 PR 15-SEP-2000; 2000US-0663870.  
 PR 06-NOV-2000; 2000US-0707351.  
 XX (HYSE-) HYSEQ INC.  
 PA Yeung G, Ford JE, Boyle BJ, Arterburn MC, Drmanac RA, Tang YT;  
 PI Liu C, Asundi V, Zhou P, Werhman T;  
 DR WPI; 2001-465571/50.  
 DR N-PSDB; AAH94156.  
 XX

PT Novel fetal proteins useful for the treatment and diagnosis of diseases  
PT associated with dysfunction of the protein e.g. cancers, immune  
PT disorders, growth disorders, thrombolytic disorders, nervous system  
PT disorders and inflammation -

XX Claim 10; Page 257; 715pp; English.

XX The invention relates to novel foetal polypeptides encoded by  
CC polynucleotides comprising one of 477 sequences fully defined in the  
CC specification. The foetal polynucleotides and polypeptides are  
CC useful in the treatment and diagnosis of diseases such as cancers,  
CC immune disorders, growth disorders (e.g. osteoporosis), thrombolytic  
CC disorders, nervous system disorders and inflammation. The present  
CC sequence is a polypeptide encoded by a cDNA assembled using  
CC an expressed sequence tag (EST) found to be expressed in human  
CC foetal tissue cDNA libraries.

XX SQ Sequence 96 AA;

Query Match 90.0%; Score 27; DB 22; Length 96;  
Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

Db 84 TCYNA 88

RESULT 38

AAG44470

ID AAG44470 standard; Protein; 190 AA.

AC AAG44470;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 55710.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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XX KW Protein identification; signal transduction pathway; metabolic pathway;  
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KW termination sequence.  
XX OS Arabidopsis thaliana.  
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XX DT 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 55708.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
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PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999;	99US-0147303.	Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
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PR 09-AUG-1999;	99US-0147493.			:							
PR 09-AUG-1999;	99US-0147935.	Db		145 NCYNA 149							
PR 10-AUG-1999;	99US-0148171.										
PR 11-AUG-1999;	99US-0148319.										
PR 12-AUG-1999;	99US-0148341.										
PR 13-AUG-1999;	99US-0148565.										
PR 13-AUG-1999;	99US-0148684.										
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PR 17-AUG-1999;	99US-0149175.										
PR 18-AUG-1999;	99US-0149426.										
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PR 20-AUG-1999;	99US-0149723.										
PR 20-AUG-1999;	99US-0149929.										
PR 23-AUG-1999;	99US-0149902.										
PR 23-AUG-1999;	99US-0149930.										
PR 25-AUG-1999;	99US-0150566.										
PR 26-AUG-1999;	99US-0150884.										
PR 27-AUG-1999;	99US-0151065.										
PR 27-AUG-1999;	99US-0151066.										
PR 27-AUG-1999;	99US-0151080.										
PR 30-AUG-1999;	99US-01511303.										
PR 31-AUG-1999;	99US-0151138.										
PR 01-SEP-1999;	99US-0151930.										
PR 07-SEP-1999;	99US-0152363.										
PR 10-SEP-1999;	99US-0153070.										
PR 13-SEP-1999;	99US-0153758.										
PR 15-SEP-1999;	99US-0154018.										
PR 16-SEP-1999;	99US-0154039.										
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PR 29-SEP-1999;	99US-0156596.										
PR 04-OCT-1999;	99US-0157117.										
PR 05-OCT-1999;	99US-0157753.										
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PR 07-OCT-1999;	99US-0158029.										
PR 08-OCT-1999;	99US-0158232.										
PR 12-OCT-1999;	99US-0158369.										
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PR 18-OCT-1999;	99US-0159584.										
PR 21-OCT-1999;	99US-0160741.										
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PR 21-OCT-1999;	99US-0160768.										
PR 21-OCT-1999;	99US-0160770.										
PR 21-OCT-1999;	99US-0160814.										
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PR 22-OCT-1999;	99US-0160981.										
PR 22-OCT-1999;	99US-0160989.										
PR 25-OCT-1999;	99US-0161404.										
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PR 26-OCT-1999;	99US-0161361.										
PR 28-OCT-1999;	99US-0161920.										
PR 28-OCT-1999;	99US-0161992.										
PR 28-OCT-1999;	99US-0161993.										
PR 29-OCT-1999;	99US-0162142.										

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Job time : 18.9 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:46 ; Search time 5.8 Seconds  
(without alignments)  
25.365 Million cell updates/sec

Title: US-10-007-790-6  
Perfect score: 30  
Sequence: 1 SCYNA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata1/iaa/5B COMB.pep.\*  
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6: /cgn2\_6/prodata1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	100.0	124	4	US-09-257-069-2
3	27	90.0	158	4	US-08-826-134-11
4	27	90.0	158	4	US-08-826-134-22
5	27	90.0	242	4	US-09-019-095A-23
6	27	90.0	281	3	US-08-808-148-4
7	27	90.0	222	4	US-09-468-738A-2
8	27	90.0	232	4	US-09-940-019-2
9	27	90.0	236	4	US-09-468-738A-23
10	27	90.0	236	4	US-09-940-019-23
11	27	90.0	645	2	US-08-592-126-144
12	27	90.0	645	2	US-08-687-080-47
13	27	90.0	1381	4	US-08-826-134-4
14	27	90.0	1384	4	US-08-826-134-2
15	27	90.0	1940	2	US-08-844-271-30
16	27	90.0	1940	4	US-09-077-955-34
17	26	86.7	14	3	US-08-331-625A-33
18	26	86.7	14	4	US-09-494-151-33
19	26	86.7	26	3	US-08-256-747C-68
20	26	86.7	26	4	US-08-834-130A-68
21	26	86.7	33	2	US-08-867-087B-63
22	26	86.7	34	2	US-08-867-087B-64
23	26	86.7	47	3	US-08-331-625A-29
24	26	86.7	47	3	US-09-100-600A-76
25	26	86.7	47	4	US-09-494-151-29
26	26	86.7	51	3	US-08-331-625A-4
27	26	86.7	51	4	US-09-494-151-4

28	26	86.7	114	2	US-08-888-366-8	Sequence 8, Appli
29	26	86.7	148	6	5180813-2	Patent No. 5180813
30	26	86.7	219	2	US-08-816-605-2	Sequence 2, Appli
31	26	86.7	250	2	US-08-867-087B-13	Sequence 13, Appli
32	26	86.7	255	1	US-08-236-918A-8	Sequence 8, Appli
33	26	86.7	255	2	US-08-816-605-9	Sequence 9, Appli
34	26	86.7	255	4	US-09-006-353A-11	Sequence 11, Appli
35	26	86.7	255	4	US-09-007-097-2	Sequence 2, Appli
36	26	86.7	255	4	US-09-150-864A-8	Sequence 8, Appli
37	26	86.7	255	4	US-09-573-986-11	Sequence 11, Appli
38	26	86.7	255	5	PCT-US96-03965-8	Sequence 8, Appli
39	26	86.7	270	4	US-09-134-001C-3187	Sequence 3187, Ap
40	26	86.7	316	4	US-09-134-001C-3736	Sequence 3736, Ap
41	26	86.7	336	1	US-07-904-073-2	Sequence 2, Appli
42	26	86.7	336	1	US-07-904-073-2	Sequence 2, Appli
43	26	86.7	336	1	US-08-442-043A-16	Sequence 16, Appli
44	26	86.7	416	1	US-08-117-083-61	Sequence 61, Appli
45	26	86.7	428	3	US-08-331-625A-43	Sequence 43, Appli

ALIGNMENTS

RESULT 1  
US-09-257-069-6  
; Sequence 6, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; CURRENT FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-6

Query Match	100.0%	Score 30;	DB 4;	Length 5;
Best Local Similarity	100.0%	Pred No. 2e+05;		
Matches	5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	SCYNA 5		
DB	1	SCYNA 5		
RESULT 2				
US-09-257-069-2				
; Sequence 2, Application US/09257069				
; Patent No. 6348580				
; GENERAL INFORMATION:				
; APPLICANT: Medical & Biological Laboratories Co., Ltd.				
; TITLE OF INVENTION: Monoclonal Antibody Specific for				
; TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate				
; FILE REFERENCE: M3-008-US				
; CURRENT APPLICATION NUMBER: US/09/257,069				
; CURRENT FILING DATE: 1999-02-24				
; PRIOR APPLICATION NUMBER: JP 1998-252921				
; PRIOR FILING DATE: 1998-09-07				
; NUMBER OF SEQ ID NOS: 10				
; SOFTWARE: Patent In Ver. 2.0				
; SEQ ID NO 2				
; LENGTH: 124				
; TYPE: PRT				
; ORGANISM: Mus musculus				
US-09-257-069-2				

Query Match 100.0%; Score 30; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 52 SCYNA 56

## RESULT 3

US-08-826-134-11  
Sequence 11, Application US/08826134A  
Patent No. 6465210  
GENERAL INFORMATION:  
APPLICANT: Peles, Elior  
TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE AXONAL CELL RECOGNITION MOLECULE CONTACTIN  
FILE REFERENCE: 7683-111  
CURRENT APPLICATION NUMBER: US/08/826,134A  
CURRENT FILING DATE: 1997-03-26  
EARLIER APPLICATION NUMBER: 60/014,199  
EARLIER FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11:  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-826-134-11

Query Match 90.0%; Score 27; DB 4; Length 158;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 95 SCYNS 99

## RESULT 4

US-08-826-134-22  
Sequence 22, Application US/08826134A  
Patent No. 6465210  
GENERAL INFORMATION:  
APPLICANT: Peles, Elior  
TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE AXONAL CELL RECOGNITION MOLECULE CONTACTIN  
FILE REFERENCE: 7683-111  
CURRENT APPLICATION NUMBER: US/08/826,134A  
CURRENT FILING DATE: 1997-03-26  
EARLIER APPLICATION NUMBER: 60/014,199  
EARLIER FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22:  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-08-826-134-22

Query Match 90.0%; Score 27; DB 4; Length 158;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 95 SCYNS 99

## RESULT 5

US-09-019-095A-23  
Sequence 23, Application US/09019095A

Patent No. 6287858  
GENERAL INFORMATION:  
APPLICANT: D'Andrea, Alan D.  
APPLICANT: Zhu, Yuan  
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate Cell Growth  
FILE REFERENCE: DFCI-435p2A2  
CURRENT APPLICATION NUMBER: US/09/019,095A  
CURRENT FILING DATE: 1998-02-05  
PRIOR APPLICATION NUMBER: PCT/US96/12884  
PRIOR FILING DATE: 1996-08-07  
PRIOR APPLICATION NUMBER: US 60/002,066  
PRIOR FILING DATE: 1995-08-09  
PRIOR APPLICATION NUMBER: US 60/019,787  
PRIOR FILING DATE: 1996-06-14  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Consensus  
US-09-019-095A-23

Query Match 90.0%; Score 27; DB 4; Length 242;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 22 NCYNA 26

## RESULT 6

US-08-808-148-4  
Sequence 4, Application US/08808148  
Patent No. 6020478  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer  
APPLICANT: Goli, Surya  
APPLICANT: Zhang, Hong Wolfe  
TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/808,148  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0218 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 755242  
US-08-808-148-4

Query Match 90.0%; Score 27; DB 3; Length 281;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 180 SCYNS 184

RESULT 7  
US-09-468-738A-2  
; Sequence 2, Application US/09468738A  
; Patent No. 6312933  
; GENERAL INFORMATION:  
; APPLICANT: Kimoto, No. 6312933ihiro  
; APPLICANT: Yamamoto, Hiroaki  
; APPLICANT: Mitsuhashi, Kazuya  
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA  
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID  
; FILE REFERENCE: 06501-050001  
; CURRENT APPLICATION NUMBER: US/09/468, 738A  
; CURRENT FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: JP 1999-171160  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: JP 1998-363130  
; PRIOR FILING DATE: 1998-12-21  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1  
; SEQ ID NO 2  
; LENGTH: 292  
; TYPE: PRP  
; ORGANISM: Kluyveromyces aestuarii  
US-09-468-738A-2

Query Match 90.0%; Score 27; DB 4; Length 292;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 192 TCYNA 196

RESULT 8  
US-09-940-019-2  
; Sequence 2, Application US/09940019  
; Patent No. 6416986  
; GENERAL INFORMATION:  
; APPLICANT: Kimoto, No. 6416986ihiro  
; APPLICANT: Yamamoto, Hiroaki  
; APPLICANT: Mitsuhashi, Kazuya  
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA  
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID  
; FILE REFERENCE: 06501-050001  
; CURRENT APPLICATION NUMBER: US/09/940, 019  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/468, 738  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: JP 1998-363130  
; PRIOR FILING DATE: 1998-12-21  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1

; SEQ ID NO 2  
; LENGTH: 292  
; TYPE: PRP  
; ORGANISM: Kluyveromyces aestuarii  
US-09-940-019-2

Query Match 90.0%; Score 27; DB 4; Length 292;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 192 TCYNA 196

RESULT 9  
US-09-468-738A-23  
; Sequence 23, Application US/09468738A  
; Patent No. 6312933  
; GENERAL INFORMATION:  
; APPLICANT: Kimoto, No. 6312933ihiro  
; APPLICANT: Yamamoto, Hiroaki  
; APPLICANT: Mitsuhashi, Kazuya  
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA  
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID  
; FILE REFERENCE: 06501-050001  
; CURRENT APPLICATION NUMBER: US/09/468, 738A  
; CURRENT FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: JP 1999-171160  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: JP 1998-363130  
; PRIOR FILING DATE: 1998-12-21  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1  
; SEQ ID NO 23  
; LENGTH: 296  
; TYPE: PRP  
; ORGANISM: Kluyveromyces aestuarii  
US-09-468-738A-23

Query Match 90.0%; Score 27; DB 4; Length 296;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 196 TCYNA 200

RESULT 10  
US-09-940-019-23  
; Sequence 23, Application US/09940019  
; Patent No. 6416986  
; GENERAL INFORMATION:  
; APPLICANT: Kimoto, No. 6416986ihiro  
; APPLICANT: Yamamoto, Hiroaki  
; APPLICANT: Mitsuhashi, Kazuya  
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA  
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID  
; FILE REFERENCE: 06501-050001  
; CURRENT APPLICATION NUMBER: US/09/940, 019  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/468, 738  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: JP 1998-363130  
; PRIOR FILING DATE: 1998-12-21  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1  
; SEQ ID NO 23  
; LENGTH: 296  
; TYPE: PRP

; ORGANISM: Kluyveromyces aestuarii  
US-09-940-019-23

Query Match 90.0%; Score 27; DB 4; Length 296;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 196 TCYNA 200

## RESULT 11

US-08-592-126-144  
; Sequence 144, Application US/08592126  
; Patent No. 5821091  
; GENERAL INFORMATION:  
; APPLICANT: Gregory Dolganov  
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory  
; TITLE OF INVENTION: Polypeptides  
; NUMBER OF SEQUENCES: 151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/592,126  
; FILING DATE:  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 4600-0111  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 144:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 645 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: G18.pgp

US-08-592-126-144

Query Match 90.0%; Score 27; DB 2; Length 645;  
Best Local Similarity 80.0%; Pred. No. 6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 609 SCYNS 613

## RESULT 12

US-08-687-080-47  
; Sequence 47, Application US/08687080  
; Patent No. 5965427

; GENERAL INFORMATION:  
; APPLICANT: Gregory Dolganov  
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof

; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,080  
; FILING DATE: 17-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/592,126  
; FILING DATE: 26-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 4600-0111.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 645 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: G18.pgp  
US-08-687-080-47

Query Match 90.0%; Score 27; DB 2; Length 645;  
Best Local Similarity 80.0%; Pred. No. 6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 609 SCYNS 613

## RESULT 13

US-08-826-134-4  
; Sequence 4, Application US/08826134A  
; Patent No. 6465210

; GENERAL INFORMATION:  
; APPLICANT: Peles, Elior

; TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RTPP-BETA AND THE  
; TITLE OF INVENTION: AXONAL CELL RECOGNITION MOLECULE CONTACTIN

; FILE REFERENCE: 7683-111

; CURRENT APPLICATION NUMBER: US/08/826,134A

; CURRENT FILING DATE: 1997-03-26

; EARLIER APPLICATION NUMBER: 60/014,199

; EARLIER FILING DATE: 1996-03-27

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1381

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-08-826-134-4

Query Match 90.0%; Score 27; DB 4; Length 1381;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 SCYNA 5
      ||||:
Db      677 SCYNS 681

RESULT 14
US-08-826-134-2
; Sequence 2, Application US/08826134A
; Patent No. 6465210
; GENERAL INFORMATION:
; APPLICANT: Peles, Elior
; TITLE OF INVENTION: CASPR/190, A FUNCTIONAL LIGAND FOR RPTP-BETA AND THE
; TITLE OF INVENTION: AXONAL CELL RECOGNITION MOLECULE CONTACTIN
; FILE REFERENCE: 7683-111
; CURRENT APPLICATION NUMBER: US/08/826,134A
; CURRENT FILING DATE: 1997-03-26
; EARLIER APPLICATION NUMBER: 60/014,199
; EARLIER FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-826-134-2

Query Match      90.0%; Score 27; DB 4; Length 1384;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      ||||:
Db      676 SCYNS 680

RESULT 15
US-08-644-271-30
; Sequence 30, Application US/08644271
; Patent No. 5814478
; GENERAL INFORMATION:
; APPLICANT: Valenzuela, et al.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
; TITLE OF INVENTION: AND LIGANDS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,271
; FILING DATE: 10-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/008,657
; FILING DATE: 15-DEC-1995
; NAME: Cobert, Robert J
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 195A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1940 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Rat Agrin
; LOCATION: 1..1940
; OTHER INFORMATION:
US-08-644-271-30

Query Match      90.0%; Score 27; DB 2; Length 1940;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      ||||:
Db      997 SCYNS 1001

RESULT 16
US-09-077-955-34
; Sequence 34, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1940
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-077-955-34

Query Match      90.0%; Score 27; DB 4; Length 1940;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      ||||:
Db      997 SCYNS 1001

RESULT 17
US-08-331-625A-33
; Sequence 33, Application US/08331625A
; Patent No. 6057436
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepper, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
```

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;
;
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-331-625A-33

Query Match 86.7%; Score 26; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
Db ||||
1 SCYN 4

RESULT 18
US-09-494-151-33
; Sequence 33, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

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;
;
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-494-151-33

Query Match 86.7%; Score 26; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
Db ||||
1 SCYN 4

RESULT 19
US-08-256-747C-68
; Sequence 68, Application US/08256747C
; Patent No. 6037448
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: GILLAM, Shirley
; APPLICANT: OU, Dawei
; APPLICANT: TINGLE, Aubrey
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,747C
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-256-747C-68
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Query Match      86.7%; Score 26; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
Db 3 SCYN 6

RESULT 20
US-08-834-130A-68
; Sequence 68, Application US/08834130A
; Patent No. 6180758
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: GILLAM, Shirley
; APPLICANT: GU, Dawei
; APPLICANT: TINGLE, Aubrey
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,130A
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-686 MTS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-834-130A-68

Query Match      86.7%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
Db 3 SCYN 6

RESULT 21
US-08-867-087B-63
; Sequence 63, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449

```

```

; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-867-087B-63

Query Match      86.7%; Score 26; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYNA 5
Db 16 CYNA 19

RESULT 22
US-08-867-087B-64
; Sequence 64, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449

```

```
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-867-087B-64

Query Match      86.7%; Score 26; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CYN 5
Db      16 CYN 19

RESULT 23
US-08-331-625A-29
; Sequence 29, Application US/08331625A
; Patent No. 6057436
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-331-625A-29

Query Match      86.7%; Score 26; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYN 4
Db      34 SCYN 37

RESULT 24
US-09-100-600A-76
; Sequence 76, Application US/09100600A
; Patent No. 6107021
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Shen, Ming
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
; TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,600A
; FILING DATE: 20-Jun-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-600A-76

Query Match      86.7%; Score 26; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYN 4
Db      4 SCYN 7

RESULT 25
US-09-494-151-29
; Sequence 29, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
```

;; Jones, Elaine V.  
;; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
;; Therefor  
;;  
;; NUMBER OF SEQUENCES: 59  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
;; Patents  
;; STREET: 709 Swedeland Road  
;; CITY: King of Prussia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19406-2799  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/494,151  
;; FILING DATE: 28-Jan-2000  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/331,625  
;; FILING DATE: <Unknown>  
;;  
;; APPLICATION NUMBER: 08/331,625  
;; APPLICATION NUMBER: US 07/698,927  
;; FILING DATE: 13-MAY-1991  
;; APPLICATION NUMBER: US 07/613,066  
;; FILING DATE: 14-NOV-1990  
;; NAME: Schreck, Patricia A.  
;; REGISTRATION NUMBER: 33,777  
;; REFERENCE/DOCKET NUMBER: SBC H85010-1  
;; TELEPHONE: (215) 270-5015  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 29:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 47 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-494-151-29  
  
Query Match 86.7%; Score 26; DB 4; Length 47;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 34 SCYN 37  
  
RESULT 26  
US-08-331-625A-4  
; Sequence 4, Application US/08331625A  
; Patent No. 6057436  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; APPLICANT: Klepfer, Sharon  
; APPLICANT: Reed, Albert Paul  
; APPLICANT: Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/331,625A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/880,194  
;; FILING DATE: 08-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/698,927  
;; FILING DATE: 13-MAY-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/613,066  
;; FILING DATE: 14-NOV-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Schreck, Patricia A.  
;; REGISTRATION NUMBER: 33,777  
;; REFERENCE/DOCKET NUMBER: SBC H85010-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5015  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 51 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
US-08-331-625A-4  
  
Query Match 86.7%; Score 26; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 1 SCYN 4  
  
RESULT 27  
US-09-494-151-4  
; Sequence 4, Application US/09494151  
; Patent No. 6372224  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Timothy J.  
; APPLICANT: Klepfer, Sharon  
; APPLICANT: Reed, Albert Paul  
; APPLICANT: Jones, Elaine V.  
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corporate  
; Patents  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/494,151  
; FILING DATE: 28-Jan-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,625

; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/698,927  
; FILING DATE: 13-MAY-1991  
; APPLICATION NUMBER: US 07/613,066  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schreck, Patricia A.  
; REGISTRATION NUMBER: 33,777  
; REFERENCE/DOCKET NUMBER: SBC H85010-1  
; TELEPHONE: (215) 270-5015  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-494-151-4  
  
Query Match 86.7%; Score 26; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 1 SCYN 4  
  
RESULT 28  
US-08-888-366-8  
; Sequence 8, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.39USC1  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-888-366-8  
  
Query Match 86.7%; Score 26; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 46 SCYN 49  
  
RESULT 29  
5180813-2  
; Patent No. 5180813  
; APPLICANT: Stinski, Mark F.  
; TITLE OF INVENTION: EARLY ENVELOPE GLYCOPROTEIN OF HUMAN  
; CYTOMEGALOVIRUS (HMCV) AND MONOCLONAL ANTIBODIES TO THE  
; GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/328,227  
; FILING DATE: 24-MAR-1989  
; SEQ ID NO: 2:  
; LENGTH: 148  
5180813-2  
  
Query Match 86.7%; Score 26; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 141 SCYN 144  
  
RESULT 30  
US-08-816-605-2  
; Sequence 2, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-2

Query Match 86.7%; Score 26; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4  
|||||  
DB 4 SCYN 7

RESULT 31  
US-08-867-087B-13  
Sequence 13, Application US/08867087B  
Patent No. 5990386  
GENERAL INFORMATION:  
APPLICANT: An, Gynheung  
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT  
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klarquist Sparkman Campbell Leigh &  
ADDRESSEE: Whinston, LLP  
STREET: One World Trade Center  
STREET: 121 S.W. Salmon Street  
STREET: Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: United States of America  
ZIP: 97204  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3-1/2 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,087B  
FILING DATE: June 2, 1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/323,449  
FILING DATE: October 14, 1994  
APPLICATION NUMBER: U.S. 08/485,981  
FILING DATE: June 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Alan. E.  
REGISTRATION NUMBER: 35,123  
REFERENCE/DOCKET NUMBER: 4630-47071  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acid residues  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-867-087B-13

Query Match 86.7%; Score 26; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYN 5  
|||||

DB 73 CYN 76

## RESULT 32

US-08-236-918A-8  
Sequence 8, Application US/08236918A  
Patent No. 5674704  
GENERAL INFORMATION:  
APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple 7.5.3  
SOFTWARE: Microsoft Word, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,918A  
FILING DATE: 06-May-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,843  
FILING DATE: 07-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-236-918A-8

Query Match 86.7%; Score 26; DB 1; Length 255;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4  
|||||  
DB 4 SCYN 7

## RESULT 33

US-08-816-605-9  
Sequence 9, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA

Query Match 86.7%; Score 26; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYN 5  
|||||

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-816-605-9

Query Match      86.7%; Score 26; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYN 4
DB      4 SCYN 7

RESULT 34
US-09-006-353A-11
; Sequence 11, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid

;
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-353A-11

Query Match      86.7%; Score 26; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYN 4
DB      4 SCYN 7

RESULT 35
US-09-007-097-2
; Sequence 2, Application US/09007097A
; Patent No. 6303121
; GENERAL INFORMATION:
; APPLICANT: KWON, BYOUNG
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/007,097A
; CURRENT FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-007-097-2

Query Match      86.7%; Score 26; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYN 4
DB      4 SCYN 7

RESULT 36
US-09-150-864A-8
; Sequence 8, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; TITLE OF INVENTION: That Binds Thereto
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens (clone: hu4-1BB)
; US-09-150-864A-8

Query Match      86.7%; Score 26; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYN 4
DB      4 SCYN 7
```

RESULT 37  
US-09-573-986-11  
; Sequence 11, Application US/09573986  
; Patent No. 6455040  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280004  
; CURRENT APPLICATION NUMBER: US/09/573,986  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-573-986-11  
  
Query Match 86.7%; Score 26; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 4 SCYN 7  
  
RESULT 38  
PCT-US96-03965-8  
; Sequence 8, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KWOS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711

TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-8  
  
Query Match 86.7%; Score 26; DB 5; Length 255;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 4 SCYN 7  
  
RESULT 39  
US-09-134-001C-3187  
; Sequence 3187, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3187  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3187  
  
Query Match 86.7%; Score 26; DB 4; Length 270;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYN 4  
Db 7 SCYN 10  
  
RESULT 40  
US-09-134-001C-3736  
; Sequence 3736, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3736  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3736  
  
Query Match 86.7%; Score 26; DB 4; Length 316;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYN 4

Db 208 SCYN 211

Search completed: July 18, 2003, 15:11:48  
Job time : 6.8 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:09:56 ; Search time 12.9 Seconds  
(without alignments) 46.031 Million cell upd

Title: US-10-007-790-6

Perfect score: 30

Sequence: 1 SCYNA 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	30	100.0	346	10	US-09-989-723-197
4	30	100.0	346	10	US-09-989-879-197
5	30	100.0	346	10	US-09-989-727-197
6	30	100.0	346	11	US-09-989-731-197
7	30	100.0	346	11	US-09-989-732-197
8	30	100.0	346	11	US-09-991-073-197
9	30	100.0	346	11	US-09-990-442-197
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## ALIGNMENTS

## RESULT 1

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US-09-989-862-197
; Sequence 197, Application US/09989862
; Publication No. US20030130182A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Trans
; FILE REFERENCE: P2730P1C58
; CURRENT APPLICATION NUMBER: US/09/98
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186

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; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C63  
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC62  
; CURRENT APPLICATION NUMBER: US/09/989, 723  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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RESULT 5

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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC65  
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Query Match 100.0%; Score 30; DB 10; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavins, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C70  
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Query Match 100.0%; Score 30; DB 11; Length 346;

Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 7

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Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David

1 APPLICANT: Desnoyers, Luc  
2 APPLICANT: Eaton, Dan L.  
3 APPLICANT: Ferrara, Napoleone  
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15 APPLICANT: Roy, Margaret Ann  
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17 APPLICANT: Tumas, Daniel  
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19 APPLICANT: Williams, P. Mickey  
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21 APPLICANT: Zhang, Zemin  
22 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
23 FILE REFERENCE: P2730PIC57  
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25 CURRENT FILING DATE: 2001-11-19  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 8

US-09-991-073-197  
; Sequence 197, Application US/09991073  
; Patent No. US2002012756A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
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 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
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 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730PIC8  
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; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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;; PRIOR APPLICATION NUMBER: 60/090429  
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1 PRIOR FILING DATE: 1998-06-25  
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5 PRIOR FILING DATE: 1998-06-25  
6 PRIOR APPLICATION NUMBER: 60/090862  
7 PRIOR FILING DATE: 1998-06-26  
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9 PRIOR FILING DATE: 1998-06-26  
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11 PRIOR FILING DATE: 1998-07-01  
12 PRIOR APPLICATION NUMBER: 60/091478  
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19 PRIOR FILING DATE: 1998-07-02  
20 PRIOR APPLICATION NUMBER: 60/091633  
21 PRIOR FILING DATE: 1998-07-02  
22 PRIOR APPLICATION NUMBER: 60/091978  
23 PRIOR FILING DATE: 1998-07-07  
24 PRIOR APPLICATION NUMBER: 60/091982  
25 PRIOR FILING DATE: 1998-07-07  
26 PRIOR APPLICATION NUMBER: 60/092182  
27 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 26+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 160 SCYNA 164

## RESULT 11

US-09-993-604-197  
Sequence 197, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16

1 PRIOR APPLICATION NUMBER: 60/062250  
2 PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred No. 2e+02; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 SCYNA 5  
Db 160 SCYNA 164

## RESULT 12

US-09-990-456-197  
; Sequence 197, Application US/09990456  
; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC22  
; CURRENT APPLICATION NUMBER: US/09/990,456  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770

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; PRIOR APPLICATION NUMBER: 60/091978  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;

Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

Db 160 SCYNA 164

RESULT 13

US-09-989-721-197

; Sequence 197, Application US/09989721

; Patent No. US20020142961A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
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; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C55  
; CURRENT APPLICATION NUMBER: US/09/989, 721  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
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 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 160 SCYNA 164  
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 US-09-992-598-197  
 ; Sequence 197, Application US/09992598  
 ; Patent No. US20020160384A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730PIC20  
 ; CURRENT APPLICATION NUMBER: US/09/992,598  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
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Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 15

US-09-989-293A-197

; Sequence 197, Application US/09989293A

; Patent No. US20020177164A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

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; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: E2730F1C66

; CURRENT APPLICATION NUMBER: US/09/989, 293A

; CURRENT FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/049787

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 160 SCYNA 164

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; Sequence 197, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
DB 160 SCYNA 164

## RESULT 17

US-09-990-444-197  
; Sequence 197, Application US/09990444  
; Publication No. US20020193300A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C19  
CURRENT APPLICATION NUMBER: US/09/990,444  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 160 SCYNA 164

## RESULT 18

US-09-991-181-197  
; Sequence 197, Application US/09991181  
; Publication No. US20020197615A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Forg, Sherman

;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
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;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC53  
;; CURRENT APPLICATION NUMBER: US/09/991,181  
;; CURRENT FILING DATE: 2001-11-16  
;; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Caps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 SCYNA 5  
Db 160 SCYNA 164

RESULT 19  
US-09-989-730-197  
; Sequence 197, Application US/09989730  
; Publication No. US20020197674A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C69  
CURRENT APPLICATION NUMBER: US/09/989,730  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 160 SCYNA 164

RESULT 20  
US-09-990-436-197  
; Sequence 197, Application US/09990436  
; Publication No. US20020198148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.

;  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C14  
; CURRENT APPLICATION NUMBER: US/09/990,436  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 11; Length 346;

Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;  
QY 1 SCVNA 5  
Db 160 SCVNA 164

RESULT 21

US-09-993-687-197  
; Sequence 197, Application US/09993687  
; Publication No. US20020198149A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC11  
; CURRENT APPLICATION NUMBER: US/09/993,687

7	PRIOR APPLICATION NUMBER: 60/089100
7	PRIOR FILING DATE: 1998-06-12
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Query Match 100.0%; Score 30; DB 11; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
Db 160 SCYNA 164

RESULT 22  
US-09-989-734-197  
Sequence 197, Application US/09989734  
Publication No. US20030003531A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C64  
CURRENT APPLICATION NUMBER: US/09/989,734  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/052250  
PRIOR FILING DATE: 1997-10-17  
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APPLICANT: Ashkenazi, Avi J.  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C64  
CURRENT APPLICATION NUMBER: US/09/989,734  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/052250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-03-20  
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; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01

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; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;

Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0;

QY 1 SCYNA 5  
Db 160 SCYNA 164

#### RESULT 23

US-09-997-653-197  
; Sequence 197, Application US/09997653  
; Publication No. US20030008297A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC38  
; CURRENT APPLICATION NUMBER: US/09/997,653  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910

1	PRIOR APPLICATION NUMBER: 60/089599	
2	PRIOR FILING DATE: 1998-06-17	
3	PRIOR APPLICATION NUMBER: 60/089600	
4	PRIOR FILING DATE: 1998-06-17	
5	PRIOR APPLICATION NUMBER: 60/089653	
6	PRIOR FILING DATE: 1998-06-17	
7	PRIOR APPLICATION NUMBER: 60/089801	
8	PRIOR FILING DATE: 1998-06-18	
9	PRIOR APPLICATION NUMBER: 60/089907	
10	PRIOR FILING DATE: 1998-06-18	
11	PRIOR APPLICATION NUMBER: 60/089908	
12	PRIOR FILING DATE: 1998-06-18	
13	PRIOR APPLICATION NUMBER: 60/089947	
14	PRIOR FILING DATE: 1998-06-19	
15	PRIOR APPLICATION NUMBER: 60/089948	
16	PRIOR FILING DATE: 1998-06-19	
17	PRIOR APPLICATION NUMBER: 60/089952	
18	PRIOR FILING DATE: 1998-06-19	
19	PRIOR APPLICATION NUMBER: 60/090246	
20	PRIOR FILING DATE: 1998-06-22	
21	PRIOR APPLICATION NUMBER: 60/090252	
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25	PRIOR APPLICATION NUMBER: 60/090349	
26	PRIOR FILING DATE: 1998-06-23	
27	PRIOR APPLICATION NUMBER: 60/090355	
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30	PRIOR FILING DATE: 1998-06-24	
31	PRIOR APPLICATION NUMBER: 60/090431	
32	PRIOR FILING DATE: 1998-06-24	
33	PRIOR APPLICATION NUMBER: 60/090435	
34	PRIOR FILING DATE: 1998-06-24	
35	PRIOR APPLICATION NUMBER: 60/090444	
36	PRIOR FILING DATE: 1998-06-24	
37	PRIOR APPLICATION NUMBER: 60/090445	
38	PRIOR FILING DATE: 1998-06-24	
39	PRIOR APPLICATION NUMBER: 60/090472	
40	PRIOR FILING DATE: 1998-06-24	
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42	PRIOR FILING DATE: 1998-06-24	
43	PRIOR APPLICATION NUMBER: 60/090540	
44	PRIOR FILING DATE: 1998-06-24	
45	PRIOR APPLICATION NUMBER: 60/090542	
46	PRIOR FILING DATE: 1998-06-24	
47	PRIOR APPLICATION NUMBER: 60/090557	
48	PRIOR FILING DATE: 1998-06-24	
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61	PRIOR APPLICATION NUMBER: 60/090862	
62	PRIOR FILING DATE: 1998-06-26	
63	PRIOR APPLICATION NUMBER: 60/090863	
64	PRIOR FILING DATE: 1998-06-26	
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66	PRIOR FILING DATE: 1998-07-01	
67	PRIOR APPLICATION NUMBER: 60/091478	
68	PRIOR FILING DATE: 1998-07-02	
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70	PRIOR FILING DATE: 1998-07-01	
71	PRIOR APPLICATION NUMBER: 60/091519	
72	PRIOR FILING DATE: 1998-07-02	
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1 PRIOR FILING DATE: 1998-07-02  
2 PRIOR APPLICATION NUMBER: 60/091633  
3 PRIOR FILING DATE: 1998-07-02  
4 PRIOR APPLICATION NUMBER: 60/091978  
5 PRIOR FILING DATE: 1998-07-07  
6 PRIOR APPLICATION NUMBER: 60/091982  
7 PRIOR FILING DATE: 1998-07-07  
8 PRIOR APPLICATION NUMBER: 60/092182  
9 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 160 SCYNA 164

## RESULT 24

US-09-993-667-197  
Sequence 197, Application US/09993667  
Publication No. US20030022187A1  
GENERAL INFORMATION:  
1 APPLICANT: Ashkenazi, Avi J.  
2 APPLICANT: Baker, Kevin P.  
3 APPLICANT: Botstein, David  
4 APPLICANT: Desnoyers, Luc  
5 APPLICANT: Eaton, Dan L.  
6 APPLICANT: Ferrara, Napoleone  
7 APPLICANT: Fong, Sherman  
8 APPLICANT: Gerber, Hanspeter  
9 APPLICANT: Gottlieb, Mary E.  
10 APPLICANT: Goddard, Audrey  
11 APPLICANT: Godowski, Paul J.  
12 APPLICANT: Grimaldi, J. Christopher  
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17 APPLICANT: Paoni, Nicholas F.  
18 APPLICANT: Roy, Margaret Ann.  
19 APPLICANT: Stewart, Timothy A.  
20 APPLICANT: Tumas, Daniel  
21 APPLICANT: Watanabe, Colin K.  
22 APPLICANT: Williams, P. Mickey  
23 APPLICANT: Wood, William I.  
24 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C4

CURRENT APPLICATION NUMBER: US/09/993,667

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

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; PRIOR FILING DATE: 1998-07-01  
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; PRIOR FILING DATE: 1998-07-02  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07

; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
  
Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCVNA 5  
Db 160 SCVNA 164  
  
RESULT 25  
US-09-997-428-197  
; Sequence 197, Application US/09997428  
; Publication No. US20030027162A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC44  
; CURRENT APPLICATION NUMBER: US/09/997,428  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Caps 0;  
Matches 5; Conservative 0; Mismatches 0;

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Db 160 SCYNA 164

RESULT 26  
US-09-997-666-197  
Sequence 197, Application US/09997666  
Publication No. US20030027163A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eston, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Grittsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavir, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C42  
CURRENT APPLICATION NUMBER: US/09/997,666  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
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Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 160 SCYNA 164

RESULT 27  
US-09-990-438-197

; Sequence 197, Application US/09990438  
; Publication No. US20030027754A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Gerritsen, Mary E.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC3  
; CURRENT APPLICATION NUMBER: US/09/990,438  
; CURRENT FILING DATE: 2001-11-14  
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
 Best Local Similarity 100.0%; Pred No. 2e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 1 SCYNA 5  
 Db 160 SCYNA 164

RESULT 28  
 US-09-990-562-197  
 ; Sequence 197, Application US/09990562  
 ; Publication No. US20030027985A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc

APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C18  
CURRENT APPLICATION NUMBER: US/09/990,562  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCVNA 5  
Db 160 SCVNA 164

## RESULT 29

US-09-990-711-197  
; Sequence 197, Application US/09990711  
; Publication No. US20030032023A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

;  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC2  
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; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-09  
;

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVNA 5

Db 160 SCVNA 164

RESULT 30

US-09-989-726-197  
; Sequence 197, Application US/09989726  
; Publication No. US20030040473A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C60  
CURRENT APPLICATION NUMBER: US/09/989,726  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/090676

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 30; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 28+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SCYNA 5
Db      160 SCYNA 164
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RESULT 31
US-09-998-156-197
; Sequence 197, Application US/09998156
; Publication No. US20030044806A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC28
; CURRENT APPLICATION NUMBER: US/09/998,156
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+00;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 160 SCYNA 164

## RESULT 32

US-09-990-437-197  
; Sequence 197, Application US/09990437  
; Publication No. US20030045463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C49  
; CURRENT APPLICATION NUMBER: US/09/990,437  
; CURRENT FILING DATE: 2001-11-16  
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; PRIOR APPLICATION NUMBER: 60/062250

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Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
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RESULT 34  
US-09-997-514-197  
; Sequence 197, Application US/09997514  
; Publication No. US20030049681A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
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; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC46  
; CURRENT APPLICATION NUMBER: US/09/997,514  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
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/ PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 26+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 160 SCYNA 164

RESULT 35
US-09-997-573-197
/ Sequence 197, Application US/09997573
/ Publication No. US20030049682A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C45
/ CURRENT APPLICATION NUMBER: US/09/997,573
/ CURRENT FILING DATE: 2001-11-15
/ PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100.0%; Score 30; DB 12; Length 346;

Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
DB 160 SCYNA 164

## RESULT 36

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; Publication No. US20030050457A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 SCVNA 5  
Db 160 SCVNA 164

## RESULT 37

US-09-990-726-197  
; Sequence 197, Application US/09990726  
; Publication No. US20030054359A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C16  
; CURRENT APPLICATION NUMBER: US/09/990, 726  
; CURRENT FILING DATE: 2001-11-14  
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Query Match 100.0%; Score 30; DB 12; Length 346;

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RESULT 38

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC40
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Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 39  
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; Publication No. US2003005404A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter

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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR APPLICATION NUMBER: 60/091633  
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;; PRIOR APPLICATION NUMBER: 60/091978  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 160 SCYNA 164

RESULT 40

US-09-990-443-197

; Sequence 197, Application US/09990443

; Publication No. US20030054987A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Forg, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC12  
;; CURRENT APPLICATION NUMBER: US/09/990,443  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
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;; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 30; DB 12; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 160 SCYNA 164

Search completed: July 18, 2003, 15:35:53  
Job time : 14.9 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:20 ; Search time 6.82 Seconds  
(without alignments)  
66.897 Million cell updates/sec

Title: US-10-007-790-7  
Perfect score: 61  
Sequence: 1 SGAYRYGVVY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	60.7	302	1 META_BACSU	P54167 bacillus su
2	37	60.7	679	1 TKT1_KULIA	Q12630 kluveromyc
3	37	60.7	695	1 TKT_PICST	P34736 pichia stip
4	37	60.7	705	1 STT3_HUMAN	P46977 homo sapien
5	37	60.7	705	1 STT3_MOUSE	P46978 mus musculu
6	36	59.0	144	1 CNIH_HUMAN	O95406 homo sapien
7	36	59.0	144	1 CNIH_MOUSE	O35372 mus musculu
8	36	59.0	144	1 CNI_DROME	P49858 drosophila
9	36	59.0	144	1 CNI_DROVI	P52159 drosophila
10	36	59.0	408	1 G10A_DROME	P58950 drosophila
11	36	59.0	408	1 G47B_DROME	P58961 drosophila
12	36	59.0	679	1 TKT1_YEAST	P23254 saccharomyc
13	35	57.4	64	1 Y64_IANBD	P03773 bacterioph
14	35	57.4	130	1 YEW5_YEAST	P40082 saccharomyc
15	35	57.4	253	1 PSA7_CABEL	O95005 caenorhabdi
16	35	57.4	344	1 RL3_AERPE	O9yfm2 aeropyrum p
17	35	57.4	355	1 RECA_RHOCA	P42447 rhodobacter
18	35	57.4	393	1 HXAA_HUMAN	P31260 homo sapien
19	35	57.4	399	1 HXAA_MOUSE	P31310 mus musculu
20	35	57.4	540	1 ASDI_NEUCR	P78710 neurospora
21	35	57.4	1124	1 YPHG_ECOLI	P76585 escherichia
22	35	57.4	1501	1 SNQ2_YEAST	P32568 saccharomyc
23	34	55.7	77	1 FER7_METJA	O58132 methanococc
24	34	55.7	92	1 GONI_CAVPO	O54713 cavia porce
25	34	55.7	207	1 NP1_RHOPR	Q26239 rhodnius pr
26	34	55.7	208	1 PSB5_HUMAN	P28074 h proteasom
27	34	55.7	209	1 PSB5_MOUSE	O55234 mus musculu
28	34	55.7	259	1 KDKA_XYLFA	O9pbj1 xyliella fas
29	34	55.7	314	1 META_STRPN	O97pm9 streptococc
30	34	55.7	338	1 RFAJ_ECOLI	P27129 escherichia
31	34	55.7	351	1 RL3_SULSO	O9uxa8 sulfolobus
32	34	55.7	373	1 G10B_DROME	O9vy22 drosophila
33	34	55.7	387	1 RL3A_SCHPO	P40372 schizosacch

34	34	55.7	387	1 RL3B_SCHPO	P36584 schizosacch
35	34	55.7	677	1 TKT1_CANAL	O94039 candida alb
36	34	55.7	681	1 TKT2_YEAST	P33315 saccharomyc
37	33.5	54.9	1090	1 PULA_KLEPN	P07206 klebsiella
38	33.5	54.9	1096	1 PULA_KLEAE	P07811 klebsiella
39	33	54.1	105	1 RNMS_ASPSA	P00653 aspergillus
40	33	54.1	119	1 VTU3_DROME	Q06521 drosophila
41	33	54.1	195	1 CSL4_HUMAN	O9y3b2 homo sapien
42	33	54.1	238	1 DSBC_ERWCH	P39691 erwinia chr
43	33	54.1	253	1 Y990_CAMJE	P45489 campylobact
44	33	54.1	255	1 AMPM_TREPA	O83814 treponema p
45	33	54.1	256	1 PSB5_CHICK	P34065 gallus gall

ALIGNMENTS

RESULT 1  
META\_BACSU  
ID META\_BACSU STANDARD; PRT; 302 AA.  
AC P54167;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Homoserine O-succinyltransferase (EC 2.3.1.46) (Homoserine O-transuccinylase) (HTS).  
GN META OR METB.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168 / Marburg;  
RX MEDLINE=96349105; PubMed=8760912;  
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D., Serror P.;  
RT "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome.";  
RL Microbiology 142:2005-2016(1996).  
RN [2]  
RP IDENTIFICATION OF PROBABLE FRAMESHIFT.  
RA Bairoch A.;  
RL Unpublished observations (DEC-2000).  
CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + L-homoserine = CoA + O-succinyl-L-homoserine.  
CC -!- PATHWAY: Methionine biosynthesis; HTS variant; first step.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE HTS FAMILY.  
CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 221.  
CC -----  
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CC -----  
DR EMBL; L77246; AAA96625.1; ALT\_FRAME.  
DR EMBL; Z99115; CAB14109.1; ALT\_FRAME.  
DR Subtilist; BG11534; meta.  
DR TIGRFAMS; TIGR01001; meta; 1.  
KW Methionine biosynthesis; Transferase; Acyltransferase;  
KW Complete proteome.  
FT ACT\_SITE 142 142 POTENTIAL.  
SQ SEQUENCE 302 AA; 35451 MW; 1BE392C62D30321F CRC64;

Query Match 60.7%; Score 37; DB 1; Length 302;  
Best Local Similarity 66.7%; Pred.No.16;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SGAYRYGVV 9

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Db 147 AGLYYHYGV 155
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RESULT 2
TKT1_KLULA
ID_TKT1_KLULA STANDARD; PRT; 679 AA.
AC Q12630; 1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Transketolase (EC 2.2.1.1) (TK).
GN TKL1.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
PC STRAIN-CBS 2359/152;
RX MEDLINE=97153463; PubMed=9000376;
RA Jacoby J.J., Heinisch J.J.;
RT "Analysis of a transketolase gene from Kluyveromyces lactis reveals
RT that the yeast enzymes are more related to transketolases of
RT prokaryotic origins than to those of higher eukaryotes.";
RL Curr. Genet. 31:15-21(1997).
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL; Z26486; CAA81260.1; -
DR PIR; S37439; S37439.
DR HSSP; P23254; ITRK.
DR InterPro; IPR000360; Transketolase.
DR Pfam; PF00456; transketolase; 1.
DR Pfam; PF02779; transket_pyr; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR TIGRFAMs; TIGR00232; tktlase_bact; 1.
DR PROSITE; PS00801; TRANSKETOLASE_1; 1.
DR PROSITE; PS00802; TRANSKETOLASE_2; 1.
DR TRANSFERASE; Thiamine pyrophosphate.
KW TRANSFERASE; Thiamine pyrophosphate.
SQ SEQUENCE 679 AA; 73703 MW; BC5F3CF61A78CDA4 CRC64;
Query Match 60.7%; Score 37; DB 1; Length 679;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGAYRYGV 9
||| |||
Db 407 SGRYIRYGV 415
RESULT 3
TKT_PICST
ID_TKT_PICST STANDARD; PRT; 695 AA.
AC P34736; 1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Transketolase (EC 2.2.1.1) (TK).
GN TKT.
OS Pichia stipitis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=28985;
RN [1]
PC STRAIN-CBS 2359/152;
RX MEDLINE=97153463; PubMed=9000376;
RA Jacoby J.J., Heinisch J.J.;
RT "Analysis of a transketolase gene from Kluyveromyces lactis reveals
RT that the yeast enzymes are more related to transketolases of
RT prokaryotic origins than to those of higher eukaryotes.";
RL Curr. Genet. 31:15-21(1997).
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL; U65983; AAB05935.1; -
DR HSSP; P23254; ITRK.
DR InterPro; IPR000360; Transketolase.
DR Pfam; PF00456; transketolase; 1.
DR Pfam; PF02779; transket_pyr; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR TIGRFAMs; TIGR00232; tktlase_bact; 1.
DR PROSITE; PS00801; TRANSKETOLASE_1; 1.
DR PROSITE; PS00802; TRANSKETOLASE_2; 1.
DR TRANSFERASE; Thiamine pyrophosphate.
KW TRANSFERASE; Thiamine pyrophosphate.
SQ SEQUENCE 679 AA; 73703 MW; BC5F3CF61A78CDA4 CRC64;
Query Match 60.7%; Score 37; DB 1; Length 679;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGAYRYGV 9
||| |||
Db 407 SGRYIRYGV 415
RESULT 4
STT3_HUMAN
ID STT3_HUMAN STANDARD; PRT; 705 AA.
AC P46977;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral
DE membrane protein 1) (TMC).
GN ITM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
PC SEQUENCE FROM N.A.
RX MEDLINE=96435424; PubMed=8838310;
RA Hong G., Deleersnijder W., Kozak C.A., van Marck E., Tylzanowski P.,
RA Merregaert J.;
RT "Molecular cloning of a highly conserved mouse and human integral
RT membrane protein (Itm1) and genetic mapping to mouse chromosome 9.";
RL Genomics 31:295-300(1996).
CC -1- FUNCTION: INVOLVED IN PROTEIN GLYCOSYLATION. EITHER REQUIRED FOR
CC THE ASSEMBLY OF THE OLIGOSACCHARYL TRANSFERASE (OTASE) COMPLEX
CC OR REQUIRED IN SUBSTOICHIOMETRIC AMOUNTS FOR OTASE ACTIVITY
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE STT3 FAMILY.
```

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CC EMBL; L38961; AAB05994.1; -  
CC Genew; HGNC:6172; ITM1.  
CC MIM; 601134; -  
CC InterPro; IPR003674; OTase\_STT3.  
CC Pfam; PF02516; STT3; 1.  
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KW Transmembrane.  
FT TRANSMEM 18 38 POTENTIAL.  
FT TRANSMEM 83 103 POTENTIAL.  
FT TRANSMEM 115 135 POTENTIAL.  
FT TRANSMEM 138 158 POTENTIAL.  
FT TRANSMEM 170 190 POTENTIAL.  
FT TRANSMEM 209 229 POTENTIAL.  
FT TRANSMEM 236 259 POTENTIAL.  
FT TRANSMEM 301 321 POTENTIAL.  
FT TRANSMEM 360 380 POTENTIAL.  
FT TRANSMEM 384 404 POTENTIAL.  
FT TRANSMEM 406 426 POTENTIAL.  
FT TRANSMEM 454 474 POTENTIAL.  
FT TRANSMEM 573 593 POTENTIAL.  
SQ SEQUENCE 705 AA; 80471 MW; DBF50C217EA40AE4 CRC64;  
  
Query Match 60.7%; Score 37; DB 1; Length 705;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 644 YRFGQVY 651  
  
RESULT 5  
STT3\_MOUSE  
ID STT3\_MOUSE STANDARD; PRT; 705 AA.  
AC P46978;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral  
DE membrane protein 1).  
GN ITM1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Mandibular condyle;  
RX MEDLINE=96435424; PubMed=8838310;  
RA Hong G., Deleersnijder W., Kozak C.A., van Marck E., Tylzanowski P.,  
RA Mergaert J.;  
RT "Molecular cloning of a highly conserved mouse and human integral  
RT membrane protein (itm1) and genetic mapping to mouse chromosome 9";  
RL Genomics 31:295-300(1996).  
CC -!- FUNCTION: INVOLVED IN PROTEIN GLYCOSYLATION. EITHER REQUIRED FOR  
CC THE ASSEMBLY OF THE OLIGOSACCHARYL TRANSFERASE (OTASE) COMPLEX  
CC OR REQUIRED IN SUBSTOICHIOMETRIC AMOUNTS FOR OTASE ACTIVITY  
CC (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE STT3 FAMILY.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; L34260; AAB47775.1; -  
CC MGD; MGI:105124; Itm1.  
CC InterPro; IPR003674; OTase\_STT3.  
CC Pfam; PF02516; STT3; 1.  
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KW Transmembrane.  
FT TRANSMEM 19 39 POTENTIAL.  
FT TRANSMEM 83 103 POTENTIAL.  
FT TRANSMEM 115 135 POTENTIAL.  
FT TRANSMEM 138 158 POTENTIAL.  
FT TRANSMEM 170 190 POTENTIAL.  
FT TRANSMEM 209 229 POTENTIAL.  
FT TRANSMEM 236 259 POTENTIAL.  
FT TRANSMEM 301 321 POTENTIAL.  
FT TRANSMEM 360 380 POTENTIAL.  
FT TRANSMEM 384 404 POTENTIAL.  
FT TRANSMEM 406 426 POTENTIAL.  
FT TRANSMEM 459 479 POTENTIAL.  
FT TRANSMEM 573 593 POTENTIAL.  
SQ SEQUENCE 705 AA; 80597 MW; CD1D796D0479F321 CRC64;  
  
Query Match 60.7%; Score 37; DB 1; Length 705;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 644 YRFGQVY 651  
  
RESULT 6  
CNH\_HUMAN  
ID CNH\_HUMAN STANDARD; PRT; 144 AA.  
AC O95406;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cornichon homolog (TCAM77).  
GN CNH OR CNIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Carcinoma;  
RA Plisov S.Y., Ivanov S.V., Lerman M., Perantoni A.O.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=20499367; PubMed=11042152;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells";  
RL Genome Res. 10:1546-1560(2000).  
RN [3]  
RP SEQUENCE OF 11-144 FROM N.A.  
RX MEDLINE=99227056; PubMed=10209299;  
RA Utku N., Bulwin G.-C., Beinke S., Heinemann T., Beato F., Randall J.,  
RA Schnieders B., Sandhoff K., Volk H.-D., Milford E., Gullans S.R.;  
RT "The human homolog of Drosophila cornichon protein is differentially  
RT expressed in allocated T-cells";  
RL Biochim Biophys Acta 1449:203-210(1999).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LIVER, SKELETAL  
CC MUSCLE, PANCREAS, ADRENAL MEDULLA AND CORTEX, THYROID, TESTIS,

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CC SPLEEN, APPENDIX, PERIPHERAL BLOOD LYMPHOCYTES AND BONE MARROW.
CC LOWER EXPRESSION FOUND IN BRAIN, PLACENTA, LUNG, KIDNEY, OVARY,
CC SMALL INTESTINE, STOMACH, LYMPH NODE, THYMUS AND FETAL LIVER.
CC -/- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC -----
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CC -----
DR EMBL; AF104398; AAC98388.1; -
DR EMBL; AF070854; AAD20960.1; -
DR EMBL; AF031379; AAD32301.1; -
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
DR PROSITE; PS01340; Cornichon; 1.
KW Transmembrane
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
SQ SEQUENCE 144 AA; 16699 MW; 59BD114D24C455CD CRC64;
Query Match 59.0%; Score 36; DB 1; Length 144;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 YRYGVVY 11
DB 132 YYLYGMIV 139
RESULT 7
ID CNIH_MOUSE STANDARD; PRT; 144 AA.
AC Q35372;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cornichon homolog.
GN CNIH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6D2;
RX MEDLINE=991471139; PubMed=10022955;
RA Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;
RT "The mouse cornichon gene family.";
RL Dev. Genes Evol. 209:120-125(1999).
CC -/- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -/- TISSUE SPECIFICITY: EXPRESSED IN OOCYTES, AND AT A BASAL LEVEL IN
CC OVARIAN SOMATIC CELLS OF 6-WEEK-OLD MOUSE. EXPRESSED IN ADULT
CC BRAIN.
CC -/- DEVELOPMENTAL STAGE: ABUNDANT IN FULL GROWN OOCYTE AND THE
CC OVULATED UNFERTILIZED EGG, SHOWS A SLIGHT DECREASE 12 HOURS AFTER
CC FERTILIZATION. TRANSCRIPTS FROM THE ACTIVATED EMBRYONIC GENOME ARE
CC PRESENT IN THE EIGHT-CELL EMBRYO.
CC -/- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC -----
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CC -----
DR EMBL; AF022811; AAC15828.1; -
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DR MGD; MGI:1277202; Cnih.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
DR PROSITE; PS01340; CORNICHON; 1.
KW Transmembrane
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
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Query Match 59.0%; Score 36; DB 1; Length 144;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 YRYGVVY 11
DB 132 YYLYGMIV 139
RESULT 8
ID CNI_DROME STANDARD; PRT; 144 AA.
AC P49858; Q9V423;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cornichon protein.
GN CNI OR CG5855.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95300228; PubMed=7540118;
RA Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;
RT "Cornichon and the EGF receptor signaling process are necessary for
RT both anterior-posterior and dorsal-ventral pattern formation in
RT Drosophila.";
RL Cell 81:967-978(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale A., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng C., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
CC -!- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY  
CC TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES  
CC POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE  
CC ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING  
CC EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE  
CC DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC CELL OCYTE CLUSTER. IT IS HIGHLY EXPRESSED IN STAGE 1-6 EGG  
CC CHAMBERS, EXPRESSION CEASES DURING STAGE 7 AND CANNOT BE DETECTED  
CC IN STAGES 8 AND 9. DURING STAGE 10, IT IS REEXPRESSED IN THE NURSE  
CC CELLS.  
CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.  
CC  
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CC  
CC EMBL; U28069; AAA86527.1; -;  
CC EMBL; AE003415; AAP45003.1; -;  
CC EMBL; AE003650; AAP5321.1; -;  
CC FlyBase; FBgn0003339; cni.  
CC InterPro; IPR003337; Cornichon.  
CC Pfam; PF03311; Cornichon; 1.  
CC PROSITE; PS01340; CORNICHON; 1.  
CC Developmental protein; Transmembrane.  
FT TRANSMEM 11 31 POTENTIAL.  
FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
SQ SEQUENCE 144 AA; 16931 MW; 27692A3F68ECE1A9 CRC64;  
  
Query Match 59.0%; Score 36; DB 1; Length 144;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 132 YYIGVMY 139  
  
RESULT 9  
ID\_CNI\_DROVI STANDARD; PRT; 144 AA.  
AC P52159;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cornichon protein.  
GN CNI.  
OS *Drosophila virilis* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7244;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=95300228; PubMed=7540118;  
RA Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;  
RT "Cornichon and the EGF receptor signaling process are necessary for  
RT both anterior-posterior and dorsal-ventral pattern formation in  
RT *Drosophila*.";  
RL Cell 81:967-978(1995).  
CC -!- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY  
CC TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES  
CC POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE  
CC ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING  
CC EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE  
CC DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.  
CC FlyBase; FBgn0015209; Dvir\cni.  
DR InterPro; IPR003377; Cornichon.  
DR Pfam; PF03311; Cornichon; 1.  
DR PROSITE; PS01340; CORNICHON; 1.  
KW Developmental protein; Transmembrane.  
FT TRANSMEM 11 31 POTENTIAL.  
FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
SQ SEQUENCE 144 AA; 16927 MW; D0F4E65560409164 CRC64;  
  
Query Match 59.0%; Score 36; DB 1; Length 144;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 132 YYIGVMY 139  
  
RESULT 10  
ID\_GLOA\_DROME STANDARD; PRT; 408 AA.  
AC P58950;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Putative gustatory receptor 10a.  
GN GR10A.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassenaar D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
"The genome sequence of *Drosophila melanogaster*";  
Science 287:2185-2195(2000).  
[2]  
IDENTIFICATION.  
RX MEDLINE=21407712; PubMed=11516643;  
RN Dunipace L., Meister S., McNeely C., Amrein H.;  
RT "Spatially restricted expression of candidate taste receptors in the  
RT *Drosophila* gustatory system";  
RN Curr. Biol. 11:822-835(2001).  
[3]  
CONCEPTUAL TRANSLATION.  
RP Robertson H.;  
RC Unpublished observations (NOV-2001).  
RL CC -1- FUNCTION: Probable role in the gustatory response.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED  
CC RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR ENBL; AE003486; -; NOT\_ANNOTATED\_CDS.  
DR Flybase; FBgn004502; Gr10a.  
KW Hypothetical protein; Receptor; G-protein coupled receptor;  
KW Transmembrane; Glycoprotein; Multigene family.  
KW DOMAIN 1 20 EXTRACELLULAR (POTENTIAL).  
FT FT TRANSMEM 21 38 1 (POTENTIAL).  
FT FT DOMAIN 39 48 CYTOPLASMIC (POTENTIAL).  
FT FT TRANSMEM 49 69 2 (POTENTIAL).  
FT FT DOMAIN 70 86 3 (POTENTIAL).  
FT FT TRANSMEM 87 107 3 (POTENTIAL).  
FT FT DOMAIN 108 144 4 (POTENTIAL).  
FT FT TRANSMEM 145 165 4 (POTENTIAL).  
FT FT DOMAIN 166 270 5 (POTENTIAL).  
FT FT TRANSMEM 271 291 5 (POTENTIAL).  
FT FT DOMAIN 292 304 6 (POTENTIAL).  
FT FT TRANSMEM 305 325 6 (POTENTIAL).  
FT FT DOMAIN 326 381 7 (POTENTIAL).  
FT FT TRANSMEM 382 402 7 (POTENTIAL).  
FT FT DOMAIN 403 408 7 (POTENTIAL).  
FT FT CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL).  
FT FT CARBOHYD 205 205 63FEBB27DD8B56AD CRC64;  
SQ SEQUENCE 408 AA; 48391 MW; 63FEBB27DD8B56AD CRC64;

Qy	Query Match	59.0%;	Score 36;	DB 1;	Length 408;
	Best Local Similarity	75.0%;	Pred. No. 33;		
	Matches	6;	Conservative	1;	Mismatches 1; Indels 0; Gaps
Qy	4 YRYGVVY 11				
Dd	18 FYRIGHVY 25				
RESULT 11					
ID	G47B DROME	STANDARD;	PRT;	408 AA.	
AC	P58961;				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Putative gustatory receptor 47b.				
GN	GR47B.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;				
OC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
ON	NCBI_TaxID=7227;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Berkeley;				
RX	MEDLINE=20196006; PubMed=10731132;				
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,				
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Benson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,				
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,				
RA	Fosler C., Gabriellian A.E., Garg N.S., Galbart W.M., Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,				
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,				
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,				
RA	Spier E., Spradling A.C., Scapleton M., Strong R., Sun E.,				
RA	SVarskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,				
RA	Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,				
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,				
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,				
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;				
RT	"The genome sequence of Drosophila melanogaster.;"				
RL	Science 287:2185-2195(2000)				
RP	[2]				
RN	CONCEPTUAL TRANSLATION.				
RA	Robertson H.;				
RL	Unpublished observations (NOV-2001).				
CC	-!- FUNCTION: Probable role in the gustatory response.				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).				
CC	-!- SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED				

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CC -----
CC EMBL: AE003486; -; NOT ANNOTATED_CDS.
DR FLYBase: FBgn041241; Gr47b.
KW Hypothetical protein; Receptor; G-protein coupled receptor;
KW Transmembrane; Glycoprotein; Multigene family.
FT DOMAIN 1 20 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 21 38 1 (POTENTIAL).
FT DOMAIN 39 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 2 (POTENTIAL).
FT DOMAIN 70 86 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 87 107 3 (POTENTIAL).
FT DOMAIN 108 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 165 4 (POTENTIAL).
FT DOMAIN 166 270 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 271 291 5 (POTENTIAL).
FT DOMAIN 292 304 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 305 325 6 (POTENTIAL).
FT DOMAIN 326 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 402 7 (POTENTIAL).
FT DOMAIN 403 408 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 408 AA; 48391 MW; 63FEBB27DDB856AD CRC64;

Query Match 59.0%; Score 36; DB 1; Length 408;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YYRYGVVY 11
Db 18 FYRYGVVY 25
:|||||

RESULT 12
TKTL YEAST STANDARD; PRT; 679 AA.
AC P23254;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transketolase 1 (EC 2.2.1.1) (TK 1).
GN TKL1 OR YPR074C OR YP9499.29C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92144611; PubMed=1737042;
RA Fletcher T.S., Kwee I.L., Nakada T., Largman C., Martin B.M.;
RT "DNA sequence of the yeast transketolase gene.";
RL Biochemistry 31:1892-1896(1992).
RN [2]
RN SEQUENCE FROM N.A.
RN STRAIN=W303-1A;
RX MEDLINE=94043273; PubMed=8226984;
RA Sundstroem M., Lindqvist Y., Schneider G., Hellman U., Ronne H.;
RT "Yeast TKL1 gene encodes a transketolase that is required for
RT efficient glycolysis and biosynthesis of aromatic amino acids.";
RL J. Biol. Chem. 268:24346-24352(1993).
RN [3]
RN SEQUENCE FROM N.A.
RN STRAIN=S288c / AB972;
RX MEDLINE=97313271; PubMed=9169875;

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RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoerge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Church C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunnicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schramm S., Schroeder M., Sidcu A.M., Tettelin H.,
RA Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
RN [4]
RN SEQUENCE OF 1-35.
RP MEDLINE=92253546; PubMed=1812485;
RX Nixon P.F., Duggleby R.G.;
RT "The N-terminal amino acid sequence of yeast transketolase.";
RL Protein Seq. Data Anal. 4:325-326(1991).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92331588; PubMed=1628611;
RA Lindqvist Y., Schneider G., Ermler U., Sundstroem M.;
RT "Three-dimensional structure of transketolase, a thiamine diphosphate
RT dependent enzyme, at 2.5-A resolution.";
RL EMBO J. 11:2373-2379(1992).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=94231561; PubMed=8176731;
RA Nikola M., Lindqvist Y., Schneider G.;
RT "Refined structure of transketolase from Saccharomyces cerevisiae at
RT 2.0-A resolution.";
RL J. Mol. Biol. 238:387-404(1994).
RN [7]
RP MUTAGENESIS OF HIS, AND X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=98062276; PubMed=9398292;
RA Wikner C., Nilsson U., Meshalkina L., Udekwu C., Lindqvist Y.,
RA Schneider G.;
RT "Identification of catalytically important residues in yeast
RT transketolase.";
RL Biochemistry 36:15643-15649(1997).
RN [8]
RP MUTAGENESIS OF HIS-102.
RX MEDLINE=96085137; PubMed=8521838;
RA Wikner C., Meshalkina L., Nilsson U., Baeckstroem S., Lindqvist Y.,
RA Schneider G.;
RT "His103 in yeast transketolase is required for substrate recognition
RT and catalysis.";
RL Eur. J. Biochem. 233:750-755(1995).
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE. REQUIRES MAGNESIUM IONS FOR
CC CATALYTIC ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
CC -----
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CC -----
CC EMBL: M63302; AAA35168.1; -
CC ENBL: X73224; CAA51693.1; -
CC EMBL: Z49219; CAA89191.1; -
CC EMBL: Z71255; CAA94982.1; -

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DR PRINTS; PR00142; RECA.
DR PRODOM; PD000229; RECA. 1.
DR PROSITE; PS00321; RECA. 1; 1.
DR PROSITE; PS00162; RECA. 2; 1.
DR PROSITE; PS00163; RECA. 3; 1.
DR KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP BIND 78 85 ATP (BY SIMILARITY).
SQ SEQUENCE 355 AA; 38027 MW; 64E408A33A2DE77E CRC64;

Query Match 57.4%; Score 35; DB 1; Length 393;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYRG 8
DB 299 SGAWYSYG 306

RESULT 18
HXAA_HUMAN
ID HXAA_HUMAN STANDARD; PRT; 393 AA.
AC P31260; Q15949; O43605; O43370;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A10 (Hox-1.8) (PL).
GN HOXA10 OR HOX1.8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91288229; PubMed=1676505;
RA Lowrey P., Corral J.C., Detmer K., Lebeau M.M., Deaven L.,
RA Lawrence H.J., Largman C.;
RT "A human Hox 1 homeobox gene exhibits myeloid-specific expression of
RT alternative transcripts in human hematopoietic cells.";
RL Nucleic Acids Res. 19:3443-3449(1991).
RN [2]
SEQUENCE FROM N.A.
RA Mi X., Winters J.L., Stevens D.B., Fleischman R.A.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RA Bradshaw H., Hinds K., Keppler D.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE OF 301-383 FROM N.A.
RX MEDLINE=90046832; PubMed=2573064;
RA Shen W.-F., Largman C., Lowrey P., Corral J.C., Detmer K.,
RA Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
RT "Lineage-restricted expression of homeobox-containing genes in human
RT hematopoietic cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
RN [5]
SEQUENCE OF 319-384 FROM N.A.
RX MEDLINE=90098876; PubMed=2574852;
RA Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio E.,
RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
RT "The human HOX gene family.";
RL Nucleic Acids Res. 17:10385-10402(1989).
RN [6]
SEQUENCE OF 332-370 FROM N.A.
RX MEDLINE=94145486; PubMed=7906121;
RA Castonovo V., Kusaka M., Chariot A., Gielen J., Sobel M.;
RT "Homeobox genes: potential candidates for the transcriptional control
RT of the transformed and invasive phenotype.";
RL Biochem. Pharmacol. 47:137-143(1994).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC BINDS TO THE DNA SEQUENCE 5'-AA(AT)TTTATTAC-3'.
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CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PL1 (SHOWN HERE) AND 2/PL2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE ABD-B HOMEBOX FAMILY.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A NUMBER OF
CC FRAMESHIFTS.
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CC -----
CC EMBL; X58430; CAB86198.1; ALT_FRAME.
CC EMBL; AF040714; AAB96917.1; -.
CC EMBL; AC004080; -. NOT ANNOTATED_CDS.
CC EMBL; M30599; AAA36006.1; -.
CC EMBL; S69027; AAD14030.1; -.
CC EMBL; S69029; AAD14031.1; -.
CC PIR; S14930; S14930.
CC PIR; S26402; S26402.
CC PIR; A34425; A34425.
CC HSSP; P02833; 9ANT.
CC TRANSFAC; T01713; -.
CC Genew; HGNC:5100; HOXA10.
CC MIM; 142957; -.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00711; HOMEBOX_2; 1.
CC KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation; Alternative splicing.
FT DOMAIN 26 39 POLY-GLY.
FT DOMAIN 78 89 POLY-GLY.
FT DOMAIN 116 120 POLY-PRO.
FT DOMAIN 124 133 POLY-PRO.
FT DOMAIN 208 215 POLY-GLY.
FT DOMAIN 256 259 POLY-PRO.
FT DOMAIN 319 378 HOMEBOX.
FT VARSPPLIC 1 299 MISSING (IN ISOFORM 2).
FT VARSPPLIC 300 370 DSI -> MCQ (IN ISOFORM 2).
FT CONFLICT 1 6 MSCS -> MFCTRVSQGLSAPFAKLSHNNVLMGE
FT CONFLICT 69 69 G -> R (IN REF. 1).
FT CONFLICT 136 137 OA -> HR (IN REF. 1).
FT CONFLICT 332 332 L -> S (IN REF. 4).
FT CONFLICT 334 334 L -> F (IN REF. 4).
FT CONFLICT 370 370 R -> P (IN REF. 4).
SQ SEQUENCE 393 AA; 40536 MW; 20F89542582D6F25 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 393;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11
DB 38 GGYAHGVVY 47

RESULT 19
HXAA_MOUSE
ID HXAA_MOUSE STANDARD; PRT; 399 AA.
AC P31310;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A10 (Hox-1.8).
GN HOXA10 OR HOXA-10 OR HOX-1.8.
```

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=CD-1; TISSUE=Kidney;  
 RX MEDLINE=92073356; PubMed=7862151;  
 RA Benson G.V., Nguyen T.-H.E., Maas R.L.;  
 RT "The expression pattern of the murine Hoxa-10 gene and the sequence  
 RT recognition of its homeodomain reveal specific properties of  
 RT Abdominal B-like genes.";  
 RL Mol. Cell. Biol. 15:1591-1601(1995).  
 RN [2]  
 RP SEQUENCE OF 325-384 FROM N.A.  
 RX MEDLINE=92073356; PubMed=1683707;  
 RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., Potter S.S.;  
 RT "Identification of 10 murine homeobox genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).  
 RN [3]  
 RP SEQUENCE OF 346-370 FROM N.A.  
 RX STRAIN=C57BL/6; TISSUE=Spleen;  
 RC MEDLINE=92073357; PubMed=1720547;  
 RA Murtha M.T., Leckman J.F., Ruddle F.H.;  
 RT "Detection of homeobox genes in development and evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10711-10715(1991).  
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTATTAC-3'.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IT  
 CC IS RESTRICTED TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS.  
 CC ALSO FOUND IN DEVELOPING GUT AND UROGENITAL TRACT. IN ADULT  
 CC TISSUE, BOTH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM 1 IS EXPRESSED  
 CC IN SKELETAL MUSCLE.  
 CC -!- DEVELOPMENTAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY 9  
 CC TO DAY 12 AND THEN DECLINES TO DAY 15.  
 CC -!- SIMILARITY: BELONGS TO THE ABD-B HOMEBOX FAMILY.  
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 CC EMBL; L08757; AAA67125.1; -;  
 CC EMBL; M81659; AAA63312.1; -;  
 CC PIR; F38809; F38809.  
 CC PIR; F37290; F37290.  
 CC HSP; P02833; 9ANT.  
 CC TRANSFAC; T01715; -;  
 CC MGD; MGI:96171; Hoxa10.  
 CC InterPro; IPR001356; Homeobox.  
 CC Pfam; PF00046; Homeobox; 1.  
 CC PRINTS; PR00024; HOMEBOX.  
 CC ProDom; PD000010; Homeobox; 1.  
 CC SMART; SM00389; HOX; 1.  
 CC PROSITE; PS00027; HOMEBOX\_1; 1.  
 CC PROSITE; PS00071; HOMEBOX\_2; 1.  
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 CC Transcription regulation; Alternative splicing.  
 KW DOMAIN 26 38 GLY-RICH.  
 FT DOMAIN 77 90 POLY-GLY.  
 FT DOMAIN 113 144 GLN/PRO-RICH.  
 FT DOMAIN 215 222 POLY-GLY.  
 FT DOMAIN 271 274 POLY-GLY.  
 FT DNA\_BIND 325 384 HOMEBOX.

FT VARSPPLIC 1 305 MISSING (IN ISOFORM 2).  
 FT VARSPPLIC 306 DSL -> MCQ (IN ISOFORM 2).  
 SQ SEQUENCE 399 AA; 41415 MW; 7529624FC6057042 CRC64;  
 Query Match 57.4%; Score 35; DB 1; Length 399;  
 Best Local Similarity 60.0%; Pred. No. 48;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAYRYGVVY 11  
 Db 37 GGYAHGGVY 46  
 RESULT 20  
 ASD1 NEUCR STANDARD; PRT; 540 AA.  
 ID ASD1 NEUCR STANDARD; PRT; 540 AA.  
 AC P78710;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative rhannogalacturonase precursor (EC 4.2.2.-)  
 DE (Rhannogalacturonan lyase) (RGase) (Ascus development protein 1) (Asd-  
 DE 1).  
 GN ASD-1.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]\_TaxID=5141;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97321283; PubMed=9178004;  
 RA Nelson M.A., Merino S.T., Metzberg R.L.;  
 RT "A putative rhannogalacturonase required for sexual development of  
 RT Neurospora crassa.";  
 RL Genetics 146:531-540(1997).  
 CC -!- FUNCTION: COULD BE A PECTINOLYTIC ENZYME THAT HYDROLYSES THE  
 CC ALPHA-L-RHAMNOPYRANOSYL-(1,4)-ALPHA-D-GALACTURONOPYRANOSYL  
 CC GLYCOSIDIC LINKAGE BY BETA-ELIMINATION, THEREBY GENERATING  
 CC OLIGOSACCHARIDES TERMINATING AT THE NON-REDUCING END WITH A HEX-4-  
 CC ENOPYRANOSYLURONIC ACID RESIDUE.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED PREFERENTIALLY DURING THE SEXUAL  
 CC CYCLE AND ESSENTIAL FOR NORMAL SEXUAL DEVELOPMENT.  
 CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 4.  
 CC -----  
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 CC -----  
 CC EMBL; U70861; AAB39649.1; -;  
 CC Lyase; Glycoprotein; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 540 PUTATIVE RHAMNOCALACTURONASE.  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 540 AA; 58011 MW; B4638A1B93A28A0 CRC64;  
 Query Match 57.4%; Score 35; DB 1; Length 540;  
 Best Local Similarity 70.0%; Pred. No. 65;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAYRYGVVY 11  
 Db 488 GAYRGYGVY 497  
 RESULT 21  
 YPHG\_ECOLI STANDARD; PRT; 1124 AA.  
 ID YPHG\_ECOLI  
 AC P76585;

```
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yphg.
GN YPHG OR B2549.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
CC -----
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CC -----
DR EMBL; AE000341; AAC75602.1; -
DR EcoGene; EG13468; yphg.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 5.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1124 AA; 127284 MW; EA3F919BC8F491F2 CRC64;
Query Match 57.4%; Score 35; DB 1; Length 1124;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 SGAYRYGV 9
Db 68 SGAYRYGV 76
RESULT 22
SNQ2_YEAST STANDARD; PRT; 1501 AA.
ID SNQ2_YEAST
AC P32568;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE SNQ2 protein.
GN SNQ2 OR YDR011W OR YD8119.16.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX Medline=93173094; PubMed=8437567;
RA Servos J., Haase E., Brendel M.;
RT "Gene SNQ2 of Saccharomyces cerevisiae, which confers resistance to
RT 4-nitroquinoline-N-oxide and other chemicals, encodes a 169 kDa
RT protein homologous to ATP-dependent permeases.";
RL Mol. Gen. Genet. 236:214-218 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX Murphy L., Richards C., Gentles S., Harris D., Barrell B.G.,
RA Rajandream M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=97051598; PubMed=8896275;
RA Eide L.G., Sander C., Prydz H.;
RT "Sequencing and analysis of a 35.4 kb region on the right arm of
RT chromosome IV from Saccharomyces cerevisiae reveal 23 open reading
RT frames.";
RL Yeast 12:1085-1090 (1996).
RN [4]
RP CHARACTERIZATION, AND SEQUENCE OF 1243-1247.
RX MEDLINE=95355421; PubMed=7629127;
RA Decottignies A., Lambert L., Catty P., Degand H., Epping E.A.,
RA Moye-Rowley W.S., Balzi E., Goffeau A.;
RT "Identification and characterization of SNQ2, a new multidrug ATP
RT binding cassette transporter of the yeast plasma membrane.";
RL J. Biol. Chem. 270:18150-18157 (1995)
CC -!- FUNCTION: COULD BE AN ATP-DEPENDENT PERMEASE. CONFERS HYPER-
CC RESISTANCE TO THE MUTAGENS 4-NITROQUINOLINE-N-OXIDE (4-NQO) AND
CC TRIAZOQUONE, AS WELL AS TO THE CHEMICALS SULPHOMETHURON METHYL
CC PHENANTHROLINE WHEN PRESENT IN MULTIPLE COPIES. EXHIBITS
CC NUCLEOSIDE TRIPHOSPHATASE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
CC -----
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CC -----
DR EMBL; X66732; CAA47270.1; -
DR EMBL; Z48008; CAA88071.1; -
DR EMBL; X95966; CAA65203.1; -
DR EMBL; Z74307; CAA98831.1; -
DR PIR; S30918; S30918.
DR -SGD; S0002418; SNQ2.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005285; PDR.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transportr; 2.
DR SMART; SM00382; AAA; 1.
DR TIGRfams; TIGR00956; 3a01205; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transmembrane; Glycoprotein; Transport.
FT TRANSMEM 521 541 POTENTIAL.
FT TRANSMEM 554 574 POTENTIAL.
FT TRANSMEM 600 620 POTENTIAL.
FT TRANSMEM 628 648 POTENTIAL.
FT TRANSMEM 664 680 POTENTIAL.
FT TRANSMEM 771 789 POTENTIAL.
FT TRANSMEM 1190 1212 POTENTIAL.
FT TRANSMEM 1216 1236 POTENTIAL.
FT TRANSMEM 1277 1296 POTENTIAL.
FT TRANSMEM 1333 1352 POTENTIAL.
FT TRANSMEM 1455 1475 POTENTIAL.
FT NP_BIND 889 896
FT CONFLICT 78 78 V -> E (IN REF. 1).
SQ SEQUENCE 1501 AA; 168766 MW; 96BE3D30CCFB76AC CRC64;
Query Match 57.4%; Score 35; DB 1; Length 1501;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 SGAYRYGVV 11
Db 548 SGAFSRGGVLY 558
RESULT 23
FERT_METJA STANDARD; PRT; 77 AA.
ID FERT_METJA
AC Q58132;
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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative ferredoxin MJ0722.
GN MJ0722.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sulton C.J., White G., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sulton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Overbeek R., Kirkness E.F., Tomb J.-F., Adams M.D., Reich C.I.,
RA Kerevack R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
CC ELECTRONS PROBABLY IN THE CO-DEHYDROGENASE COMPLEX
CC (BY SIMILARITY).
CC -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
CC
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CC
CC -----
CC EMBL; U67519; AAB98718.1; -.
CC HSSP; P00193; 1DUR.
CC TIGR; MJ0722; -.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC Pfam; PF00037; 4Fe4SFRDXIN.
CC PRINTS; PR00353; 4FE4SFRDXIN.
CC PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
KW Hypothetical protein; Electron transport; Iron-sulfur; 4Fe-4S;
KW Complete proteome.
FT METAL 12 12 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 15 15 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 18 18 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 22 22 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 45 45 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 48 48 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 51 51 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 55 55 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 77 AA; 8847 MW; 7514C8E87906A879 CRC64;
Query Match 55.7%; Score 34; DB 1; Length 77;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SGAYRYGVVY 11
Db 34 NGKYAYDVEY 44
RESULT 24
GONI_CAVPO STANDARD; PRT; 92 AA.
AC O54713;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
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DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)
DE (luteinizing hormone releasing hormone I) (Gonadotropin releasing
DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I].
GN GNRH1 OR GNRH OR LHRH.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley white; TISSUE=Hypothalamus;
RX MEDLINE=97462693; PubMed=9322920;
RA Jimenez-Linan M., Rubin B.S., King J.C.;
RT "Examination of guinea pig luteinizing hormone-releasing hormone gene
RT reveals a unique decapeptide and existence of two transcripts in the
RT brain.";
RL Endocrinology 138:4123-4130 (1997).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
CC THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
CC HORMONES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
CC
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CC
CC -----
CC EMBL; AF033346; AAB87688.1; -.
CC InterPro; IPR002012; GnRH.
CC InterPro; IPR004079; GonadoliberinI.
CC Pfam; PF00446; GnRH; 1.
CC PRINTS; PR01541; GONADOLIBRNI.
CC PROSITE; PS00473; GnRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Placenta; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 92 PROGONADOLIBERIN I.
FT PEPTIDE 24 33 GONADOLIBERIN I.
FT PEPTIDE 37 92 GNRH-ASSOCIATED PEPTIDE I.
FT ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
FT ACT_SITE 26 26 ACTIVITY (BY SIMILARITY).
FT MOD_RES 24 24 PYROLIDONE CARBOXYLIC ACID (BY
FT MOD_RES 33 33 SIMILARITY).
FT MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP) (BY
FT MOD_RES 92 92 SIMILARITY).
SQ SEQUENCE 92 AA; 10279 MW; ACF74613F456D663 CRC64;
Query Match 55.7%; Score 34; DB 1; Length 92;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 SGAYRYGVV 9
Db 22 SQYWSYGV 30
RESULT 25
NPI_RHOPR STANDARD; PRT; 207 AA.
AC Q26239;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nitrophorin 1 precursor (NPI).
OS Rhodnius prolixus (Triatomid bug).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae; Triatominae;
OC Rhodnius.
```

OX NCBI\_TaxID=L3249;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Salivary gland;  
RA MEDLINE=95238361; PubMed=7721773;  
RX Champagne D.E., Nuesenzweig R.H., Ribeiro J.M.C.;  
RT "Purification, partial characterization, and cloning of nitric oxide-  
carrying heme proteins (nitrophorins) from salivary glands of the  
RT blood-sucking insect Rhodnius prolixus.";  
RL J. Biol. Chem. 270:8691-8695(1995).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RC TISSUE=Salivary gland;  
RX MEDLINE=98206297; PubMed=9546222;  
RA Weichsel A., Andersen J.F., Champagne D.E., Walker F.A.,  
RA Montfort W.R.;  
RT "Crystal structures of a nitric oxide transport protein from a blood-  
sucking insect.";  
RL Nat. Struct. Biol. 5:304-309(1998).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RA Ding X.D., Weichsel A., Andersen J.F., Shokhireva T.K., Balfour C.,  
RA Pierik A., Averill B.A., Montfort W.R., Walker F.A.;  
RL Submitted (JUN-1998) to the PDB data bank.  
CC -1- FUNCTION: HEME-BASED PROTEIN THAT DELIVER NITRIC OXIDE GAS (NO) TO  
CC THE VICTIM WHILE FEEDING, RESULTING IN VASODILATION AND INHIBITION  
CC OF PLATELET AGGREGATION. ALSO BIND TIGHTLY TO HISTAMINE, WHICH IS  
CC RELEASED BY THE HOST TO INDUCE WOUND HEALING.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: EXPRESSED BY THE SALIVARY GLANDS.  
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CC -----  
DR EMBL; L39654; AAA74407.1; -;  
DR PDB; 1NP1; 27-MAY-98.  
DR PDB; 2NP1; 27-MAY-98.  
DR PDB; 3NP1; 12-AUG-98.  
DR PDB; 4NP1; 11-NOV-98.  
DR InterPro; IPR02351; Nitrophorin.  
DR Pfam; PF02087; Nitrophorin; 1.  
KW Heme; Vasodilator; Signal; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 207 NITROPHORIN 1.  
FT DISULFID 25 145  
FT DISULFID 64 194  
FT METAL 82 82 IRON (HEME PROXIMAL LIGAND).  
SQ SEQUENCE 207 AA; 22763 MW; 4AB9EE803FDA0EB8 CRC64;  
Query Match 55.7%; Score 34; DB 1; Length 207;  
Best Local Similarity 54.5%; Pred. No. 38;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 SGAYRYGVVY 11  
Db 124 SGNYTFTVMY 134  
RESULT 26  
ID PSB5 HUMAN STANDARD; PRT; 208 AA.  
AC P28074; Q16242;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 13-JUN-2002 (Rel. 41, Last annotation update)  
DE Proteasome subunit beta type 5 precursor (EC 3.4.25.1) (Proteasome  
DE epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase  
DE complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6)

DE (Proteasome subunit MB1).  
GN PSMB5 OR LMPX.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94345396; PubMed=8066462;  
RA Akiyama K.-Y., Yokota K.-Y., Kagawa S., Shimbara N., Tamura T.,  
RA Akioka H., Nothwang H.G., Noda C., Tanaka K., Ichihara A.;  
RT "cDNA cloning and interferon gamma down-regulation of proteasomal  
RT subunits X and Y.";  
RL Science 265:1231-1234(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Abdulla S., Beck S., Behlich M., Jackson A., Nakamura T.,  
RA Trowsdale J.;  
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95120465; PubMed=7820546;  
RA Bellich M.P., Glynn R.J., Senger G., Sheer D., Trowsdale J.;  
RT "Proteasome components with reciprocal expression to that of the MHC-  
RT encoded LMP proteins.";  
RL Curr. Biol. 4:769-776(1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 5-30.  
RX MEDLINE=90167111; PubMed=2306472;  
RA Lee L.W., Moonaw C.R., Orth K., McGuire M.J., DeMartino G.N.,  
RA Slaughter C.A.;  
RT "Relationships among the subunits of the high molecular weight  
RT proteinase, macropain (proteasome).";  
RL Biochim. Biophys. Acta 1037:178-185(1990).  
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX  
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG,  
CC PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR  
CC SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC  
CC ACTIVITY. MAY CATALYZE BASAL PROCESSING OF INTRACELLULAR ANTIGENS.  
CC -1- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad  
CC specificity.  
CC -1- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal  
CC proteolytic pathway.  
CC -1- SUBUNIT: The proteasome is composed of at least 15 non identical  
CC subunits which form a highly ordered ring-shaped structure. This  
CC subunit can be displaced by the equivalent immune-specific subunit  
CC PSMB8.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B.  
CC -----  
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CC -----  
DR EMBL; D29011; BAA06097.1; -;  
DR EMBL; X95586; CAA64838.1; ALT\_INIT.  
DR EMBL; S74378; AAB33092.1; ALT\_INIT.  
DR EMBL; BC004146; AA04146.1; -;  
DR PIR; S08189; S08189.  
DR HSSP; P30656; 1RYP.  
DR MEROPS; T01.012; -;  
DR Genew; HGNC:9542; PSMB5.  
DR MIM; 600306; -;  
DR InterPro; IPR000243; Proteasome\_B.

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CC -----  
DR ENBL; AB003306; BAA24917.1; ALT\_INIT.  
DR ENBL; AB003304; BAA24916.1; ALT\_INIT.  
DR ENBL; AF060091; AAD50536.1; ALT\_INIT.  
DR HSSP; P30656; ILYP.  
DR MEROPS; T01.012; -.  
DR MGD; MGI.1194513; Psmb5.  
DR InterPro; IPR000243; Proteasome\_B.  
DR InterPro; IPR001353; Proteasome; 1.  
DR Pfam; PF00227; Proteasome; 1.  
DR PRINTS; PR00141; PROTEASOME.  
DR PROSITE; PS00854; PROTEASOME\_B; 1.  
DR Proteasome; Hydrolase; Protease; Zymogen.  
DR PROPEP 1 4 BY SIMILARITY.  
DR CHAIN 5 209 PROTEASOME SUBUNIT BETA TYPE 5.  
DR SEQUENCE 209 AA; 22967 MW; 873B58A9A84C7794 CRC64;  
  
Query Match 55.7%; Score 34; DB 1; Length 209;  
Best Local Similarity 60.0%; Pred. No. 39;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 SGAYRYGVV 10  
||: ||||:  
DB 134 SGSVYGVV 143  
  
RESULT 28  
ID KDKA\_XYLFA STANDARD; PRT; 259 AA.  
KK KDKA\_XYLFA  
ID KDKA\_XYLFA STANDARD; PRT; 259 AA.  
AC Q9PBJ1;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 3-deoxy-D-manno-octulosonic acid kinase (EC 2.7.1.-) (XDO kinase).  
DS KDKA OR XF2153.  
GN Xylella fastidiosa.  
OS Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
OC Xylella  
NCBI\_TaxID=2371;  
OX [1]  
RN  
RP  
SEQUENCE FROM N.A.  
RC STRAIN=9a5C;  
RX MEDLINE=20365717; PubMed=10910347;  
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
RA Bueno M.R.P., Colombo A.A., Camargo L.E.A., Cartaro D.M., Carrer H.,  
RA Calauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,  
RA Pacinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
RA Machado M.A., Madeira A.N.B.N., Madeira H.M.F., Marino C.L.,  
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,  
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;  
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";

RL Nature 406:151-159(2000).  
CC -!- FUNCTION: ATP-dependent phosphorylation of 3-deoxy-D-manno-  
CC octulosonic acid at the 4-OH position (By similarity).  
CC -!- PATHWAY: Lipopolysaccharide core biosynthesis.  
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE KDKA FAMILY.  
CC -----  
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CC -----  
DR EMBL; AF004029; AAF84952.1; -;  
KW Lipopolysaccharide biosynthesis; Transferase; Kinase; Membrane;  
KW ATP-binding; Complete proteome.  
FT ACT SITE 185 185 POTENTIAL.  
SQ SEQUENCE 259 AA; 29999 MW; 453D6EA79E6A9823 CRC64;  
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Query Match 55.7%; Score 34; DB 1; Length 259;  
Best Local Similarity 54.5%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
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QY 1 SGAYVRYGVY 11  
Db 128 AACVYRVGVY 138  
-----  
RESULT 29  
META\_STRPN STANDARD; PRT; 314 AA.  
ID META\_STRPN  
AC Q97PM9;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Homoserine O-succinyltransferase (EC 2.3.1.46) (Homoserine O-  
DE transsuccinylase) (HTS).  
GN META OR SP1576.  
OS Streptococcus pneumoniae.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1313;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TIGR4;  
RX MEDLINE=21357209; PubMed=11463916;  
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,  
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,  
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,  
RA Unayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,  
RA Holtzapfle E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,  
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,  
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,  
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;  
RT "Complete genome sequence of a virulent isolate of Streptococcus  
RT pneumoniae".  
RL Science 293:498-506(2001).  
CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + L-homoserine = CoA + O-  
CC succinyl-L-homoserine.  
CC -!- PATHWAY: Methionine biosynthesis; HTS variant; first step.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE HTS FAMILY.  
CC -----  
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CC -----

DR EMBL; AF007452; AAK75662.1; -;  
DR TIGR; SP1576; -;  
DR TIGRAME; TIGR01001; metaA; 1.  
KW Methionine biosynthesis; Transferase; Acyltransferase;  
KW Complete proteome.  
FT ACT SITE 142 142 POTENTIAL.  
SQ SEQUENCE 314 AA; 36926 MW; 9CA22016E26A4F24 CRC64;  
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Query Match 55.7%; Score 34; DB 1; Length 314;  
Best Local Similarity 66.7%; Pred. No. 58;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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QY 1 SGAYVRYGV 9  
Db 147 AGLYRYGV 155  
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RESULT 30  
RFAJ\_ECOLI STANDARD; PRT; 338 AA.  
ID RFAJ\_ECOLI  
AC F27129;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Lipopolysaccharide 1,2-glucosyltransferase (EC 2.4.1.58).  
GN RFAJ OR WAAJ OR B3626.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=92325066; PubMed=1624461;  
RA Pradel E., Parker C.T., Schnaitman C.A.;  
RT "Structures of the rfaB, rfaI, rfaJ, and rfaS genes of Escherichia  
RT coli K-12 and their roles in assembly of the lipopolysaccharide  
RT core".  
RL J. Bacteriol. 174:4736-4745(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=94316500; PubMed=8041620;  
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;  
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the  
RT Nucleic Acids Res. 22:2576-2586(1994).  
CC -!- CATALYTIC ACTIVITY: UDP-glucose + lipopolysaccharide = UDP + D-  
CC glucosyl-lipopolysaccharide.  
CC -!- PATHWAY: Lipopolysaccharide core biosynthesis.  
CC -!- SIMILARITY: TO S.TYPHIMURIUM RFAJ AND TO RPAJ.  
CC -----  
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CC -----  
DR EMBL; M80599; AAA24087.1; -;  
DR EMBL; U00039; AAB18603.1; -;  
DR EMBL; AB000440; AAC76650.1; -;  
DR PIR; D42982; D42982.  
DR EcoGene; EGI1353; rfaJ.  
DR InterPro; IPR002495; GT 8.  
DR Pfam; PF01501; Glyco transf 8; 1.  
KW Lipopolysaccharide biosynthesis; Glycosyltransferase; Transferase;  
KW Complete proteome.  
FT CONFLICT 310 338 RKHLLVQHYSIGITAGVCLCRKYRK -> DINIF  
FT (IN REF. 1).  
SQ SEQUENCE 338 AA; 39040 MW; 819428EA13F1959A CRC64;

Query Match 55.7%; Score 34; DB 1; Length 338;  
 Best Local Similarity 60.0%; Pred. No. 62;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11  
 176 GQFNSGVVY 185

Db ID\_RL3 SULSO STANDARD; PRT; 351 AA.  
 AC QPXA8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 50S ribosomal protein L3P  
 GN RPL3P OR RPL3AB OR SS00719 OR C10\_011.  
 OS Sulfolobus solfataricus.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxID=2287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
 RX MEDLINE=20165948; PubMed=10701121;  
 RA Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,  
 RA Gaasterland T., Curtis B., Duguet M., Erauso G., Faguy D.,  
 RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,  
 RA Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,  
 RA St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,  
 RA Ragan M.A., Sengen C.W.;  
 RT "Gene content and organization of a 281-kbp contig from the genome of  
 RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";  
 RL Genome 43:116-136(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
 RX MEDLINE=21332296; PubMed=11427726;  
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
 RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,  
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
 RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.;  
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
 CC -!- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.  
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 CC -----  
 CC EMBL; Y18930; CAB57584.1; -;  
 DR EMBL; AE006897; AAK41018.1; -;  
 DR InterPro; IPR000597; Ribosomal\_L3.  
 DR Pfam; PF00297; Ribosomal\_L3; 1.  
 DR ProDom; PD001374; Ribosomal\_L3; 1.  
 DR PROSITE; PS00474; RIBOSOMAL\_L3; 1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 351 AA; 33670 MW; 06D86BA37FA38008 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 351;  
 Best Local Similarity 50.0%; Pred. No. 64;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVV 10  
 :|: |||:

Db ID\_GLOB\_DROME STANDARD; PRT; 373 AA.  
 AC QVYZ2;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Putative gustatory receptor 10b.  
 GN GR10B OR CGI2622.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostali M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jallil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.-S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -!- FUNCTION: Probable role in the gustatory response.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED  
 CC RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; AE003486; AAF48041.1; -;

```

DR FlyBae: FBgn0030297; Gr10b.
DR InterPro: IPR004117; 7tm.6.
DR Pfam: PF02949; 7tm.6; 1.
KW Hypothetical protein; Receptor; G-protein coupled receptor;
KW Transmembrane; Glycoprotein; Multigene family.
FT DOMAIN 1 8
FT TRANSMEM 9 29
FT DOMAIN 30 82
FT TRANSMEM 83 103
FT DOMAIN 104 132
FT TRANSMEM 133 153
FT DOMAIN 154 170
FT TRANSMEM 171 191
FT DOMAIN 192 230
FT TRANSMEM 231 251
FT DOMAIN 252 273
FT TRANSMEM 274 294
FT DOMAIN 295 350
FT TRANSMEM 351 371
FT DOMAIN 372 373
FT CARBOHYD 192 192
SQ SEQUENCE 373 AA; 44030 MW; 57CF481BF6139B14 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 373;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YRYGVVY 11
DB 59 YRYAMTY 66

RESULT 33
RL3A SCHPO STANDARD; PRT; 387 AA.
AC P40372;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L3-A.
GN RPL3A OR SPAC17A5.03.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=94237476; PubMed=8181745;
RA Liebhich I., Kohler G., Witt I., Gross T., Kauffer N.F.;
RT "Two genes encoding ribosomal protein L3 of Schizosaccharomycetes pombe
RL and their proximal promoter regions.";
RL Gene 142:119-122(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Art R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

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RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wamburt R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR L3 IN S.POMBE.
CC -!- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U00798; AAL19655.1; -
CC EMBL; Z98849; CAB11503.1; -
CC InterPro: IPR000597; Ribosomal_L3.
CC Pfam: PF00297; Ribosomal_L3; 1.
CC PROSITE; PS00474; RIBOSOMAL_L3; 1.
KW Ribosomal protein; Multigene family.
FT INIT MET 0 0 BY SIMILARITY.
SQ SEQUENCE 387 AA; 43671 MW; C97252D7DCECA492 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 387;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAYRYGVV 10
DB 308 GGFVRYGVV 316

RESULT 34
RL3B SCHPO STANDARD; PRT; 387 AA.
AC P36584;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L3-B.
GN RPL3B OR SPAPB85.06C.
OS Schizosaccharomycetes pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=94237476; PubMed=8181745;
RA Liebhich I., Kohler G., Witt I., Gross T., Kauffer N.F.;
RT "Two genes encoding ribosomal protein L3 of Schizosaccharomycetes pombe
RL and their proximal promoter regions.";
RL Gene 142:119-122(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Art R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

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RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas H., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shipakowski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe";  
RL Nature 415:871-880(2002).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L3 IN S. POMBE.  
CC -1- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.  
CC  
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CC  
CC EMBL: X57734; CAA40901.1; -.  
DR EMBL: AL590902; CAC37425.1; -.  
DR PIR: S25592; S25592.  
DR InterPro: IPR000597; Ribosomal\_L3.  
DR Pfam: PF00297; Ribosomal\_L3; 1.  
DR PROSITE: PS00474; RIBOSOMAL\_L3; 1.  
KW Ribosomal protein; Multigene family.  
FT INIT MET 0 BY SIMILARITY.  
SQ SEQUENCE 387 AA; 43685 MW; 5A75FBE94CE13C8B CRC64;  
  
Query Match 55.7%; Score 34; DB 1; Length 387;  
Best Local Similarity 66.7%; Pred. No. 71;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 GAYRYGVV 10  
DB 308 GGFVRYGVV 316  
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RESULT 35  
TKTL\_CANAL STANDARD; PRT; 677 AA.  
AC 094039;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Transketolase 1 (EC 2.2.1.1) (TK 1).  
GN TKTL OR CA41C10.05C.  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1161;  
RA Taylor K., Harris D., Barrell B.G., Rajandream M.A.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde  
CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.  
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE. REQUIRES MAGNESIUM IONS FOR  
CC CATALYTIC ACTIVITY.  
CC  
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CC -1- SUBUNIT: HOMODIMER (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.  
CC  
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CC  
CC EMBL: AL033501; CAA21989.1; -.  
DR HSSP: P23254; ITRK.  
DR InterPro: IPR000360; Transketolase.  
DR Pfam: PF00456; transketolase; 1.  
DR Pfam: PF02779; transket pyr; 1.  
DR Pfam: PF02780; transketolase\_C; 1.  
DR TIGRFAMs: TIGR00232; tktlase\_Bact; 1.  
DR PROSITE: PS00801; TRANSKETOLASE\_1; 1.  
DR PROSITE: PS00802; TRANSKETOLASE\_2; 1.  
KW Transferase; Thiamine pyrophosphate; Magnesium.  
FT ACT SITE 100 100 BY SIMILARITY.  
SQ SEQUENCE 677 AA; 73773 MW; CE0516127B885D2A CRC64;  
  
Query Match 55.7%; Score 34; DB 1; Length 677;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 GAYRYGVV 9  
DB 406 GVIYRGV 413  
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RESULT 36  
TKT2\_YEAST STANDARD; PRT; 681 AA.  
AC P3315;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Transketolase 2 (EC 2.2.1.1) (TK 2).  
GN TKL2 OR YBR117C OR YBR0912.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetales; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c;  
RX MEDLINE=94039074; PubMed=7916691;  
RA Schaeff-Gerstenschlager I., Mannhaupt G., Vetter I., Zimmermann F.K.,  
RA Feldmann H.;  
RT TKL2, a second transketolase gene of Saccharomycetes cerevisiae.  
RT Cloning, sequence and deletion analysis of the gene.;  
RL Eur. J. Biochem. 217:487-492(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c;  
RX MEDLINE=95208357; PubMed=7900426;  
RA Mannhaupt G., Stucka R., Ehnlé S., Vetter I., Feldmann H.;  
RT "Analysis of a 70 kb region on the right arm of yeast chromosome II.";  
RL Yeast 10:1363-1381(1994).  
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde  
CC 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.  
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE. REQUIRES MAGNESIUM IONS FOR  
CC CATALYTIC ACTIVITY.  
CC  
CC -1- SUBUNIT: HOMODIMER (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.  
CC  
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X73532; CAA51937.1; -
CC EMBL; X78993; CAA55619.1; -
CC EMBL; Z35985; CAA85074.1; -
CC PIR; S37809; S37809.
CC PIR; S34170; S34170.
CC HSP; P23254; ITRK.
CC SGD; S0000321; TKL2.
CC InterPro; IPR000360; Transketolase.
CC Pfam; PF00456; transketolase_1.
CC Pfam; PF02779; transket_pyr; 1.
CC Pfam; PF02780; transketolase_C; 1.
CC TIGRFAMs; TIGR00232; tktlase_bact; 1.
CC PROSITE; PS00801; TRANSKETOLASE_1; 1.
CC PROSITE; PS00802; TRANSKETOLASE_2; 1.
CC Transferase; Thiamine pyrophosphate; Magnesium; Multigene family.
KW TRANSFERASE; 681 AA; 75029 MW; 84D7477916D136D5 CRC64;
SQ SEQUENCE 681 AA; 75029 MW; 84D7477916D136D5 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 681;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9
Db 408 AGRYRYGV 416
: || || || ||
PULA_KLEPN STANDARD; PRT; 1090 AA.
ID_PULA_KLEPN STANDARD; PRT; 1090 AA.
AC P07206;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pullulanase precursor (EC 3.2.1.41) (Alpha-dextrin endo-1,6-alpha-
DE glucosidase) (Pullulan 6-glucanohydrolase).
GN PULA.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UNF 5023;
RX MEDLINE=90205629; PubMed=2181242;
RA Kornacker M.G., Pugsley A.P.;
RT "Molecular characterization of pula and its product, pullulanase, a
RT secreted enzyme of Klebsiella pneumoniae UNF5023.";
RL Mol. Microbiol. 4:73-85(1990).
RN [2]
RP SEQUENCE OF 1-62 FROM N.A.
RX MEDLINE=86033621; PubMed=3902792;
RA Chapon C., Raibaud O.;
RT "Structure of two divergent promoters located in front of the gene
RT encoding pullulanase in Klebsiella pneumoniae and positively
RT regulated by the malt product.";
RL J. Bacteriol. 164:639-645(1985).
RN [3]
RP SEQUENCE OF 944-1090 FROM N.A.
RX MEDLINE=89291709; PubMed=2661532;
RA D'Enfert C., Pugsley A.P.;
RT "Klebsiella pneumoniae pils gene encodes an outer membrane
RT lipoprotein required for pullulanase secretion.";
RL J. Bacteriol. 171:3673-3679(1989).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
CC linkages in pullulan and in amylopectin and glycogen, and the
CC alpha- and beta-limit dextrans of amylopectin and glycogen.
CC -|- SUBUNIT: HOMOTRIMER.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).
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CC -|- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL; X52181; CAA36431.1; -
CC EMBL; M12503; AAA25087.2; -
CC EMBL; M29097; AAA61976.1; -
CC PIR; A25025; A25025.
CC PIR; A32880; A32880.
CC PIR; S11823; S11823.
CC InterPro; IPR000461; Alpha amylase.
CC InterPro; IPR004193; Isoamylase_N.
CC Pfam; PF00128; alpha-amylase; 1.
CC Pfam; PF02922; isoamylase_N; 1.
CC Pfam; PF03714; PUD; 1.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Hydrolase; Glycosidase; Membrane; Lipoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1090 PULLULANASE.
FT LIPID 20 20 N-ACYL DIGLYCERIDE.
FT ACT_SITE 684 684 BY SIMILARITY.
FT ACT_SITE 713 713 BY SIMILARITY.
FT ACT_SITE 841 841 BY SIMILARITY.
FT CONFLICT 6 6 R -> C (IN REF. 2).
FT CONFLICT 10 10 V -> F (IN REF. 2).
FT CONFLICT 15 15 V -> I (IN REF. 2).
FT CONFLICT 23 23 G -> S (IN REF. 2).
FT CONFLICT 31 31 N -> S (IN REF. 2).
FT CONFLICT 34 34 T -> N (IN REF. 2).
FT CONFLICT 36 36 D -> DGNP (IN REF. 2).
FT CONFLICT 55 58 TAVE -> MATA (IN REF. 2).
SQ SEQUENCE 1090 AA; 118098 MW; 240AE7DFB3FF1BD6 CRC64;

Query Match 54.9%; Score 33.5; DB 1; Length 1090;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 GAYRYGV-VY 11
Db 361 GAFYRYAMTVY 371
||:||||:|
PULA_KLEAE STANDARD; PRT; 1096 AA.
AC P07811;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pullulanase precursor (EC 3.2.1.41) (Alpha-dextrin endo-1,6-alpha-
DE glucosidase) (Pullulan 6-glucanohydrolase).
GN PULA.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W70;
RX MEDLINE=87194626; PubMed=3155373;
RA Katsuragi N., Takizawa N., Murooka Y.;
RT "Entire nucleotide sequence of the pullulanase gene of Klebsiella
RT aerogenes W70.";
RL J. Bacteriol. 169:2301-2306(1987).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
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CC linkages in pullulan and in amylopectin and glycogen, and the  
 CC alpha- and beta-limit dextrins of amylopectin and glycogen.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 CC (Probable).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: M16187; AAA25124.1; ALT\_SEQ.  
 CC PIR: A26879; A26879.  
 CC InterPro: IPR000461; Alpha amylase.  
 CC InterPro: IPR004193; Isoamylase\_N.  
 CC InterPro: IPR005323; PUD.  
 CC Pfam: PF00128; alpha-amylase; 1.  
 CC Pfam: PF02922; isoamylase\_N; 1.  
 CC Pfam: PF03714; PUD; 1.  
 CC PROSITE: PS00013; PROKAR LIPOPROTEIN; 1.  
 CC Hydrolase; Glycosidase; Membrane; Lipoprotein; Signal.  
 CC FT SIGNAL 1 19  
 CC FT CHAIN 20 1096 PULLULANASE.  
 CC FT LIPID 20 20 N-ACYL DIGLYCERIDE.  
 CC FT ACT\_SITE 694 694 BY SIMILARITY.  
 CC FT ACT\_SITE 723 723 BY SIMILARITY.  
 CC FT ACT\_SITE 851 851 BY SIMILARITY.  
 CC SQ SEQUENCE 1096 AA; 119335 MW; FE7D9167CDACFD79 CRC64;  
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 CC Query Match 54.9%; Score 33.5; DB 1; Length 1096;  
 CC Best Local Similarity 63.6%; Pred. No. 2.4e+02;  
 CC Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
 CC  
 CC QY 2 GAYRYGV-VY 11  
 CC ||||| :||  
 CC Db 371 GAFRYAMTVV 381  
 CC  
 CC RESULT 39  
 CC ID RNMS ASPSA STANDARD; PRT; 105 AA.  
 CC AC P00653;  
 CC DT 21-JUL-1986 (Rel. 01, Created)  
 CC DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Guanyl-specific ribonuclease Ms (EC 3.1.27.3) (RNase Ms).  
 CC OS Aspergillus saitoi (Aspergillus phoenicis).  
 CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 CC OC Euriotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 CC OX NCBI\_TaxID=5063;  
 CC RN [1]  
 CC RP SEQUENCE.  
 CC RX MEDLINE=82239267; PubMed=7096302;  
 CC RA Watanabe H., Ohgi K., Irie M.;  
 CC RT "Primary structure of a minor ribonuclease from Aspergillus saitoi.";  
 CC RL J. Biochem. 91:1495-1509(1982).  
 CC RN [2]  
 CC RP REVISIONS TO 52-54; 80 AND 95.  
 CC RX MEDLINE=91257303; PubMed=1646118;  
 CC RA Watanabe H., Ohgi K., Irie M.;  
 CC RL Unpublished results, cited by:  
 CC RL Nonaka T., Mitsui Y., Irie M., Nakamura K.T.;  
 CC RL FEBS Lett. 283:207-209(1991).  
 CC RN [3]  
 CC RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 CC RX MEDLINE=91257303; PubMed=1646118;  
 CC RA Nonaka T., Mitsui Y., Irie M., Nakamura K.T.;  
 CC RT "Three-dimensional structure of ribonuclease Ms\*3'-guanylic acid

RT complex at 2.5-A resolution.";  
 RL FEBS Lett. 283:207-209(1991).  
 CC -1- CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to  
 CC nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in  
 CC G-P with 2', 3'-cyclic phosphate intermediates. FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEASE N1/T1 FAMILY.  
 CC PIR: A00800; NEASTP.  
 CC PDB: 1RDS; 31-OCT-93.  
 CC DR PDB; IRMS; 31-OCT-93.  
 CC DR InterPro: IPR000026; Ribonuc N1T1.  
 CC DR Pfam: PF00545; ribonuclease; 1.  
 CC KW Hydrolase; Nuclease; Endonuclease; 3D-structure.  
 CC FT DISULFID 3 11  
 CC FT ACT\_SITE 7 102  
 CC FT ACT\_SITE 39 39  
 CC FT ACT\_SITE 57 57  
 CC FT ACT\_SITE 76 76  
 CC FT ACT\_SITE 91 91  
 CC FT STRAND 5 7  
 CC FT TURN 8 9  
 CC FT STRAND 10 12  
 CC FT STRAND 14 29  
 CC FT TURN 30 31  
 CC FT STRAND 34 34  
 CC FT STRAND 35 36  
 CC FT STRAND 37 37  
 CC FT STRAND 39 41  
 CC FT TURN 44 45  
 CC FT STRAND 55 59  
 CC FT TURN 62 63  
 CC FT STRAND 75 80  
 CC FT TURN 81 82  
 CC FT STRAND 85 90  
 CC FT TURN 92 93  
 CC FT STRAND 100 101  
 CC FT STRAND 103 103  
 CC SQ SEQUENCE 105 AA; 11332 MW; 94CF56D109242EFD CRC64;  
 CC  
 CC Query Match 54.1%; Score 33; DB 1; Length 105;  
 CC Best Local Similarity 50.0%; Pred. No. 30;  
 CC Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 CC  
 CC QY 1 SGAYRYGVV 10  
 CC ||||| :||  
 CC Db 52 SGTYYEYPI 61  
 CC  
 CC RESULT 40  
 CC ID VTU3 DROME STANDARD; PRT; 119 AA.  
 CC AC Q06521;  
 CC DT 01-OCT-1996 (Rel. 34, Created)  
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 CC DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 CC DE Vitelline membrane protein Vm34Ca precursor.  
 CC GN VM34CA OR VM34C.1.  
 CC OS Drosophila melanogaster (Fruit fly).  
 CC OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 CC OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 CC OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 CC OX NCBI\_TaxID=7227;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=94123988; PubMed=8293994;  
 CC RA Scherer L.J., Harris D.H., White M.K., Steel L.S., Jin J.,  
 CC RA Petri W.H.;  
 CC RT "Comparative analysis of the sequence and structure of two Drosophila  
 CC RT melanogaster genes encoding vitelline membrane proteins.";  
 CC RL Gene 136:121-127(1993).  
 CC RN [2]  
 CC RP SEQUENCE OF 1-96 FROM N.A.  
 CC RX STRAIN=Daekwanryeong;  
 CC RX MEDLINE=85257433; PubMed=3926479;

RA Mindrinos M.N., Scherer L.J., Garcini F.J., Kwan H., Jacobs K.A.,  
RA Petri W.H.;  
RT "Isolation and chromosomal location of putative vitelline membrane  
RL genes in Drosophila melanogaster.";  
RN EMBO J. 4:147-153(1985).  
[3]  
RP SEQUENCE OF 69-106 FROM N.A.  
RC STRAIN-Oregon-R;  
RX MEDLINE=8905296; PubMed=3143615;  
RA Scherer L.J., Harris D.H., Petri W.H.;  
RT "Drosophila vitelline membrane genes contain a 114 base pair region  
RL of highly conserved coding sequence.";  
Dev. Biol. 130:786-788(1988).  
CC -1- FUNCTION: MAJOR EARLY EGG SHELL PROTEIN.  
CC -1- TISSUE SPECIFICITY: FOLLICLE CELLS.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING VITELLINE MEMBRANE  
CC BIOSYNTHESIS.  
CC -1- SIMILARITY: A 38 AMINO ACIDS REGION (VM DOMAIN) IS CONSERVED IN  
CC DROSOPHILA VITELLINE MEMBRANE PROTEINS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; L08852; AAC37200.1; -;  
DR EMBL; X01802; CAA25933.1; -;  
DR EMBL; M22700; AAA29018.1; -;  
DR FlyBase; FBgn0003983; Vm34Ca.  
KW Signal; Structural protein; Eggshell.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 119 VITELLINE MEMBRANE PROTEIN VM34CA.  
FT DOMAIN 69 106 VM DOMAIN.  
FT CONFLICT 96 96 A -> R (IN REF. 2).  
SQ SEQUENCE 119 AA; 11934 MW; 2F06298E52005BFC CRC64;  
  
Query Match 54.1%; Score 33; DB 1; Length 119;  
Best Local Similarity 54.5%; Pred. No. 33;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 SGAYRYGVVY 11  
Db 102 AGAYSQYAPVY 112

Search completed: July 18, 2003, 15:07:17  
Job time : 8.82 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:40 ; Search time 28.38 Seconds  
(without alignments)  
79.863 Million cell updates/sec

Title: US-10-007-790-7

Perfect score: 61  
Sequence: 1 SGAYRYGVVY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriopl.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	46	75.4	306	16 Q97HX0	Q97hx0 clostridium
2	41	67.2	580	16 Q8XUY2	Q8xuy2 ralstonia s
3	41	67.2	942	17 Q8RU74	Q8tj74 methanosarc
4	40	65.6	1343	12 Q91FM9	Q91fm9 chilo iride
5	40	65.6	1548	5 Q9NGQ6	Q9ngq6 drosophila
6	40	65.6	1805	5 Q9VZM1	Q9vzm1 drosophila
7	39	63.9	441	16 Q9X1M3	Q9x1m3 thermotoga
8	39	63.9	452	13 Q8UW45	Q8uw45 fugu rubrip
9	39	63.9	517	10 Q64882	Q64882 arabidopsis
10	39	63.9	1389	3 Q94474	Q94474 schizosacch
11	38	62.3	740	5 Q96281	Q96281 plasmodium
12	38	62.3	914	10 Q96301	Q96301 arabidopsis
13	38	62.3	911	10 Q8RVB2	Q8rvb2 lycopersico
14	38	62.3	932	10 Q82039	Q82039 petunia hyp
15	38	62.3	944	10 Q82422	Q82422 hordeum vul
16	38	62.3	1416	5 Q77309	Q77309 plasmodium

17	38	62.3	1417	5 Q77310	Q77310 plasmodium
18	37	60.7	79	9 Q9B041	Q9b041 mycobacteri
19	37	60.7	209	16 Q9PAU5	Q9pau5 xylella fas
20	37	60.7	218	13 Q57331	Q57331 brachydanio
21	37	60.7	255	13 Q9PUS4	Q9pus4 brachydanio
22	37	60.7	265	10 Q9SE35	Q9se35 cylindrothe
23	37	60.7	317	3 Q06328	Q06328 saccharomyc
24	37	60.7	384	10 Q23165	Q23165 arabidopsis
25	37	60.7	409	10 Q9LEB4	Q9leb4 nicotiana p
26	37	60.7	492	10 Q94K88	Q94k88 arabidopsis
27	37	60.7	560	4 Q14520	Q14520 homo sapien
28	37	60.7	574	17 Q26815	Q26815 methanobact
29	37	60.7	705	4 Q8WUB4	Q8wub4 homo sapien
30	37	60.7	705	4 Q8TE35	Q8te35 homo sapien
31	37	60.7	742	2 Q9L3J5	Q9l3j5 clostridium
32	37	60.7	1350	5 Q95YI8	Q95yi8 plasmodium
33	37	60.7	1787	10 Q8S6N1	Q8s6n1 oryza sativ
34	36	59.0	241	11 Q9WVQ5	Q9wvq5 mus musculu
35	36	59.0	242	4 Q9Y318	Q9y318 homo sapien
36	36	59.0	242	4 Q96HK2	Q96hk2 homo sapien
37	36	59.0	242	4 Q96GX9	Q96gx9 homo sapien
38	36	59.0	242	4 Q8WVU2	Q8wv2 homo sapien
39	36	59.0	252	5 Q8SV24	Q8sv24 encephalito
40	36	59.0	339	16 Q8REE0	Q8ree0 fusobacteri
41	36	59.0	358	3 Q9HFZ2	Q9hfr2 candida alb
42	36	59.0	372	17 Q8TWQ1	Q8twq1 methanopyru
43	36	59.0	391	5 Q44148	Q44148 caenorhabdi
44	36	59.0	421	16 Q92KJ8	Q92kj8 helicobacte
45	36	59.0	429	16 Q8Y1B8	Q8y1b8 ralstonia s

#### ALIGNMENTS

#### RESULT 1

Q97HX0 PRELIMINARY; PRT; 306 AA.  
AC Q97HX0;  
DT 01-OCT-2001 (Tremblrel. 18, Created)  
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)  
DE Uncharacterized phage related protein.  
GN CAC1886.  
OS Clostridium acetobutylicum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
OC Clostridiales; Clostridiaceae; Clostridium.  
OX NCBI\_TaxID=1488;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
RX MEDLINE=21359325; PubMed=11466286;  
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Daly M.J.,  
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P.,  
RA Bennett G.N., Koonin E.V., Smith D.R.;  
RT "Genome sequence and comparative analysis of the solvent-producing  
RT bacterium Clostridium acetobutylicum";  
RL J. Bacteriol. 183:4823-4838(2001).  
DR EMBL; A8007697; AAK79850.1; -.  
KW Complete proteome.  
SQ SEQUENCE 306 AA; 33526 MW; 783B0B46A803254A CRC64;

Query Match 75.4%; Score 46; DB 16; Length 306;  
Best Local Similarity 87.5%; Pred. No. 2.8;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11

Db 117 YRYGVVY 124

#### RESULT 2

Q8XUY2

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ID QBXUV2 PRELIMINARY; PRT; 580 AA.
AC QBXUV2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical signal peptide protein RSC3051.
GN RSC3051 OR RS00492.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR ENBL; AL646073; CAD16760.1; -.
DR InterPro; IPR000567; SBP_bac1.
DR Pfam; PF01547; SBP_bacterial_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 580 AA; 64531 MW; 18C8E00E37CAD51F CRC64;

Query Match 67.2%; Score 41; DB 16; Length 580;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAYRYGVV 10
Db 139 GTHRYGVV 147
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|:|||||

RESULT 3
QBXTJ74 PRELIMINARY; PRT; 942 AA.
ID QBXTJ74;
AC QBXTJ74;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein MA3914.
GN MA3914.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nuebaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Maylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McKernan K., Talama D.E., Grahame D.A., Guss A.M.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR ENBL; AE011103; AM07465.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 942 AA; 105833 MW; 6A5801A0566B47FB CRC64;

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Query Match 67.2%; Score 41; DB 17; Length 942;
Best Local Similarity 63.6%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVV 11
Db 213 TGSYYSYTVVY 223
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|:|||||

RESULT 4
Q91FM9 PRELIMINARY; PRT; 1343 AA.
ID Q91FM9;
AC Q91FM9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 295L.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RC Deltus H., Darai G., Fluegel R.M.;
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
RT in mice.";
RL J. Virol. 49:609-614(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
RT in mice.";
RL Med. Microbiol. Immunol. 175:43-53(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321126; PubMed=2820141;
RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,
RA Deltus H., Darai G.;
RT "Molecular cloning and physical mapping of the genome of insect
RT iridescent virus type 6: further evidence for circular permutation of
RT the viral genome.";
RL Virology 160:66-74(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073752; PubMed=3201750;
RA Fischer M., Schnitzler P., Deltus H., Darai G.;
RT "Identification and characterization of the repetitive DNA element in
RT the genome of insect iridescent virus type 6.";
RL Virology 167:485-496(1988).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196996; PubMed=1549908;
RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
RA Darai G.;
RT "Identification and mapping of origins of DNA replication within the
RT DNA sequences of the genome of insect iridescent virus type 6.";
RL Virus Genes 6:19-32(1992).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93118242; PubMed=1475907;
RA Sonntag K.C., Darai G.;
RT "Characterization of the third origin of DNA replication of the genome
RT of insect iridescent virus type 6.";
RL Virus Genes 6:333-342(1992).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=93260401; PubMed=8492091;
RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
RT "Identification of the gene encoding the major capsid protein of
RT insect iridescent virus type 6 by polymerase chain reaction.";
RL J. Gen. Virol. 74:873-879(1993).
RN [8]
RP SEQUENCE FROM N.A.

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XX MEDLINE=94167241; PubMed=8121799;  
RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,  
RA Delius H., Darai G.;  
RT "Identification of genes encoding zinc finger proteins, non-histone  
RT chromosomal HMG protein homologues, and a putative GTP phosphohydrolase  
RT in the genome of Chilo iridescent virus.";  
RL Nucleic Acids Res. 22:158-166(1994).  
RN [9]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94353641; PubMed=8073636;  
RA Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;  
RA "Chilo iridescent virus encodes a putative helicase belonging to a  
RT distinct family within the 'DEAD/H' superfamily: implications for the  
RT evolution of large DNA viruses.";  
RL Virus Genes 8:151-158(1994).  
RN [10]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95213160; PubMed=7698884;  
RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;  
RT "Identification of the primary structure and the coding capacity of  
RT the genome of insect iridescent virus type 6 between the genome  
RT coordinates 0.310 and 0.347 (7990 bp).";  
RL Intervirology 37:287-297(1994).  
RN [11]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94292906; PubMed=8021587;  
RA Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,  
RA Koonin E.V., Darai G.;  
RT "Insect iridescent virus type 6 encodes a polypeptide related to the  
RT largest subunit of eukaryotic RNA polymerase II.";  
RL J. Gen. Virol. 75:1557-1567(1994).  
RN [12]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98141693; PubMed=9482589;  
RA Bahr U., Tidona C.A., Darai G.;  
RT "The DNA sequence of Chilo iridescent virus between the genome  
RT coordinates 0.101 and 0.391; similarities in coding strategy between  
RT insect and vertebrate iridoviruses.";  
RL Virus Genes 15:235-245(1997).  
RN [13]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99125223; PubMed=9926400;  
RA Muller K., Tidona C.A., Bahr U., Darai G.;  
RT "Identification of a thymidylate synthase gene within the genome of  
RT Chilo iridescent virus.";  
RL Virus Genes 17:243-258(1998).  
RN [14]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99383793; PubMed=10456793;  
RA Muller K., Tidona C.A., Darai G.;  
RT "Identification of a gene cluster within the genome of Chilo  
RT iridescent virus encoding enzymes involved in viral DNA replication  
RT and processing.";  
RL Virus Genes 18:243-264(1999).  
RN [15]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21342589; PubMed=11448171;  
RA Jakob N.J., Muller K., Bahr U., Darai G.;  
RT "Analysis of the First Complete DNA Sequence of an Invertebrate  
RT Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";  
RL Virology 286:182-196(2001).  
RN [16]  
RP SEQUENCE FROM N.A.  
RA Jakob N.J., Mueller K., Bahr U., Darai G.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF303741; AAR82156.1; -  
SQ SEQUENCE 1343 AA; 156514 MW; 8267646EA7CDAD0D CRC64;  
Query Match 65.6%; Score 40; DB 12; Length 1343;  
Best Local Similarity 75.08; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 YYYRGVYV 11

Db 714 YYRYGTM 721  
RESULT 5  
Q9NGQ6 PRELIMINARY; PRT; 1548 AA.  
AC Q9NGQ6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Cytoplasmic protein encode.  
GN ENC OR CG10847.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Van Buskirk C., Hawkins N.C., Schubach T.;  
RT "Encore is a member of a novel class of proteins and affects multiple  
RT processes in Drosophila oogenesis.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF243382; AAF68440.1; -  
DR FlyBase; FBgn0004875; enc.  
DR InterPro; IPR001374; R3H.  
DR Pfam; PF01424; R3H; 1.  
DR SMART; SM00393; R3H; 1.  
SQ SEQUENCE 1548 AA; 164364 MW; F2423CE7E7D5D0CF CRC64;  
Query Match 65.6%; Score 40; DB 5; Length 1548;  
Best Local Similarity 54.5%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 SCAYRYGVYV 11  
Db 1475 SGVYFKYGTQY 1485  
RESULT 6  
Q9VZM1 PRELIMINARY; PRT; 1805 AA.  
AC Q9VZM1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE CG10847 protein.  
GN ENC OR CG10847.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Chew S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003479; AAF47799.1; -.
DR FlyBase; FBgn004875; enc.
DR InterPro; IPR001374; R3H.
DR Pfam; PF01424; R3H; 1.
DR SMART; SM00393; R3H; 1.
SQ SEQUENCE 1805 AA; 187054 MW; A96A090E568F18E6 CRC64;

Query Match 65.6%; Score 40; DB 5; Length 1805;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SGAYRYGVVY 11
Db 1754 SGVYKYGQVY 1764

RESULT 7
ID Q9X1M3 PRELIMINARY; PRT; 441 AA.
AC Q9X1M3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE MG-protoporphyrin IX monomethyl ester oxidative cyclase-related
DE protein.
GN TM1537.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001800; AAD36604.1; -.
DR TIGR; TM1537; -.
KW Complete proteome.
SQ SEQUENCE 441 AA; 51038 MW; D096EC15A46A04D8 CRC64;

Query Match 63.9%; Score 39; DB 16; Length 441;
Best Local Similarity 70.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 2 GAYRYGVVY 11
Db 12 GYYRLGAVY 21

RESULT 8
ID Q8UW45 PRELIMINARY; PRT; 452 AA.
AC Q8UW45;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pancreatic carboxypeptidase A1.
GN CPAL.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Avelle K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W.,
RA Bouffard G.G., Brinkley C., Brooks S., Dietrich N.L., Granite S.,
RA Guan X., Gupta J., Ho S.-L., Idol J.R., Karlins E., Lee-Lin S.-Q.,
RA Legaepi R., Lim M., Maduro Q.L., Maduro V.B., Masiello C.,
RA Mastrian S.D., McCloskey J.C., McDowell J., Pearson R., Prasad A.,
RA Shevchenko Y., Snyder B., Stantrop S., Thomas J.W., Thomas P.J.,
RA Tionsgon E.E., Touchman J.W., Tsurgeon C., Vogt J.L., Walker M.A.,
RA Wetherby K.D., Zhang L.-H., Green E.D.;
RT "NISC Comparative Sequencing Initiative";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC090119; AAL40361.1; -.
DR InterPro; IPR003146; Propep M14.
DR InterPro; IPR000834; Zn_carbopept.
DR Pfam; PF02244; Propep M14; 1.
DR Pfam; PF00246; Zn_carbopept. 1.
DR PRINTS; PR00765; CRBOXYPTASEA.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; UNKNOWN_1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
KW Carboxypeptidase.
SQ SEQUENCE 452 AA; 50824 MW; 7CF7BC6E601955EF CRC64;

Query Match 63.9%; Score 39; DB 13; Length 452;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAYRYGVVY 10
Db 378 GYYRYGSI 386

RESULT 9
ID Q64882 PRELIMINARY; PRT; 517 AA.
AC Q64882;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative beta-glucosidase (At2g44480/P411.29).
GN AT2G44480.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
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RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Adams L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Cronin M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nietman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP RP
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Lim J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004521; AAC16094.1; -.
DR EMBL; AY074629; AAL69445.1; -.
DR HSSP; P26205; ICBG.
DR InterPro; IPR001360; GH 1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GUHYDLASE1.
DR ProDom; PD000650; GH 1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
SQ SEQUENCE 517 AA; 59120 MW; 1A9E4DD65EE1A760 CRC64;

Query Match 63.9%; Score 39; DB 10; Length 517;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11
| ||| |||
Db 477 GYKRYGLVY 486

RESULT 10
O94474 PRELIMINARY; PRT; 1389 AA.
AC O94474
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 157.9 kDa protein C1919.05 in chromosome III.
GN SPCC1919.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Harris D.E., Murphey L.D., Rajandream M.A., Barrell B.G.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 TPR DOMAINS.
DR EMBL; AL035075; CAA22636.1; -.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 9.
DR SMART; SM00028; TPR; 5.
KW Hypothetical protein; Transmembrane; TPR domain; Repeat.
FT REPEAT 39 881 POTENTIAL.
FT REPEAT 578 606 TPR 1.
FT REPEAT 653 681 TPR 2.
FT REPEAT 681 681 TPR 3.
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FT REPEAT 687 715 TPR 4.
FT REPEAT 762 790 TPR 5.
FT REPEAT 933 961 TPR 6.
SQ SEQUENCE 1389 AA; 157874 MW; FC5C9A785034AFE0 CRC64;

Query Match 63.9%; Score 39; DB 3; Length 1389;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AYRYGVV 9
| ||| |||
Db 540 AYRYGI 546

RESULT 11
O96281 PRELIMINARY; PRT; 740 AA.
AC O96281
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 88.3 kDa protein.
GN PFB0945W.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551;
RA Gardner M.J., Tettein H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shalton S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perle M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
DR EMBL; AB001428; AAC71978.1; -.
DR InterPro; IPR002160; Kunitz_legume.
DR PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 740 AA; 88263 MW; 983C34B795942CC8 CRC64;

Query Match 62.3%; Score 38; DB 5; Length 740;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11
| ||| |||
Db 188 FVKYGIY 195

RESULT 12
O96301 PRELIMINARY; PRT; 914 AA.
AC O96301
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SPINDLY.
GN SPINDLY OR P24K9.29.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP RP
RC STRAIN=COLUMBIA;
RX MEDLINE=96392406; PubMed=8799194;
RA Jacobsen S.E., Binkowski K.A., Olszewski N.E.;
RT "SPINDLY, a tetratricopeptide repeat protein involved in gibberellin
RT signal transduction in Arabidopsis.";
```

Proc. Natl. Acad. Sci. U.S.A. 93:9292-9296(1996).

[2]

SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,  
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R.,  
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
"Arabidopsis thaliana chromosome 3 BAC F24K9 genomic sequence.";  
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

EMBL; U62135; AAC49446.1; -;  
DR EMBL; AC008153; AAG51433.1; -;  
DR InterPro; IPR001440; TPR.  
DR Pfam; PF00515; TPR; 11.  
DR SMART; SM00028; TPR; 9.  
SQ SEQUENCE 914 AA; 101429 MW; A881D84BB5C33493 CRC64;

Query Match 62.3%; Score 38; DB 10; Length 914;  
Best Local Similarity 77.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11  
||| ||||  
Db 188 AYYNLGVVY 196

RESULT 13

Q8RVB2 PRELIMINARY; PRT; 931 AA.

AC Q8RVB2;  
DT 01-JUN-2002 (TrEMBLrel..21, Created)  
DT 01-JUN-2002 (TrEMBLrel..21, Last sequence update)  
DE SPY protein.  
GN SPY.

OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]

SEQUENCE FROM N.A.

RA Greb T., Schmitz G., Theres K.;  
RT "Spindly and Procera encode different components of the GA signal.  
Transduction pathway in tomato.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ312093; CAC85168.1; -;  
DR EMBL; AJ312094; CAC85169.1; -;  
SQ SEQUENCE 931 AA; 103491 MW; 1933A81C48132C62 CRC64;

Query Match 62.3%; Score 38; DB 10; Length 931;  
Best Local Similarity 77.8%; Pred. No. 2.7e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11  
||| ||||  
Db 193 AYYNLGVVY 201

RESULT 14

O82039 PRELIMINARY; PRT; 932 AA.

AC O82039;  
DT 01-NOV-1998 (TrEMBLrel..08, Created)  
DT 01-NOV-1998 (TrEMBLrel..08, Last sequence update)  
DE SPINDLY protein.  
GN SPY.

OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
OX NCBI\_TaxID=4102;  
RN [1]

SEQUENCE FROM N.A.

STRAIN=CV. VR; TISSUE=ANTHERS;

Izhaki A., Weiss B.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y17720; CAA76834.1; -;  
DR InterPro; IPR001440; TPR.  
DR Pfam; PF00515; TPR; 10.  
DR SMART; SM00028; TPR; 9.  
SQ SEQUENCE 932 AA; 103939 MW; 4F0896631302D95D CRC64;

Query Match 62.3%; Score 38; DB 10; Length 932;  
Best Local Similarity 77.8%; Pred. No. 2.7e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11  
||| ||||  
Db 193 AYYNLGVVY 201

RESULT 15

O82422 PRELIMINARY; PRT; 944 AA.

AC O82422;  
DT 01-NOV-1998 (TrEMBLrel..08, Created)  
DT 01-NOV-1998 (TrEMBLrel..08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel..19, Last annotation update)  
DE Gibberellin action negative regulator SPY.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticaceae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=CV. HIMALAYA;  
RX MEDLINE=98299840; PubMed=9634587;  
RA Robertson M., Swain S.M., Chandler P.M., Olszewski N.E.;  
RT "Identification of a negative regulator of gibberellin action, HvSPY,  
in barley.";  
RL Plant Cell 10:995-1007(1998).  
DR EMBL; AF035820; AAC36055.1; -;  
DR InterPro; IPR001440; TPR.  
DR Pfam; PF00515; TPR; 11.  
DR SMART; SM00028; TPR; 9.  
SQ SEQUENCE 944 AA; 103828 MW; CBEAD8B0DICE2F88 CRC64;

Query Match 62.3%; Score 38; DB 10; Length 944;  
Best Local Similarity 77.8%; Pred. No. 2.7e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11  
||| ||||  
Db 179 AYYNLGVVY 187

RESULT 16

O77309 PRELIMINARY; PRT; 1416 AA.

AC O77309; O77307;  
DT 01-NOV-1998 (TrEMBLrel..08, Created)  
DT 01-OCT-2000 (TrEMBLrel..15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel..19, Last annotation update)  
DE PFC0110W, MAL3P1.2 protein.  
GN PFC0110W, MAL3P1.2.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=3D7;  
RX MEDLINE=99376085; PubMed=10448855;  
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,  
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,

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RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum";
RL Nature 400:532-538(1999).
DR EMBL; Z97348; CAB10571.3; -.
SQ SEQUENCE 1416 AA; 167488 MW; 1E15EF2D1CD91BB5 CRC64;

Query Match          62.3%; Score 38; DB 5; Length 1416;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11
Db 863 FYKGYIY 870

RESULT 17
O77310 PRELIMINARY; PRT; 1417 AA.
ID O77310; O77311.
AC O77310; O77311.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PFC0120W, MAL3P1.5 protein.
GN PFC0120W, MAL3P1.5.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum";
RL Nature 400:532-538(1999).
DR EMBL; Z97348; CAB10572.2; -.
SQ SEQUENCE 1417 AA; 167241 MW; AE7AA0E54B5B1130 CRC64;

Query Match          62.3%; Score 38; DB 5; Length 1417;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11
Db 861 FYKGYIY 868

RESULT 18
O9B041 PRELIMINARY; PRT; 79 AA.
ID O9B041
AC O9B041;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp80.
GN 80.
OS Mycobacteriophage Bxb1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=148603;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20572070; PubMed=11123671;
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RA Mediavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R.,
RA Hendrix R.W., Hatfull G.F.;
RT "Genome organization and characterization of mycobacteriophage bxb1.";
RL Mol. Microbiol. 38:955-970(2000).
DR EMBL; AF271693; AAG59785.1; -.
SQ SEQUENCE 79 AA; 9138 MW; 5B35665968154089 CRC64;

Query Match          60.7%; Score 37; DB 9; Length 79;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYG 8
Db 33 NGAYTYG 20

RESULT 19
O9PAU5 PRELIMINARY; PRT; 209 AA.
ID O9PAU5
AC O9PAU5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Xf2400.
GN Xf2400.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE004049; AAF85199.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 209 AA; 23902 MW; 37D0A0EA7FB1B62D CRC64;

Query Match          60.7%; Score 37; DB 16; Length 209;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11
Db 28 GAFISYGIY 37
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RESULT 23
Q06328      PRELIMINARY;      PRT;      317 AA.
AC Q06328;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to YBR147W.
GN YDR352W OR D9476.6.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Du Z.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28372; AAB64788.1; -.
DR SGD; S0002760; YDR352W.
SQ SEQUENCE 317 AA; 35179 MW; F6A41A2175E05C75 CRC64;

Query Match      60.7%; Score 37; DB 3; Length 317;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAYRYGVVY 11
DB      87 GQYRYGVVH 96

RESULT 24
O23165      PRELIMINARY;      PRT;      384 AA.
AC O23165;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 41.4 kDa protein.
GN C7A10.150 OR AT4G37210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Vos P., Heijnen L., Mewes H.W., Schueller C.,
RA Chalwatiz N.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
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RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99707; CAB16777.1; -.
DR EMBL; AL161591; CAB80387.1; -.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 3.
KW Hypothetical protein.
SQ SEQUENCE 384 AA; 41370 MW; 5A46D0EBE92557DD CRC64;

Query Match      60.7%; Score 37; DB 10; Length 384;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 AYRYGVV 9
DB     124 AYRYGVL 130

RESULT 25
Q9LEB4      PRELIMINARY;      PRT;      409 AA.
AC Q9LEB4;
ID Q9LEB4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RNA binding protein 45.
GN RBP45.
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20555308; PubMed=11105760;
RA Lorkovic Z.J., Wicczorek Kirk D.A., Klahre U., Hemmings-Mieszcak M.,
RA Filipowicz W.;
RT "RBP45 and RBP47, two oligouridylate-specific hnRNP-like proteins
RT interacting with poly(A)+ RNA in nuclei of plant cells.";
RL RNA 6:1610-1624(2000).
DR EMBL; AJ292767; CAC01237.1; -.
DR HSSP; P11940; 1CVJ.
DR ANU-2DPAGE; Q9LEB4; -.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 409 AA; 45243 MW; 145EE701A89AF01D CRC64;

Query Match      60.7%; Score 37; DB 10; Length 409;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GAYRYGVVY 11
DB     370 GAYRYGVVY 379

RESULT 26
Q94K88      PRELIMINARY;      PRT;      492 AA.
AC Q94K88;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 52.3 kDa protein.
GN AT4G37210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
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RN SEQUENCE FROM N.A.
RP Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G.,
RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene AT4g37210 (GI:7270704).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RP Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4g37210 (GI:7270704).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370189; AAK44004.1; -.
DR EMBL; AY062946; AAL33778.1; -.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 3.
KW Hypothetical protein.
SQ SEQUENCE 492 AA; 52275 MW; 25ED16561586AD01 CRC64;

Query Match 60.7%; Score 37; DB 10; Length 492;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AYRYGV 9
Db 124 AYRYVGL 130

RESULT 27
QI4520 PRELIMINARY; PRT; 560 AA.
AC Q14520; O00663;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE HGF activator like protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Kitamura N.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RP MEDLINE-96425001; PubMed-8827452;
RA Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
RA Tomita M.;
RT "Purification and characterization of a novel hyaluronan-binding
RT protein (PHBP) from human plasma: it has three EGF, a kringle and a
RT serine protease domain, similar to hepatocyte growth factor
RT activator.";
RL J. Biochem. 119:1157-1165(1996).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL; D49742; BAA08576.1; -.
DR EMBL; S83182; AAB46909.1; -.
DR HSP; P00763; IDPO.
DR MEROPS; S01.033; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.

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DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF 1; 3.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Serine protease.
SQ SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;

Query Match 60.7%; Score 37; DB 4; Length 560;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVV 10
Db 519 GYYVIGIV 527

RESULT 28
Q26815 PRELIMINARY; PRT; 574 AA.
AC Q26815;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cell surface glycoprotein (S-layer protein).
GN MTH719.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]_TaxID=187420;
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000851; AAB85224.1; -.
KW Complete proteome.
SQ SEQUENCE 574 AA; 61922 MW; B41D17CBE53C8CDE CRC64;

Query Match 60.7%; Score 37; DB 17; Length 574;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVV 11
Db 504 SGGWYRHGRLY 514

RESULT 29
Q8WUB4 PRELIMINARY; PRT; 705 AA.

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AC Q9WUB4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 80.5 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020965; AAH20965.1; -.  
DR InterPro; IPR003674; OTase\_STT3.  
DR Pfam; PF02516; STT3; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 705 AA; 80529 MW; 71426CA559B51C4 CRC64;  
  
Query Match 60.7%; Score 37; DB 4; Length 705;  
Best Local Similarity 75.0%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 644 YYRFGQVY 651  
  
RESULT 30  
Q8TE35 PRELIMINARY; PRT; 705 AA.  
AC Q8TE35;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Transmembrane protein.  
GN TMC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bellacosa A.A.B.; Testa J.J.R.;  
RT "Isolation, characterization and mapping to human chromosome 11q24-25  
RT of a gene, TMC, encoding a highly conserved putative transmembrane  
RT protein."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L47337; AAL77539.1; -.  
SQ SEQUENCE 705 AA; 80603 MW; C5A48A1E92A89250 CRC64;  
  
Query Match 60.7%; Score 37; DB 4; Length 705;  
Best Local Similarity 75.0%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 644 YYRFGQVY 651  
  
RESULT 31  
Q9L3J5 PRELIMINARY; PRT; 742 AA.  
AC Q9L3J5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Endo-1,4-glucanase (EC 3.2.1.4).  
GN CELN.  
OS Clostridium thermocellum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
OC Clostridiales; Clostridiaceae; Clostridium.

OX NCBI\_TaxID=1515;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F7;  
RA Zverlov V.V., Schwarz W.H.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ275974; CAB76935.1; -.  
DR HSSP; P26221; 1TF4.  
DR InterPro; IPR001956; CBD 3.  
DR InterPro; IPR002105; Dockerin\_1.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR001701; GH\_9.  
DR Pfam; PF00942; CBM\_3; 1.  
DR Pfam; PF00404; Dockerin\_1; 2.  
DR Pfam; PF00759; Glyco hydro\_9; 1.  
DR PROSITE; PS00448; CLQS\_CELLULOSE\_RPT; 1.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
DR PROSITE; PS00592; GLYCOSYL\_HYDROL\_F9\_1; 1.  
DR PROSITE; PS00698; GLYCOSYL\_HYDROL\_F9\_2; 1.  
KW Glycosidase; Hydrolase.  
SQ SEQUENCE 742 AA; 82181 MW; D901768CF2C36F8 CRC64;  
  
Query Match 60.7%; Score 37; DB 2; Length 742;  
Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GAYRYG 8  
Db 46 GAYNYG 52  
  
RESULT 32  
Q95YI8 PRELIMINARY; PRT; 1350 AA.  
AC Q95YI8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Pyrophosphatase.  
GN PYRPHIA-P.  
OS Plasmodium yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5861;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17X;  
RA Kaneko O., Tsuboi T., Shirano M., Tachibana M., Ling I.T., Howell S.,  
RA Cao Y.M., Holder A.A., Torii M.;  
RT "The high molecular mass thopy protein, Rphp1, is coded by a member  
RT of the CLAG multigene family in plasmodium falciparum and P. yoelii."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
DR EMBL; AB060735; BAB70677.1; -.  
KW Hydrolase.  
SQ SEQUENCE 1350 AA; 161922 MW; A27EE34A2F1A471A CRC64;  
  
Query Match 60.7%; Score 37; DB 5; Length 1350;  
Best Local Similarity 62.5%; Pred. No. 6.1e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db 847 YYKFGVLY 854  
  
RESULT 33  
Q8S6N1 PRELIMINARY; PRT; 1787 AA.  
AC Q8S6N1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative gag-pol polypeptide.

GN OSJNBA0073L01.17.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Eriarthroideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPONBARE;  
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,  
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,  
RA Jin S.S., Koo H., Ziemann V., Hsiao J., Blunt S., Vanaken S.S.,  
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,  
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
RT "Oryza sativa chromosome 10 BAC OSJNBA0073L01 genomic sequence.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC092548; AAM18738.1; -  
KW Polyprotein.  
SQ SEQUENCE 1787 AA; 202958 MW; CBDFE5D6D7F0260E CRC64;  
  
Query Match 60.7%; Score 37; DB 10; Length 1787;  
Best Local Similarity 62.5%; Pred. No. 8.3e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 YRYGVVY 11  
Db - - - - -  
418 YRYGVVY 425  
  
RESULT 34  
Q9WVQ5 PRELIMINARY; PRT; 241 AA.  
AC Q9WVQ5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE MWRP19 (Monocyte macrophage 19).  
GN MWRP19 OR MWR19.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sha S., Aoki Y., Nishi Y.;  
RT "A cDNA sequence from murine monocyte-macrophage.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY GLAND;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB028863; BAA78906.1; -  
DR EMBL; BC028434; AAB28434.1; -  
DR MGD; MGI:1926788; Mmrp19.  
DR InterPro; IPR001303; Aldolase\_II\_N.  
DR Pfam; PF00596; Aldolase\_II; 1.  
SQ SEQUENCE 241 AA; 26949 MW; 4366CF4AD2239DB8 CRC64;  
  
Query Match 59.0%; Score 36; DB 11; Length 241;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SGAYRY 7  
Db - - - - -  
148 SGYRY 154  
  
RESULT 35  
Q9Y318 PRELIMINARY; PRT; 242 AA.  
AC Q9Y318  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE CGI-29 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20272150; PubMed=10810093;  
RA Lai C.-H., Chou C.-Y., Chang L.-Y., Liu C.-S., Lin W.-C.;  
RT "Identification of Novel Human Genes Evolutionarily Conserved in  
RT Caenorhabditis elegans by Comparative Proteomics.";  
RL Genome Res. 10:703-713(2000).  
DR EMBL; AF132963; AAD27738.1; -  
DR InterPro; IPR001303; Aldolase\_II\_N.  
DR Pfam; PF00596; Aldolase\_II; 1.  
SQ SEQUENCE 242 AA; 27012 MW; 7B99194024C77D5B CRC64;  
  
Query Match 59.0%; Score 36; DB 4; Length 242;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SGAYRY 7  
Db - - - - -  
149 SGYRY 155  
  
RESULT 36  
Q96HK2 PRELIMINARY; PRT; 242 AA.  
AC Q96HK2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Similar to CGI-29 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC008440; AAB08440.1; -  
DR InterPro; IPR001303; Aldolase\_II\_N.  
DR Pfam; PF00596; Aldolase\_II; 1.  
SQ SEQUENCE 242 AA; 27112 MW; 691C60447B723C1B CRC64;  
  
Query Match 59.0%; Score 36; DB 4; Length 242;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SGAYRY 7  
Db - - - - -  
149 SGYRY 155  
  
RESULT 37  
Q96GX9 PRELIMINARY; PRT; 242 AA.  
AC Q96GX9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE CGI-29 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

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RC TISSUR-EYE;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009077; AAH09077.1; -.
DR InterPro: IPR001303; Aldolase II_N.
DR Pfam: PF00596; Aldolase II; 1_-.
SQ SEQUENCE 242 AA; 27125 MW; 9B8D5D1435D6775A CRC64;

Query Match          59.0%; Score 36; DB 4; Length 242;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYR 7
DB 149 SGGYRY 155

RESULT 38
Q8WVU2 PRELIMINARY; PRT; 242 AA.
AC Q8WVU2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 27.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC017594; AAH17594.1; -.
DR InterPro: IPR001303; Aldolase II_N.
DR Pfam: PF00596; Aldolase II; 1_-.
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27215 MW; F8C4A371E3C63FC2 CRC64;

Query Match          59.0%; Score 36; DB 4; Length 242;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYR 7
DB 149 SGGYRY 155

RESULT 39
Q8SV24 PRELIMINARY; PRT; 252 AA.
AC Q8SV24;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative ATP binding protein.
GN ECU07_0540.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyrecaillade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
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RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL: AL590447; CAD25586.1; -.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 28571 MW; AA3318F2EFBBB286 CRC64;

Query Match          59.0%; Score 36; DB 5; Length 252;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11
DB 123 GRYFKGVVY 132

RESULT 40
Q8REE0 PRELIMINARY; PRT; 339 AA.
AC Q8REE0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Galactoside transport system permease protein mgIC.
GN FN1167.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL: AB010622; AAL93363.1; -.
KW Complete proteome.
SQ SEQUENCE 339 AA; 36234 MW; CF1CFBDC4A878111 CRC64;

Query Match          59.0%; Score 36; DB 16; Length 339;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYRG 8
DB 241 SGAYYAFG 248

Search completed: July 18, 2003, 15:09:45
Job time : 30.38 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:01:44 ; Search time 37.18 Seconds  
(without alignments)  
39.423 Million cell updates/sec

Title: US-10-007-790-8

Perfect score: 57

Sequence: 1 RASENIYSYLP 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_101002.\*

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- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	57	100.0	11	21	Murine PIP3 recogn
2	57	100.0	107	21	Murine PIP3 recogn
3	50	87.7	11	23	Murine MC-1 antibo
4	50	87.7	92	23	Murine MC-1 antibo
5	50	87.7	99	18	Anti-DNA antibody
6	50	87.7	99	18	Anti-DNA antibody
7	50	87.7	99	18	Anti-DNA antibody
8	50	87.7	99	18	Anti-DNA antibody
9	50	87.7	107	17	Humanised ID10 ant
10	50	87.7	107	18	Anti-DNA antibody

11	50	87.7	107	23	AAE22189	Murine MC-1 antibo
12	50	87.7	109	19	AAW46483	8019 VK antibody.
13	50	87.7	126	12	AAAR12235	Mouse Mab 2G12 L c
14	50	87.7	127	12	AAAR12357	Light (kappa) chai
15	50	87.7	214	17	AAW05828	Humanised ID10 ant
16	50	87.7	243	15	AAAR53148	VH and VL of Mab P
17	50	87.7	256	23	AAU72864	P4-15 single chain
18	50	87.7	268	21	AAU44972	Recombinant mouse
19	50	87.7	268	21	AAU44973	Recombinant mouse
20	50	87.7	495	23	AAE22193	Murine CCR5xCD3 bi
21	50	87.7	503	23	AAU72873	3B10xP5-2 bispecif
22	47	82.5	107	12	AAAR11985	Anti-placental alk
23	47	82.5	107	12	AAAR11987	Human anti-placent
24	46	80.7	107	16	AAAR78971	Light chain variab
25	46	80.7	224	22	AAAR75038	TRO005 HuMab kappa
26	44	77.2	128	17	AAW03721	Anti-human gp19 MA
27	44	77.2	171	17	AAW03725	Humanised Mab 39-1
28	43	75.4	11	21	AAU92161	Murine 15B8 light
29	43	75.4	107	21	AAU92157	Murine 15B8 light
30	42	73.7	258	23	ABB05962	Monoclonal antiod
31	42	73.7	258	23	ABB05963	Monoclonal antiod
32	42	73.7	258	23	ABB05990	Mouse monoclonal a
33	42	73.7	258	23	ABB05991	Mouse and human ch
34	42	73.7	258	23	ABB05992	Mouse and human ch
35	42	73.7	258	23	ABB05993	Mouse and human ch
36	42	73.7	258	23	ABB05994	Human monoclonal a
37	42	73.7	258	23	ABB05995	Human monoclonal a
38	42	73.7	258	23	ABB05996	Human monoclonal a
39	42	73.7	258	23	ABB05997	Human monoclonal a
40	42	73.7	287	23	ABB05982	Monoclonal antiod
41	41	71.9	11	16	AAAR77201	Mouse anti-human I
42	41	71.9	11	18	AAW27350	CDR1 from murine a
43	41	71.9	104	13	AAAR30010	Light chain variab
44	41	71.9	108	16	AAAR79160	Human IGE receptor
45	41	71.9	108	18	AAW27360	Light chain variab

ALIGNMENTS

RESULT 1	
AA187660	
ID	AA187660 standard; Protein; 11 AA.
XX	
AC	AA187660;
XX	
DT	11-AUG-2000 (first entry)
XX	
DE	Murine PIP3 recognizing Mab variable region light chain CDR1 region.
XX	
KW	PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR1;
KW	immunogen; antibody; light chain; complementarity determining region.
XX	
OS	Mus sp.
XX	
PN	JP2000083664-A.
XX	
PD	28-MAR-2000.
XX	
PF	07-SEP-1998; 98JP-0252921.
XX	
PR	07-SEP-1998; 98JP-0252921.
XX	
PA	(FUKU/) FUKUI Y.
PA	(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX	
DR	WPI; 2000-353334/31.
XX	
PT	A monoclonal antibody recognizing
PT	phosphatidylinositol-3,4,5-triphosphate
XX	
PS	Claim 10; Page 13; 15pp; Japanese.
XX	

CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain complementarity determining region, CDRI described in the method of  
 CC the invention.  
 CC  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 |||||  
 Db 1 RASENIYSYLP 11

RESULT 2  
 AAY87656  
 ID AAY87656 standard; Protein; 107 AA.

AC AAY87656;  
 DT 11-AUG-2000 (first entry)

DE Murine PIP3 recognizing Mab variable region light chain protein.  
 XX  
 XX PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;  
 KW immunogen; antibody; light chain.  
 XX  
 XX Mus sp.

OS JP2000083664-A.  
 PN 28-MAR-2000.  
 XX

XX 07-SEP-1998; 98JP-0252921.  
 XX 07-SEP-1998; 98JP-0252921.

PA (FUKU/) FUKUI Y.  
 PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.  
 DR N-PSDB; AAY87656.

XX A monoclonal antibody recognizing  
 PT phosphatidylinositol-3,4,5-triphosphate -  
 XX Claim 6; Page 12; 15pp; Japanese.

XX This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region light  
 CC chain described in the method of the invention.  
 CC

SQ Sequence 107 AA;

Query Match 100.0%; Score 57; DB 21; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 |||||  
 Db 24 RASENIYSYLP 34

RESULT 3  
 AAE22197  
 ID AAE22197 standard; peptide; 11 AA.

XX AAE22197;

XX 25-JUL-2002 (first entry)

XX Murine MC-1 antibody light chain variable domain (VL) CDRI peptide.

XX Chemokine construct; human immunodeficiency virus 1; allergic disease;  
 KW skin disease; immunological disorder; autoimmune disease; psoriasis;  
 KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
 KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
 KW inflammatory renal disease; HIV-1; transplant rejection; murine; CDRI;  
 KW light chain variable domain; VL; complementarity determining region 1;  
 KW MC-1; antibody.

XX Mus sp.

OS WO2002020615-A2.

PN 14-MAR-2002.

XX 10-SEP-2001; 2001WO-EP10433.

XX 08-SEP-2000; 2000EP-0119694.

PR 05-SEP-2001; 2001US-0948004.

XX (MICR-) MICROMET AG.

XX Mack M, Schloendorff D, Spring M;

PI WPI; 2002-362240/39.

XX Use of an antibody and/or chemokine construct that binds to a chemokine  
 PT receptor, for eliminating cells latently infected with primate  
 PT immunodeficiency virus, or treating, preventing and alleviating immune  
 PT disorders -

XX Disclosure; Page 116; 117pp; English.

XX The invention relates to the use of an antibody and/or chemokine  
 CC construct that binds a chemokine receptor for preparing a pharmaceutical  
 CC composition for eliminating cells latently infected with a primate  
 CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They  
 CC are used in gene therapy and as vaccines. The antibody and/or chemokine  
 CC construct is also used for preparing a pharmaceutical composition for  
 CC treating, preventing and/or alleviating immunological disorders  
 CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes  
 CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin  
 CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
 CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
 CC renal diseases and inflammatory bowel diseases (inflammatory diseases  
 CC and transplant rejections. The present sequence is murine MC-1 antibody  
 CC light chain variable domain (VL) complementarity determining region 1  
 CC (CDRI) peptide.

XX Sequence 11 AA;

Query Match 87.7%; Score 50; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 10

Db 1 RASENIYSYLP 10

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RESULT 4
AAE22190
ID AAE22190 standard; Protein; 92 AA.
XX AC
XX AAE22190;
XX AC
XX AC
DT 25-JUL-2002 (first entry)
XX AC
XX Murine MC-1 antibody light chain variable domain (VL) (1) #2.
XX AC
XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
XX KW skin disease; immunological disorder; autoimmune disease; psoriasis;
XX KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
XX KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
XX KW inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;
XX KW MC-1 antibody; VL; light chain variable domain; chemokine receptor 5.
XX AC
XX Mus sp.
XX AC
XX WO200220615-A2.
XX AC
XX 14-MAR-2002.
XX AC
XX 10-SEP-2001; 2001WO-BP10433.
XX AC
XX 08-SEP-2000; 2000EP-0119694.
XX AC
XX 05-SEP-2001; 2001US-0948004.
XX AC
XX (MICR-) MICROMET AG.
XX AC
XX Mack M, Schloendorff D, Spring M;
XX AC
XX WPI; 2002-362240/39.
XX AC
XX N-PSDB; AAD35249.
XX AC
XX Use of an antibody and/or chemokine construct that binds to a chemokine
XX PT receptor, for eliminating cells latently infected with primate
XX PT immunodeficiency virus, or treating, preventing and alleviating immune
XX PT disorders -
XX AC
XX Claim 12; Page 49-50; 117pp; English.
XX AC
XX The invention relates to the use of an antibody and/or chemokine
XX CC construct that binds a chemokine receptor for preparing a pharmaceutical
XX CC composition for eliminating cells latently infected with a primate
XX CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
XX CC are used in gene therapy and as vaccines. The antibody and/or chemokine
XX CC construct is also used for preparing a pharmaceutical composition for
XX CC treating, preventing and/or alleviating immunological disorders
XX CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes
XX CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
XX CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
XX CC such as inflammatory joint diseases (chronic arthritis), inflammatory
XX CC renal diseases and inflammatory bowel diseases and graft versus host
XX CC and transplant rejections. The present sequence is murine MC-1 antibody
XX CC light chain variable domain (VL)(1). This antibody is specific for
XX CC human chemokine receptor 5 (CCR5).
XX AC
XX Sequence 92 AA;
XX AC
XX Query Match 87.7%; Score 50; DB 23; Length 92;
XX AC
XX Best Local Similarity 100.0%; Pred.No. 0.045;
XX AC
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
XX AC
Qy 1 RASENIYSYL 10
Db 16 RASENIYSYL 25
XXXXXXXXXX
XXXXXXXXXX
RESULT 5
AAW04587

```

```
QY      1 RASENIYSYL 10
Db      |||||
      16 RASENIYSYL 25

RESULT 6
AAW04596
ID AAW04596 standard; Protein; 99 AA.
XX
AC AAW04596;
XX
DT 12-AUG-1997 (first entry)
XX
DE Anti-DNA antibody 9f11 light chain variable region.
XX
KW Light chain; variable region; anti-DNA; monoclonal; antibody;
KW MAb 9f11; hairpin; diagnosis; inflammatory glomerulonephritis;
KW systemic lupus erythematosus; screening; treatment; prevention;
KW SLE; disease.
XX
OS Mus spp.
XX
FH Key Location/Qualifiers
FT Region 1..22 /label= framework_I
FT Region 23..27 /label= CDR_I
FT Region 28..41 /label= framework_II
FT Region 42..58 /label= CDR_II
FT Region 59..90 /label= framework_III
FT Region 91..102 /label= CDR_III
FT Region 103..115 /label= J_region
XX WO9636361-A1.
XX
XX 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
XX 18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Glick GD, Swanson PC;
XX
XX WPI; 1997-011854/01.
XX N-PSDB; AAT43741.
XX
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX develop prods. for diagnosis and treatment of disorders, e.g.
XX glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 8; 102pp; English.
XX
XX The present sequence is the light chain variable region of the
XX anti-DNA monoclonal antibody (MAb) 9f11, which has a high affinity
XX for single stranded DNA, low or no affinity for double stranded DNA
XX and specifically binds a DNA hairpin. The MAb can be used to diagnose
XX disorders associated with the pathological complexation of DNA,
XX e.g. inflammatory glomerulonephritis and systemic lupus
XX erythematosus. It can also be used to generate reagents to screen
XX for pharmaceutical agents, and treat and/or prevent an above
XX disorder.
XX Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
XX from which were then fused with Sp2/0 myeloma cells to give
XX hybridomas producing the anti-DNA MAb. 9f11 was found to react
XX strongly with single stranded DNA and poly(dT), and weakly with
XX poly(dG).
```

```
XX
SQ Sequence 99 AA;
Query Match 87.7%; Score 50; DB 18; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.049; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY      1 RASENIYSYL 10
Db      |||||
      16 RASENIYSYL 25

RESULT 7
AAW04597
ID AAW04597 standard; Protein; 99 AA.
XX
AC AAW04597;
XX
DT 12-AUG-1997 (first entry)
XX
DE Anti-DNA antibody 15b10 light chain variable region.
XX
KW Light chain; variable region; anti-DNA; monoclonal; antibody;
KW MAb 15b10; hairpin; diagnosis; inflammatory glomerulonephritis;
KW systemic lupus erythematosus; screening; treatment; prevention;
KW SLE; disease.
XX
OS Mus spp.
XX
FH Key Location/Qualifiers
FT Region 1..22 /label= framework_I
FT Region 23..27 /label= CDR_I
FT Region 28..41 /label= framework_II
FT Region 42..58 /label= CDR_II
FT Region 59..90 /label= framework_III
FT Region 91..102 /label= CDR_III
FT Region 103..115 /label= J_region
XX WO9636361-A1.
XX
XX 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
XX 18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Glick GD, Swanson PC;
XX
XX WPI; 1997-011854/01.
XX N-PSDB; AAT43742.
XX
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX develop prods. for diagnosis and treatment of disorders, e.g.
XX glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 8; 102pp; English.
XX
XX The present sequence is the light chain variable region of the
XX anti-DNA monoclonal antibody (MAb) 15b10, which has a high affinity
XX for single stranded DNA, low or no affinity for double stranded DNA
XX and specifically binds a DNA hairpin. The MAb can be used to diagnose
XX disorders associated with the pathological complexation of DNA,
XX e.g. inflammatory glomerulonephritis and systemic lupus
XX erythematosus. It can also be used to generate reagents to screen
XX for pharmaceutical agents, and treat and/or prevent an above
XX disorder.
XX Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
XX from which were then fused with Sp2/0 myeloma cells to give
XX hybridomas producing the anti-DNA MAb. 9f11 was found to react
XX strongly with single stranded DNA and poly(dT), and weakly with
XX poly(dG).
```

```

CC for pharmaceutical agents, and treat and/or prevent an above
CC disorder.
CC Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
CC from which were then fused with Sp2/0 myeloma cells to give
CC hybridomas producing the anti-DNA Mab. 15b10 was found to react
CC strongly with single stranded DNA and poly(dT), and weakly with
CC poly(dG).
XX
XX
SQ Sequence 99 AA;
Query Match 87.7%; Score 50; DB 18; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASENIYSYL 10
Db 16 RASENIYSYL 25
|||||
|||||
RESULT 8
AAW04598
ID ID AAW04598 standard; Protein; 99 AA.
XX
XX AC AAW04598;
XX
XX 12-AUG-1997 (first entry)
XX
XX Anti-DNA antibody 5f3 light chain variable region.
DE
XX
XX Light chain; variable region; anti-DNA; monoclonal; antibody;
KW Mab 5f3; hairpin; diagnosis; inflammatory glomerulonephritis;
KW KW systemic lupus erythematosus; screening; treatment; prevention;
KW KW SLE; disease.
XX
XX
OS Mus spp.
XX
XX Key Location/Qualifiers
FH Region 1..22
FT /label= framework_I
FT Region 23..27
FT /label= CDR_I
FT Region 28..41
FT /label= framework_II
FT Region 42..58
FT /label= CDR_II
FT Region 59..90
FT /label= framework_III
FT Region 91..102
FT /label= CDR_III
FT Region 103..115
FT /label= J_region
XX
XX WO9636361-A1.
XX
XX 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
XX 18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Gluck GD, Swanson PC;
PI
XX WPI; 1997-011854/01.
DR
XX N-PSDB; AAT43743.
XX
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 8; 102pp; English.
XX
XX

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PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Gingrich R, Link BK, Tso JY, Weiner G;  
 XX  
 DR WPI; 1996-412742/41.  
 XX  
 XX New bispecific antibody reactive with both T or NK cells and  
 PT malignant B cells - also their humanised forms and hybridomas  
 PT producing them, useful for treating or preventing leukaemia,  
 PT lymphoma and myeloma  
 XX  
 XX Claim 14; Fig 4a; 85pp; English.  
 PS  
 CC The variable region (AAW05822) of the humanised ID10 antibody light  
 CC chain (AAW05828) consists of human R3.5H5G kappa-light chain variable  
 CC region framework (substd. at 5 positions with mouse or consensus  
 CC human amino acids) and complementarity determining regions from the  
 CC murine ID10 antibody specific for a 28/32 kDa heterodimeric antigen  
 CC present on the surface of malignant B-cells. It can be coexpressed  
 CC with humanised ID10 heavy chain (see also AAW05829) in e.g. mouse  
 CC myeloma NSO cells. Humanised antibody fragments can be incorporated  
 CC into novel bispecific antibodies reactive with both effector cell  
 CC antigens (see also AAW05824-25, AAW05826 and AAW05830) and malignant  
 CC B-cells.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 87.7%; Score 50; DB 17; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RASENIYSYL 10  
 DB 24 RASENIYSYL 33  
 RESULT 10  
 ID AAW07439 standard; Protein; 107 AA.  
 XX  
 AC AAW07439;  
 XX  
 DT 12-AUG-1997 (first entry)  
 DE Anti-DNA antibody 9f11 group light chain variable region.  
 XX  
 KW Light chain; variable region; anti-DNA; monoclonal; antibody;  
 KW 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis;  
 KW systemic lupus erythematosus; screening; treatment; prevention;  
 KW SLE; disease; consensus; putative.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..23 /label= framework\_I  
 FT Region 24..34 /label= CDR\_I  
 FT Region 35..49 /label= framework\_II  
 FT Region 50..56 /label= CDR\_II  
 FT Region 57..88 /label= framework\_III  
 FT Region 89..97 /label= CDR\_III  
 FT Region 98..107 /label= J\_region  
 XX  
 PN WO9636361-A1.  
 XX  
 PD 21-NOV-1996.  
 XX

PF 16-MAY-1996; 96WO-US07113.  
 XX  
 PR 18-MAY-1995; 95US-0443540.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Glick GD, Swanson PC;  
 XX  
 DR WPI; 1997-011854/01.  
 DR N-PSDB; AAT43808.  
 XX  
 PT Anti-DNA antibody which specifically binds DNA hairpin - useful to  
 PT develop prods. for diagnosis and treatment of disorders, e.g.  
 PT glomerulonephritis or systemic lupus erythematosus  
 XX  
 PS Example; Fig 9; 102pp; English.  
 XX  
 CC The present sequence is the light chain variable region of the  
 CC group 9f11 putative consensus anti-DNA monoclonal antibody (MAB),  
 CC which has a high affinity for single stranded DNA, low or no  
 CC affinity for double stranded DNA and specifically binds a DNA  
 CC hairpin. The MAB can be used to diagnose disorders associated with the  
 CC pathological complexation of DNA, e.g. inflammatory  
 CC glomerulonephritis and systemic lupus erythematosus. It can also be  
 CC used to generate reagents to screen for pharmaceutical agents, and  
 CC treat and/or prevent an above disorder.  
 CC The sequence was derived by aligning homologous anti-DNA MAB,  
 CC whose sequences have been published, as well as several MAB of  
 CC other specificities obtained from a database search.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 87.7%; Score 50; DB 18; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RASENIYSYL 10  
 DB 24 RASENIYSYL 33  
 RESULT 11  
 ID AAE22189 standard; Protein; 107 AA.  
 XX  
 AC AAE22189;  
 XX  
 DT 25-JUL-2002 (first entry)  
 DE Murine MC-1 antibody light chain variable domain (VL) (1) #1.  
 XX  
 KW Chemokine construct; human immunodeficiency virus 1; allergic disease;  
 KW skin disease; immunological disorder; autoimmune disease; psoriasis;  
 KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
 KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
 KW inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;  
 KW MC-1 antibody; VL; light chain variable domain; Chemokine receptor 5.  
 XX  
 OS Mus sp.  
 XX  
 PN WO20020615-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-EP10433.  
 XX  
 PR 08-SEP-2000; 2000EP-0119694.  
 PR 05-SEP-2001; 2001US-0948004.  
 XX  
 PA (MICR-) MICROMET AG.  
 XX  
 PD Mack M, Schloendorff D, Spring M;  
 XX



```
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASENIYSYL 10
Db 44 RASENIYSYL 53
RESULT 14
AAR12357 standard; Protein; 127 AA.
XX AC AAR12357;
XX 15-AUG-1991 (first entry)
DE Light (kappa) chain variable region of murine 2G12 immuno-
DE globulin.
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX Mus musculus.
XX WO9107493-A.
XX 30-MAY-1991.
XX 13-NOV-1990; 90WO-US06615.
XX 13-NOV-1989; 89US-0433730.
XX (XOMA-) XOMA CORP.
XX (GREC) GREEN CROSS CORP.
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX WPI; 1991-178044/24.
XX N-PSDB; AAQ12059.
XX New chimeric mouse-human antibodies - used to detect, kill and
XX remove HIV-1 antigen from sample
XX Disclosure; fig 8; 107pp; English.
XX This is the light (kappa)-chain variable (V) region of a mouse
XX monoclonal antibody (Mab), 2G12, and is specific for an HIV-1
XX viral antigen. It is used in the construction of a chimeric
XX MAb comprising heavy and light chains having murine V regions
XX and human C regions. The chimeric MABs are more effective than
XX murine MAB 2G12 since they have an increased compatibility in
XX humans. The heavy and light chain V-regions are joined by
XX manipulating their respective joining (J) regions to generate
XX restriction enzyme recognition sites. The chimeric MABs can be
XX used as immunoconjugates, in association with e.g. toxins for HIV
XX treatment. They can also be used in diagnosis of HIV.
XX See also AAQ12056-58 and AAQ12060-63.
XX Sequence 127 AA;
Query Match 87.7%; Score 50; DB 12; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASENIYSYL 10
Db 44 RASENIYSYL 53
RESULT 15
AAW05828
ID AAW05828 standard; Protein; 214 AA.
XX AC AAW05828;
XX 27-JAN-1997 (first entry)
```

```
XX Humanised ID10 antibody light chain.
DE
XX B-cell lymphoma; humanised antibody; bispecific antibody;
KW myeloma; leukaemia; hybridoma; monoclonal antibody.
XX
XX Chimeric Homo sapiens;
OS Chimeric Mus sp.
XX
XX Key Location/Qualifiers
FH Domain 1..107
FT /label= Variable_domain
FT Region 24..33
FT /label= CDR1
FT Region 49..55
FT /label= CDR2
FT Region 89..97
FT /label= CDR3
FT Domain 108..214
FT /label= Human_C-kappa_domain
XX
XX WO9626964-A1.
XX
XX 06-SEP-1996.
XX
XX 29-FEB-1996; 96WO-US02754.
XX
XX 01-MAR-1995; 95US-0397411.
XX
XX (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Gingrich R, Link BK, Tso JY, Weiner G;
XX WPI; 1996-412742/41.
XX
XX New bispecific antibody reactive with both T or NK cells and
XX malignant B cells - also their humanised forms and hybridomas
XX producing them, useful for treating or preventing leukaemia,
XX lymphoma and myeloma
XX
XX Example 4; Fig 4c; 85pp; English.
XX
XX The humanised ID10 antibody light chain (AAW05828) includes a
XX variable region (see also AAW05822) consisting of human R3 SHG light
XX chain variable region framework and complementarity determining
XX regions from the murine ID10 antibody specific for a 28/32 kDa
XX antigen found on the surface of malignant B-cells. It can be
XX coexpressed with humanised ID10 heavy chain (see also AAW05829) in
XX mammalian host cells. Bispecific antibodies can be constructed that
XX include a first binding fragment comprising humanised M291 heavy and
XX light chain variable regions (see also AAW05826, AAW05830), and a second
XX binding fragment comprising humanised ID10 heavy and light chain
XX variable regions. Such antibodies are reactive with both T or NK
XX cells and malignant B cells, and have therapeutic and diagnostic
XX applns.
XX
XX Sequence 214 AA;
Query Match 87.7%; Score 50; DB 17; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASENIYSYL 10
Db 24 RASENIYSYL 33
RESULT 16
AAR53148
ID AAR53148 standard; Protein; 243 AA.
XX
XX AAR53148;
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XX 07-DEC-1994 (first entry)
XX VH and VL of MAb PR1.
XX
XX PE38KDEL; plasmid; PUL140; heavy; chain; light; variable region; VH;
XX VL; monoclonal antibody; MAb; PR1; PCR; amplify; PR1-hybridoma RNA;
XX primer; complementarity determining regions; CDR; drug; cytotoxin;
XX prostate cell associated antigen; radioisotope; PCAA; prostate;
XX cells; cancer; diagnosis; benign prostate hyperplasia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Protein 1..118 /label= PR1 VH
XX Peptide 119..133 /label= Linker
XX Protein 134..243 /label= PR1 VL
XX
XX WO9409150-A.
XX
XX 28-APR-1994.
XX
XX 22-SEP-1993; 93WO-US09166.
XX
XX 08-OCT-1992; 92US-0958140.
XX
XX (USSH ) US SEC DEPT HEALTH.
XX
XX Pastan IH;
XX
XX WPI; 1994-151334/18.
XX N-PSDB; AAQ64476.
XX
XX Monoclonal antibody specific for prostate cells - used in the
XX diagnosis and treatment of conditions involving abnormal growth
XX of prostate cells, esp prostate cancer.
XX
XX Example 3; Fig 1; 64pp; English.
XX
XX This sequence is encoded by the PE38KDEL fragment of the plasmid
XX PUL140 and represents the heavy chain and light chain variable regions
XX (VH and VL) of the monoclonal antibody (MAb) PR1. The cDNA encoding
XX this sequence was derived by PCR amplification of reverse transcribed
XX PR1-hybridoma RNA using the primer sequences given in AAQ64477-81. The
XX VH and VL complementarity determining regions (CDRs) are used in the
XX construction of the MAb of the invention which competes with PR1
XX for binding to a prostate cell associated antigen. The MAb of the
XX invention can be used for targeting a drug, cytotoxin or radioisotope
XX to prostate cells of a patient suffering from prostate cancer. It can
XX also be used for diagnosing the presence of prostate cancer in an
XX individual and for the diagnosis and treatment of other conditions
XX involving abnormal growth of prostate cells, eg. benign prostate
XX hyperplasia. The MAb reacts strongly with prostate cancer cells but
XX only weakly with a few other normal human tissues. The effect of
XX therapy on normal prostate cells does not threaten the overall health
XX of the patient.
XX
XX Sequence 243 AA;
XX
XX Query Match 87.7%; Score 50; DB 15; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
XX Matches 10; Conservative 0;
XX
XX QY 1 RASENIYSYL 10
XX Db 157 RASENIYSYL 166
XX
XX RESULT 17
XX AAU72864

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ID AAU72864 standard; Protein; 256 AA.
XX
AC AAU72864;
XX
DT 26-FEB-2002 (first entry)
XX
DE P4-15 single chain Fv.
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
XX P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
XX
OS Homo sapiens.
XX
XX WO200171005-A2.
XX
XX 27-SEP-2001.
XX
XX 26-MAR-2001; 2001WO-EP03414.
XX
XX 24-MAR-2000; 2000EP-0106467.
XX
XX (KUFE/) KUFER P.
XX
XX Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
XX Mayer M, Hofmeister R;
XX
XX WPI: 2002-055119/07.
XX N-PSDB; AAS97138.
XX
XX Multifunctional polypeptides comprising binding sites that specifically
XX recognise extracellular groups of the NKG2D receptor complex and
XX domains which function as receptors or ligands, useful for treating
XX cancers and infectious diseases -
XX
XX Example 7; Fig 16; 114pp; English.
XX
XX The invention relates to a multifunctional polypeptide comprising a
XX domain with a binding site that specifically recognises an extracellular
XX group of the NKG2D receptor complex and a second domain which functions
XX as a receptor or ligand. The polypeptide and its associated
XX polynucleotide are used for the preparation of a pharmaceutical
XX composition for the treatment of cancer, infections and/or autoimmune
XX conditions. The cancer may be a tumour of the head and neck, stomach,
XX oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
XX larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
XX bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
XX The infectious diseases can be caused by viruses, bacteria, fungi,
XX protozoa or helminths. The autoimmune diseases include multiple
XX sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
XX uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
XX diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
XX autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
XX receptor and the polypeptides of the invention.
XX
XX Sequence 256 AA;
XX
XX Query Match 87.7%; Score 50; DB 23; Length 256;
XX Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
XX Matches 10; Conservative 0;
XX
XX QY 1 RASENIYSYL 10
XX Db 161 RASENIYSYL 170
XX
XX RESULT 18
XX

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AA44972  
ID AA44972 standard; Protein; 268 AA.  
XX  
AC AA44972;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Recombinant mouse anti-rotavirus antibody (Clone 11).  
XX  
KW Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;  
XX VH; light chain variable region; VL; pCANTAB 5E vector; treatment;  
KW probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;  
KW immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Region 6..116  
FT Region /label= Mouse\_Heavy\_chain\_variable\_region  
FT Region 117..151  
FT Region /label= Linker\_region  
FT Region 152..250  
FT Region /label= Mouse\_Light\_chain\_variable\_region  
FT Domain 254..266  
FT /label= E tag domain  
FT /note= "Enables immunodetection and immunoaffinity  
FT purification of the recombinant antibody"  
XX  
PN WO200006764-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 29-JUL-1999; 99WO-US17296.  
XX  
PR 30-JUL-1998; 98US-0094697.  
XX  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX  
PI Fahl WE, Letchworth GJ, Mueller GC, Savage AK, Loo D;  
XX WPI; 2000-195315/17.  
DR N-PSDB; AA250508.  
XX  
PT Composition for supplementing or replacing an immune response against  
PT gastrointestinal pathogens in e.g. newborn infants, comprises probiotic  
PT microorganisms expressing antibodies specific for the gastrointestinal  
PT pathogens -  
XX  
PS Disclosure; Fig 1; 48pp; English.  
XX  
CC The present sequence is the recombinant mouse anti-rotavirus antibody.  
CC It comprises of mouse heavy chain (VH) and light chain (VL) variable  
CC regions joined by a linker. The recombinant antibody encoding DNA is  
CC inserted into pCANTAB 5E expression vector (clone 11). The vector is  
CC used to transform probiotic bacteria like, Lactobacilli for expression  
CC and secretion of recombinant anti-rotavirus antibodies. The antibodies  
CC have antibacterial and antiviral activity. Antibody-expressing probiotic  
CC bacteria can be administered for treatment of gastrointestinal (GI)  
CC tract infections and to immunise neonates, humans or immunosuppressed/  
CC immunodeficient adults acutely exposed to a bolus of GI pathogen.  
XX  
SQ Sequence 268 AA;

Query Match 87.7%; Score 50; DB 21; Length 268;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
DB 166 RASENIYSYL 175

RESULT 19  
AA44973  
ID AA44973 standard; Protein; 268 AA.  
XX  
AC AA44973;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Recombinant mouse anti-rotavirus antibody (Clone 22).  
XX  
KW Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;  
XX VH; light chain variable region; VL; pCANTAB 5E vector; treatment;  
KW probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;  
KW immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Region 6..116  
FT Region /label= Mouse\_Heavy\_chain\_variable\_region  
FT Region 117..152  
FT Region /label= Linker\_region  
FT Region 153..250  
FT Region /label= Mouse\_Light\_chain\_variable\_region  
FT Domain 254..266  
FT /label= E tag domain  
FT /note= "Enables immunodetection and immunoaffinity  
FT purification of the recombinant antibody"  
XX  
PN WO200006764-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 29-JUL-1999; 99WO-US17296.  
XX  
PR 30-JUL-1998; 98US-0094697.  
XX  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX  
PI Fahl WE, Letchworth GJ, Mueller GC, Savage AK, Loo D;  
XX WPI; 2000-195315/17.  
DR N-PSDB; AA250509.  
XX  
PT Composition for supplementing or replacing an immune response against  
PT gastrointestinal pathogens in e.g. newborn infants, comprises probiotic  
PT microorganisms expressing antibodies specific for the gastrointestinal  
PT pathogens -  
XX  
PS Disclosure; Fig 2; 48pp; English.  
XX  
CC The present sequence is the recombinant mouse anti-rotavirus antibody.  
CC It comprises of mouse heavy chain (VH) and light chain (VL) variable  
CC regions joined by a linker. The recombinant antibody encoding DNA is  
CC inserted into pCANTAB 5E expression vector (clone 22). The vector is  
CC used to transform probiotic bacteria like, Lactobacilli for expression  
CC and secretion of recombinant anti-rotavirus antibodies. The antibodies  
CC have antibacterial and antiviral activity. Antibody-expressing probiotic  
CC bacteria can be administered for treatment of gastrointestinal (GI)  
CC tract infections and to immunise neonates, humans or immunosuppressed/  
CC immunodeficient adults acutely exposed to a bolus of GI pathogen.  
XX  
SQ Sequence 268 AA;

Query Match 87.7%; Score 50; DB 21; Length 268;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
DB 166 RASENIYSYL 175



## RESULT 22

AAR11985  
ID AAR11985 standard; Protein; 107 AA.

XX AC AAR11985;  
XX DT 31-JUL-1991 (first entry)

XX DE Anti-placental alkaline phosphatase Vκ.  
XX KW Placental alkaline phosphatase; antibody; cancer; light chain;  
XX KW PLAP; CDR.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
XX FT Region 24..34  
FT /label= CDR1  
FT Region 50..56  
FT /label= CDR2  
FT Region 89..97  
FT /label= CDR3

XX PN EP429242-A.

XX PD 29-MAY-1991.

XX PF 14-NOV-1990; 90EP-0312407.

XX PR 07-SEP-1990; 90GB-0019552.

XX PR 17-NOV-1989; 89GB-0026045.

XX PA (UNIL ) UNILEVER PLC.

XX PI Verhoeyen ME;

XX WPI; 1991-157662/22.

XX N-PSDB; AAQ11846.

XX Synthetic specific binder for human placental alkaline phosphatase - for treating and diagnosing cancers e.g. breast, ovarian and colon cancers and pleural effusions  
PS Disclosure; Fig 2; 28pp; English.

CC The murine anti-PLAP Vκ gene contains 3 CDRs which are used to reshape the human anti-PLAP Vκ gene (AAQ11848). The murine anti-PLAP Vκ gene (AAQ11845) CDRs were used to reshape the human anti-PLAP Vκ gene (AAQ11847). The specific binder for human PLAP contains at least one of the former 3 CDRs and/or at least one of the latter CDRs. The produced antibodies are more readily tolerated when administered to a human patient. Antibody reagents can be used to identify, e.g. by serum testing or imaging, and/or to treat PLAP-producing cancers. Such cancers can occur as, e.g. breast cancer, ovarian cancer and colon cancer or can manifest themselves as liquids such as pleural effusions.

XX SQ Sequence 107 AA;

Query Match 82.5%; Score 47; DB 12; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.2;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||||  
Db 24 RASENIYSV 33

## RESULT 23

AAR11987  
ID AAR11987 standard; Protein; 107 AA.

XX AC AAR11987;

XX DT 31-JUL-1991 (first entry)

XX DE Human anti-placental alkaline phosphatase Vκ.

XX KW Placental alkaline phosphatase; antibody; cancer; light chain;  
XX KW PLAP; CDR.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT Region 24..34  
FT /label= CDR1  
FT Region 50..56  
FT /label= CDR2  
FT Region 89..97  
FT /label= CDR3

XX PN EP429242-A.

XX PD 29-MAY-1991.

XX PF 14-NOV-1990; 90EP-0312407.

XX PR 07-SEP-1990; 90GB-0019552.

XX PR 17-NOV-1989; 89GB-0026045.

XX PA (UNIL ) UNILEVER PLC.

XX PI Verhoeyen ME;

XX WPI; 1991-157662/22.

XX N-PSDB; AAQ11848.

XX Synthetic specific binder for human placental alkaline phosphatase - for treating and diagnosing cancers e.g. breast, ovarian and colon cancers and pleural effusions  
PS Disclosure; Fig 1; 28pp; English.

CC The murine anti-PLAP Vκ gene (AAQ11845) contains 3 CDRs which are used to reshape the human anti-PLAP Vκ gene. The murine anti-PLAP Vκ gene (AAQ11845) CDRs were used to reshape the human anti-PLAP Vκ gene (AAQ11847). The specific binder for human PLAP contains at least one of the former 3 CDRs and/or at least one of the latter CDRs. The produced antibodies are more readily tolerated when administered to a human patient. Antibody reagents can be used to identify, e.g. by serum testing or imaging, and/or to treat PLAP-producing cancers. Such cancers can occur as, e.g. breast cancer, ovarian cancer and colon cancer or can manifest themselves as liquids such as pleural effusions.

XX SQ Sequence 107 AA;

Query Match 82.5%; Score 47; DB 12; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.2;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||||  
Db 24 RASENIYSV 33

## RESULT 24

AAR78971  
ID AAR78971 standard; Protein; 107 AA.

XX AC AAR78971;

XX DT 21-DEC-1995 (first entry)

XX

DE XX Light chain variable region for monoclonal antibody 2D5.  
XX KW Monoclonal antibody; heavy metal; mercury; variable region;  
KW light chain.  
XX OS Synthetic.  
XX PN WO9520607-A.  
XX PD 03-AUG-1995.  
XX XX 27-JAN-1995; 95WO-US01199.  
XX PF 27-JAN-1994; 94US-0187407.  
XX PR (BION-) BIONEERASKA INC.  
XX PA Lopez O, Wagner FW, Wylie DE;  
XX PI WPI; 1995-275415/36.  
XX DR N-PSDB; AAQ97509.  
XX XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
PT monoclonal antibodies, used for detecting, removing, adding or  
PT neutralising heavy metals  
XX Claim 23; Page 69; 106pp; English.  
XX XX Hybridoma antibodies have been produced with the spleen cells of  
CC BALB/c mouse that had received multiple injections of mercuric ions  
CC reacted with glutathione to produce a mercuric ion coordinate  
CC covalent compound which was covalently bound to keyhole limpet  
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23P8, 2D5,  
CC 5B6 and 3E8) were producing mAbs that were strongly positive  
CC against glutathione-mercuric ions but negative against glutathione  
CC without mercuric ions. RNA was isolated from hybridoma cells with  
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
CC by MuLV reverse transcriptase. The primers used for cDNA synthesis  
CC were complementary to the 5' end of the CH1 domain of the heavy  
CC chain expressed by the hybridoma of interest, or to the 5' and of  
CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region, in conjunction with  
CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences  
CC of the PCR amplified nucleotides were determined. These are given  
CC in AAQ97498-097510 and the deduced AA sequences in AAR79241-R79250 &  
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC sequence listings. The descriptions in the sequence listings are  
CC used here.  
XX XX Sequence 107 AA;  
SQ Query Match 80.7%; Score 46; DB 16; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.32;  
Matches 9; Conservative 0; Mismatches .1; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
DB 24 RASENIYGYL 33  
RESULT 25  
AAB75038  
ID AAB75038 standard; Protein; 224 AA.  
XX AAB75038;  
XX AAB75038;  
XX 19-JUL-2001 (first entry)  
XX TRO005 HuMab kappa chain protein sequence 1CB8K.  
XX

XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;  
KW human antibody phase display library; immunisation; transgenic animal.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200125492-A1.  
XX PD 12-APR-2001.  
XX XX 02-OCT-2000; 2000WO-US27237.  
XX PF 02-OCT-1999; 99US-0157415.  
XX PR 01-DEC-1999; 99US-0453234.  
XX XX (BIOS-) BIOSITE DIAGNOSTICS INC.  
XX PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.  
XX PI Buechler J, Valkirs G, Gray J, Lonberg N;  
XX WPI; 2001-335567/35.  
XX DR Producing a human antibody phase display library comprises providing a  
PT transgenic animal whose genome comprises human immunoglobulin genes and  
PT isolating nucleic acids encoding antibody chains from lymphatic cells -  
XX Example 37; Page 121-122; 161pp; English.  
XX PS The present invention describes a method (M1) for producing a human  
CC antibody phase display library (I), comprising: (1) providing a nonhuman  
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;  
CC (2) isolating nucleic acids encoding human antibody chains (III) from  
CC lymphatic cells; and (3) forming a library of display packages whose  
CC members comprise a nucleic acid encoding (III) which is displayed from  
CC the package. The method is used for producing a human antibody display  
CC library, e.g., a Fab phage display library. The display method may be  
CC used to screen nucleic acids encoding antibody chains obtained from  
CC immunised nonhuman transgenic animals, and from this a population of  
CC antibodies may be prepared. Production of a human monoclonal antibodies  
CC display library using this method means there is no need to immunise  
CC humans with antigens, and the difficulties faced with immortalising B  
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
CC represent sequences used in the exemplification of the present invention.  
XX XX Sequence 224 AA;  
SQ Query Match 80.7%; Score 46; DB 22; Length 224;  
Best Local Similarity 80.0%; Pred. No. 0.73;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
DB 24 RASQNIYSYL 33  
RESULT 26  
AAW03721  
ID AAW03721 standard; Protein; 128 AA.  
XX AAW03721;  
XX AAW03721;  
XX 02-APR-1997 (first entry)  
XX Anti-human gp39 MAb 39-1.106 light chain variable region.  
XX Light chain; variable region; murine; mouse; anti-human; disease;  
KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
KW diagnosis; inhibition; B-cell; activation; treatment; disorder;  
KW immune; autoimmune; allergic response; organ rejection; drug;  
KW graft versus host; cell imaging; tumour; targetted; delivery;  
KW targeted.  
XX XX

OS Mus musculus.

XX Key Location/Qualifiers

PH Peptide 1..20

FT Peptide /label= sig\_peptide

FT Peptide 21..128

FT Region /label= mat\_peptide

FT Region 44..54

FT /note= "complementarity determining region 1"

FT Region 70..76

FT /note= "complementarity determining region 2"

FT Region 109..117

FT /note= "complementarity determining region 3"

XX WO9623071-A2.

XX 01-AUG-1996.

XX 26-JAN-1996; 96WO-US01119.

XX 26-JAN-1995; 95US-0379057.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;

XX Harris LJ, Hollenbaugh D, Siadak AW;

XX WPI; 1996-362694/36.

XX N-PSDB; AAT35973.

XX Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..

XX Claim 89; Fig 6A; 167pp; English.

XX The present sequence is the light chain variable region of the murine anti-human glycoprotein (gp) 39 monoclonal antibody (Wab) 39-1.1.106 (a member of the murine kappa V subfamily). The Wab was prep'd by immunising a 6-8 week old BALB/c mouse with a gp39-CD8 fusion protein, and 3 days later harvesting and fusing spleen and CC lymph cells to mouse melanoma cells, to produce an anti-human gp39 Wab producing hybridoma. The Wab may be useful for diagnosing CC disease states, inhibiting B-cell activation and for treating CC immunological disorders, e.g. autoimmune disorders, allergic CC responses, organ rejection and graft versus host disease. It may CC also be used for imaging cells which express gp39 on their surface, CC e.g. tumour cells, and to target therapeutic agents to such cells. CC The Wab inhibits the CD40/gp39 interaction, therefore limiting both CC prim. and sec. responses to T-cell dependent antigens and Ab prodn. CC specific to these antigens. A typical compen. for intramuscular CC injection pref. contains 50 mg of Wab in 1 ml of sterile buffered CC water.

XX Sequence 128 AA;

Query Match 77.2%; Score 44; DB 17; Length 128;

Best Local Similarity 90.0%; Pred. NO. 0.95;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

DB 44 RASETIYSYL 53

RESULT 27

ID AAW03725

XX AAW03725 standard; Protein; 171 AA.

AC AAW03725;

XX 02-APR-1997 (first entry)

XX

DE Humanised MAb 39-1.1.106 light chain variable region.

XX Light chain; variable region; murine; mouse; anti-human; disease;

XX glycoprotein 39; gp39; monoclonal; antibody; 39-1.1.106; hybridoma;

XX diagnosis; inhibition; B-cell; activation; treatment; disorder;

XX immune; autoimmune; allergic response; organ rejection; drug;

XX graft versus host; cell imaging; tumour; targeted; delivery;

XX targeted; humanised.

XX Mus musculus.

XX Key Location/Qualifiers

PH Key

FT Misc-difference 2

FT /note= "corresponding codon TAG"

FT Misc-difference 11

FT /note= "corresponding codon TAA"

FT Misc-difference 157

FT /note= "corresponding codon TAA"

FT Misc-difference 165

FT /note= "corresponding codon TAA"

XX WO9623071-A2.

XX 01-AUG-1996.

XX 26-JAN-1996; 96WO-US01119.

XX 26-JAN-1995; 95US-0379057.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;

XX Harris LJ, Hollenbaugh D, Siadak AW;

XX WPI; 1996-362694/36.

XX N-PSDB; AAT36018.

XX Monoclonal antibodies specific for different epitope(s) on human gp39 - used for inhibiting B cell activation and for the diagnosis of various disorders, e.g. cancer, psoriasis etc..

XX Example 13; Fig 16; 167pp; English.

XX The present sequence is the light chain variable region of the humanised murine anti-human glycoprotein (gp) 39 monoclonal antibody (Wab) 39-1.1.106. The Wab may be useful for diagnosing CC disease states, inhibiting B-cell activation and for treating CC immunological disorders, e.g. autoimmune disorders, allergic CC responses, organ rejection and graft versus host disease. It may CC also be used for imaging cells which express gp39 on their surface, CC e.g. tumour cells, and to target therapeutic agents to such cells. CC The Wab inhibits the CD40/gp39 interaction, therefore limiting both CC prim. and sec. responses to T-cell dependent antigens and Ab prodn. CC specific to these antigens. A typical compen. for intramuscular CC injection pref. contains 50 mg of MAb in 1 ml of sterile buffered CC water.

XX Sequence 171 AA;

Query Match 77.2%; Score 44; DB 17; Length 171;

Best Local Similarity 90.0%; Pred. NO. 1.3;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

DB 66 RASETIYSYL 75

RESULT 28

ID AAY92161

XX AAY92161 standard; Peptide; 11 AA.

XX AAY92161;

AC

```

XX DT 01-AUG-2000 (first entry)
XX DE Murine 15B8 light chain variable region CDR 1.
XX PA Light chain; variable region; complementarity determining region; CDR 1;
XX KW anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic;
XX KW vascular-general; proliferative; anti-ischemic; cerebroprotective;
XX KW cardiant; agonist; antibody inhibition.
XX OS Mus musculus.
XX PN WO200018804-A1.
XX PD 06-APR-2000.
XX PF 28-SEP-1999; 99WO-US22428.
XX PR 28-SEP-1998; 98US-0102098.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Holmes SD, Erickson-miller CL, Winkler JD;
XX DR WPI; 2000-293114/25.
XX DR N-PSDB; AAA09016.
XX PT Tie2 receptor agonist antibodies useful for promoting angiogenesis in
XX PT patients suffering from strokes and myocardial infarctions
XX PS Claim 10; Page 38; 50pp; English.
XX CC This is a murine anti-Tie2 kinase receptor agonist monoclonal antibody
CC 15B8 light chain variable region. Tie2 is a single-transmembrane,
CC tyrosine kinase receptor ('Tie' stands for tyrosine kinase receptor with
CC immunoglobulin and endothelial growth factor (EGF) homology domain(s)).
CC Anti-Tie2 antibodies may be administered to enhance angiogenesis in
CC mammals suffering from ischemic disease, myocardial infarction or
CC cerebral stroke or other vascular diseases such as diabetes. It may also
CC be used to enhance endothelial cell survival and to promote
CC haematopoietic or megakaryocyte cell proliferation (claimed).
XX SQ Sequence 107 AA;

Query Match 75.4%; Score 43; DB 21; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
DB 24 RASENIYSFV 33
|||||:::

RESULT 29
AAY92157
ID AAY92157 standard; Protein; 107 AA.
XX AC AAY92157;
XX DT 01-AUG-2000 (first entry)
XX DE Murine 15B8 light chain variable region.
XX KW light chain; variable region; anti-Tie2 kinase receptor; agonist;
XX KW monoclonal antibody; 15B8; Angiogenetic; vascular-general; proliferative;
XX KW anti-ischemic; cardiant; cerebroprotective; antibody inhibition.
XX OS Mus musculus.
XX PN WO200018804-A1.
XX PD 06-APR-2000.

Query Match 75.4%; Score 43; DB 21; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.096;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
DB 1 RASENIYSFV 10
|||||:::

RESULT 30
ABB05962
ID ABB05962 standard; protein; 258 AA.
XX AC ABB05962;
XX DT 09-MAY-2002 (first entry)
XX DE Monoclonal antibody related amino acid sequence SEQ ID NO:1.
XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.
XX OS Mus sp.
XX OS Synthetic.
XX PN JP2001333780-A.
XX PD 04-DEC-2001.
XX PF 29-MAY-2000; 2000JP-0158575.
XX PR 29-MAY-2000; 2000JP-0158575.
XX PA (KEIO-) GH KEIO GIJUKU.
XX DR WPI; 2002-135945/18.
XX PT A protein fused with a monoclonal antibody against an antigen present
XX PT on cell surfaces -
XX PS Claim 14; Page 9; 24pp; Japanese.
XX CC The present invention describes a protein which is fused with a
XX CC monoclonal antibody against an antigen present on cell surface and which

```

CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal  
 CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a  
 CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the  
 CC human type monoclonal antibody to prepare a human type single-stranded  
 CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
 CC gene is expressed in a microbe to prepare a recombinant protein of the  
 CC human type single-stranded immunoprotein. Also described is a method for  
 CC introducing the above complex of monoclonal antibody-fused protein  
 CC through a cell surface receptor. The method is used for the preparation  
 CC of a monoclonal antibody-fused protein against a receptor present on cell  
 CC surface. The present sequence represents a specifically claimed amino  
 CC acid sequence from the present invention.

XX SQ Sequence 258 AA;  
 Query Match 73.7%; Score 42; DB 23; Length 258;  
 Best Local Similarity 88.9%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSY 9  
 Db 165 RTSENIYSY 173  
 | | | | | | | | | |

RESULT 31  
 ABB05963  
 ID ABB05963 standard; protein; 258 AA.

AC ABB05963;  
 XX 09-MAY-2002 (first entry)  
 DT Monoclonal antibody related amino acid sequence SEQ ID NO:2.  
 DE Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
 DE Homo sapiens.  
 OS Synthetic.

XX JP2001333780-A.  
 XX 04-DEC-2001.  
 XX 29-MAY-2000; 2000JP-0158575.  
 XX 29-MAY-2000; 2000JP-0158575.  
 XX (KEIO-) GH KEIO GIJUKU.  
 XX WPI; 2002-135945/18.  
 XX A protein fused with a monoclonal antibody against an antigen present  
 XX on cell surfaces -

XX Claim 15; Page 9; 24pp; Japanese.  
 XX The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal

CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a  
 CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC mouse type monoclonal antibody is converted to prepare a single-stranded  
 CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the  
 CC human type monoclonal antibody to prepare a human type single-stranded  
 CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
 CC gene is expressed in a microbe to prepare a recombinant protein of the  
 CC human type single-stranded immunoprotein. Also described is a method for  
 CC introducing the above complex of monoclonal antibody-fused protein  
 CC through a cell surface receptor. The method is used for the preparation  
 CC of a monoclonal antibody-fused protein against a receptor present on cell  
 CC surface. The present sequence represents a specifically claimed amino  
 CC acid sequence from the present invention.

XX SQ Sequence 258 AA;  
 Query Match 73.7%; Score 42; DB 23; Length 258;  
 Best Local Similarity 88.9%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSY 9  
 Db 165 RTSENIYSY 173  
 | | | | | | | | | |

RESULT 32  
 ABB05990  
 ID ABB05990 standard; Protein; 258 AA.

AC ABB05990;  
 XX 09-MAY-2002 (first entry)  
 DT Mouse monoclonal antibody related protein sequence BB.  
 DE Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
 DE Mus sp.  
 OS Synthetic.

XX JP2001333780-A.  
 XX 04-DEC-2001.  
 XX 29-MAY-2000; 2000JP-0158575.  
 XX 29-MAY-2000; 2000JP-0158575.  
 XX (KEIO-) GH KEIO GIJUKU.  
 XX WPI; 2002-135945/18.  
 XX N-PSDB; ABA94200.  
 XX A protein fused with a monoclonal antibody against an antigen present  
 XX on cell surfaces -

XX Example; Fig 9; 24pp; Japanese.

XX The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal  
 CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a

CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC mouse type monoclonal antibody is converted to prepare a single-stranded  
 CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the  
 CC human type monoclonal antibody to prepare a human type single-stranded  
 CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
 CC gene is expressed in a microbe to prepare a recombinant protein of the  
 CC human type single-stranded immunoprotein. Also described is a method for  
 CC introducing the above complex of monoclonal antibody-fused protein  
 CC through a cell surface receptor. The method is used for the preparation  
 CC of a monoclonal antibody-fused protein against a receptor present on cell  
 CC surface. The present sequence represents a protein sequence which is  
 CC given in an example from the present invention.

XX  
 SQ Sequence 258 AA;  
 Query Match 73.7%; Score 42; DB 23; Length 258;  
 Best Local Similarity 88.9%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RASENIYSY 9  
 | | | | |  
 Db 165 RTSENIYSY 173

RESULT 33  
 ABB05991  
 ID ABB05991 standard; Protein; 258 AA.  
 XX  
 AC ABB05991;  
 XX  
 DT 09-MAY-2002 (first entry)  
 XX  
 DE Mouse and human chimeric monoclonal antibody related protein Cvb.  
 XX  
 KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;  
 KW chimeric.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 OS Synthetic.  
 XX  
 PN JP2001333780-A.  
 XX  
 PD 04-DEC-2001.  
 XX  
 PF 29-MAY-2000; 2000JP-0158575.  
 XX  
 PR 29-MAY-2000; 2000JP-0158575.  
 XX  
 PA (KEIO-) GH KEIO GIJUKU.  
 XX  
 DR WPI; 2002-135945/18.  
 DR N-PSDB; ABA94201.  
 XX  
 PT A protein fused with a monoclonal antibody against an antigen present  
 PT on cell surfaces -  
 XX  
 PS Example; Fig 10; 24pp; Japanese.  
 XX  
 CC The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal  
 CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a  
 CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC mouse type monoclonal antibody is converted to prepare a single-stranded  
 CC mouse type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the

CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the  
 CC human type monoclonal antibody to prepare a human type single-stranded  
 CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
 CC gene is expressed in a microbe to prepare a recombinant protein of the  
 CC human type single-stranded immunoprotein. Also described is a method for  
 CC introducing the above complex of monoclonal antibody-fused protein  
 CC through a cell surface receptor. The method is used for the preparation  
 CC of a monoclonal antibody-fused protein against a receptor present on cell  
 CC surface. The present sequence represents a protein sequence which is  
 CC given in an example from the present invention.

XX  
 SQ Sequence 258 AA;  
 Query Match 73.7%; Score 42; DB 23; Length 258;  
 Best Local Similarity 88.9%; Pred. No. 5.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RASENIYSY 9  
 | | | | |  
 Db 165 RTSENIYSY 173

RESULT 34  
 ABB05992  
 ID ABB05992 standard; Protein; 258 AA.  
 XX  
 AC ABB05992;  
 XX  
 DT 09-MAY-2002 (first entry)  
 XX  
 DE Mouse and human chimeric monoclonal antibody related protein CaB.  
 XX  
 KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;  
 KW chimeric.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 OS Synthetic.  
 XX  
 PN JP2001333780-A.  
 XX  
 PD 04-DEC-2001.  
 XX  
 PF 29-MAY-2000; 2000JP-0158575.  
 XX  
 PR 29-MAY-2000; 2000JP-0158575.  
 XX  
 PA (KEIO-) GH KEIO GIJUKU.  
 XX  
 DR WPI; 2002-135945/18.  
 DR N-PSDB; ABA94202.  
 XX  
 PT A protein fused with a monoclonal antibody against an antigen present  
 PT on cell surfaces -  
 XX  
 PS Example; Fig 11; 24pp; Japanese.  
 XX  
 CC The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal  
 CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a  
 CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC mouse type monoclonal antibody is converted to prepare a single-stranded  
 CC mouse type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the

CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

XX SQ Sequence 258 AA;

Query Match 73.7%; Score 42; DB 23; Length 258;

Best Local Similarity 88.9%; Pred. No. 5.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9

DB 165 RTSENIYSY 173

RESULT 35

ABB05993

ID ABB05993 standard; Protein; 258 AA.

XX AC ABB05993;

XX DT 09-MAY-2002 (first entry)

XX DE Mouse and human chimeric monoclonal antibody related protein DB.

XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;

XX KW chimeric.

XX OS Chimeric - Mus sp.

XX OS Chimeric - Homo sapiens.

XX OS Synthetic.

XX PN JP2001333780-A.

XX PD 04-DEC-2001.

XX PF 29-MAY-2000; 2000JP-0158575.

XX PR 29-MAY-2000; 2000JP-0158575.

XX PA (KEIO-) GH KEIO GIJUKU.

XX DR WPI; 2002-135945/18.

XX DR N-PSDB; ABA94203.

XX PT A protein fused with a monoclonal antibody against an antigen present

XX PT on cell surfaces -

XX PS Example; Fig 12; 24pp; Japanese.

XX CC The present invention describes a protein which is fused with a

XX CC monoclonal antibody against an antigen present on cell surface and which

XX CC can transfer a gene by combining with the gene and containing a human

XX CC type single-stranded monoclonal antibody and a peptide which is the

XX CC combining site for the gene. Also described is a complex of a monoclonal

XX CC antibody-fused protein which is a complex of monoclonal antibody-fused

XX CC protein and a DNA, and a method for the preparation of a monoclonal

XX CC antibody-fused protein against a receptor present on cell surface in

XX CC which: (1) an mRNA extracted from a hybridoma cell having productivity of

XX CC said monoclonal antibody against a receptor present on cell surface is

XX CC used as the template to amplify a single-stranded antibody gene of a

XX CC mouse type monoclonal antibody by PCR; (2) the framework portion of the

XX CC mouse type monoclonal antibody is converted to prepare a single-stranded

XX CC antibody gene of a human type monoclonal antibody; (3) a gene encoding

XX CC the amino acid tail is added to the single-stranded antibody gene of the

XX CC human type monoclonal antibody to prepare a human type single-stranded

XX CC immunoprotein gene; and (4) the human type single-stranded immunoprotein

CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

XX SQ Sequence 258 AA;

Query Match 73.7%; Score 42; DB 23; Length 258;

Best Local Similarity 88.9%; Pred. No. 5.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9

DB 165 RTSENIYSY 173

RESULT 36

ABB05994

ID ABB05994 standard; Protein; 258 AA.

XX AC ABB05994;

XX DT 09-MAY-2002 (first entry)

XX DE Mouse and human chimeric monoclonal antibody related protein BC.

XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;

XX KW chimeric.

XX OS Chimeric - Mus sp.

XX OS Chimeric - Homo sapiens.

XX OS Synthetic.

XX PN JP2001333780-A.

XX PD 04-DEC-2001.

XX PF 29-MAY-2000; 2000JP-0158575.

XX PR 29-MAY-2000; 2000JP-0158575.

XX PA (KEIO-) GH KEIO GIJUKU.

XX DR WPI; 2002-135945/18.

XX DR N-PSDB; ABA94204.

XX PT A protein fused with a monoclonal antibody against an antigen present

XX PT on cell surfaces -

XX PS Example; Fig 13; 24pp; Japanese.

XX CC The present invention describes a protein which is fused with a  
XX CC monoclonal antibody against an antigen present on cell surface and which  
XX CC can transfer a gene by combining with the gene and containing a human  
XX CC type single-stranded monoclonal antibody and a peptide which is the  
XX CC combining site for the gene. Also described is a complex of a monoclonal  
XX CC antibody-fused protein which is a complex of monoclonal antibody-fused  
XX CC protein and a DNA, and a method for the preparation of a monoclonal  
XX CC antibody-fused protein against a receptor present on cell surface in  
XX CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
XX CC said monoclonal antibody against a receptor present on cell surface is  
XX CC used as the template to amplify a single-stranded antibody gene of a  
XX CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
XX CC mouse type monoclonal antibody is converted to prepare a single-stranded  
XX CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
XX CC the amino acid tail is added to the single-stranded antibody gene of the  
XX CC human type monoclonal antibody to prepare a human type single-stranded  
XX CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
XX CC gene is expressed in a microbe to prepare a recombinant protein of the  
XX CC human type single-stranded immunoprotein. Also described is a method for

CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.  
XX  
SQ Sequence 258 AA;

Query Match 73.7%; Score 42; DB 23; Length 258;  
Best Local Similarity 88.9%; Pred. No. 5.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9  
Db 165 RTSENIYSY 173

RESULT 37  
ABB05995  
ID ABB05995 standard; Protein; 258 AA.  
XX AC ABB05995;  
XX DT 09-MAY-2002 (first entry)  
XX DE Human monoclonal antibody related protein sequence Cvc.  
XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN JP2001333780-A.  
XX PD 04-DEC-2001.  
XX PF 29-MAY-2000; 2000JP-0158575.  
XX PR 29-MAY-2000; 2000JP-0158575.  
XX PA (KEIO-) GH KEIO GIJUKU.  
XX WPI; 2002-135945/18.  
XX DR N-PSDB; ABA94205.  
XX A protein fused with a monoclonal antibody against an antigen present  
XX on cell surfaces -  
XX Example; Fig 14; 24pp; Japanese.

CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of a monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is

CC given in an example from the present invention.  
XX  
SQ Sequence 258 AA;

Query Match 73.7%; Score 42; DB 23; Length 258;  
Best Local Similarity 88.9%; Pred. No. 5.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9  
Db 165 RTSENIYSY 173

RESULT 38  
ABB05996  
ID ABB05996 standard; Protein; 258 AA.  
XX AC ABB05996;  
XX DT 09-MAY-2002 (first entry)  
XX DE Human monoclonal antibody related protein sequence CAC.  
XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN JP2001333780-A.  
XX PD 04-DEC-2001.  
XX PF 29-MAY-2000; 2000JP-0158575.  
XX PR 29-MAY-2000; 2000JP-0158575.  
XX PA (KEIO-) GH KEIO GIJUKU.  
XX WPI; 2002-135945/18.  
XX DR N-PSDB; ABA94206.  
XX A protein fused with a monoclonal antibody against an antigen present  
XX on cell surfaces -  
XX Example; Fig 15; 24pp; Japanese.

CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
XX  
SQ Sequence 258 AA;

Query Match 73.7%; Score 42; DB 23; Length 258;  
Best Local Similarity 88.9%; Pred. No. 5.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9  
| | | | |  
Db 165 RTSENIYSY 173

RESULT 39  
ABB05997  
ID ABB05997 standard; Protein; 258 AA.  
XX AC ABB05997;  
XX DT 09-MAY-2002 (first entry)  
XX DE Human monoclonal antibody related protein sequence DC.  
XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN JP2001333780-A.  
XX PD 04-DEC-2001.  
XX PF 29-MAY-2000; 2000JP-0158575.  
XX PR 29-MAY-2000; 2000JP-0158575.  
XX PA (KEIO-) GH KEIO GIJUKU.  
XX DR WPI; 2002-135945/18.  
XX DR N-PSDB; ABA94207.  
XX PT A protein fused with a monoclonal antibody against an antigen present  
XX on cell surfaces -  
XX Example; Fig 16; 24pp; Japanese.

CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

SQ Sequence 258 AA;

Query Match 73.7%; Score 42; DB 23; Length 258;  
Best Local Similarity 88.9%; Pred. No. 5.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9  
| | | | |  
Db 165 RTSENIYSY 173

RESULT 40  
ABB05982  
ID ABB05982 standard; Protein; 287 AA.  
XX AC ABB05982;  
XX DT 09-MAY-2002 (first entry)  
XX DE Monoclonal antibody related protein sequence pBH.  
XX KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX OS Unidentified.  
XX PN JP2001333780-A.  
XX PD 04-DEC-2001.  
XX PF 29-MAY-2000; 2000JP-0158575.  
XX PR 29-MAY-2000; 2000JP-0158575.  
XX PA (KEIO-) GH KEIO GIJUKU.  
XX DR WPI; 2002-135945/18.  
XX DR N-PSDB; ABA94192.  
XX PT A protein fused with a monoclonal antibody against an antigen present  
XX on cell surfaces -  
XX Example; Fig 1; 24pp; Japanese.

CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

SQ Sequence 287 AA;

Query Match 73.7%; Score 42; DB 23; Length 287;  
Best Local Similarity 88.9%; Pred. No. 5.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSY 9  
| | | | |  
Db 179 RTSENIYSY 187

Search completed: July 18, 2003, 15:06:43  
Job time : 38.18 secs

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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:46 ; Search time 12.76 Seconds  
(without alignments)  
25.365 Million cell updates/sec

Title: US-10-007-790-8  
Perfect score: 57  
Sequence: 1 RASENIYSYLP 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/6CTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	11	4 US-09-257-069-8	Sequence 8, Appli
2	57	100.0	107	4 US-09-257-069-4	Sequence 4, Appli
3	50	87.7	94	3 US-08-881-037-68	Sequence 68, Appli
4	50	87.7	99	3 US-08-881-037-32	Sequence 32, Appli
5	50	87.7	99	3 US-08-881-037-33	Sequence 33, Appli
6	50	87.7	99	3 US-08-881-037-34	Sequence 34, Appli
7	50	87.7	99	3 US-08-881-037-35	Sequence 35, Appli
8	50	87.7	107	3 US-08-881-037-69	Sequence 69, Appli
9	50	87.7	107	3 US-08-881-037-70	Sequence 70, Appli
10	50	87.7	107	3 US-08-881-037-71	Sequence 71, Appli
11	50	87.7	107	3 US-08-881-037-72	Sequence 72, Appli
12	50	87.7	107	3 US-08-397-411-1	Sequence 1, Appli
13	50	87.7	107	3 US-08-397-411-2	Sequence 2, Appli
14	50	87.7	214	3 US-08-397-411-5	Sequence 5, Appli
15	50	87.7	227	1 US-08-681-432-2	Sequence 2, Appli
16	50	87.7	243	1 US-07-958-140-2	Sequence 2, Appli
17	50	87.7	243	5 PCT-US93-09166-2	Sequence 2, Appli
18	46	80.7	107	2 US-08-888-366-24	Sequence 24, Appli
19	44	77.2	108	2 US-08-379-057-27	Sequence 27, Appli
20	44	77.2	108	2 US-08-379-057-28	Sequence 28, Appli
21	43	77.2	128	2 US-08-379-057-12	Sequence 12, Appli
22	43	75.4	11	4 US-09-406-532-8	Sequence 8, Appli
23	43	75.4	107	4 US-09-406-532-4	Sequence 4, Appli
24	41	71.9	11	2 US-08-553-501A-62	Sequence 62, Appli
25	41	71.9	11	2 US-08-765-783A-81	Sequence 81, Appli
26	41	71.9	11	3 US-09-205-231-62	Sequence 62, Appli
27	41	71.9	11	4 US-09-416-557-81	Sequence 81, Appli

28	41	71.9	98	2	US-08-553-501A-87	Sequence 87, Appli
29	41	71.9	98	3	US-09-205-231-87	Sequence 87, Appli
30	41	71.9	106	2	US-08-553-501A-84	Sequence 84, Appli
31	41	71.9	106	2	US-08-553-501A-86	Sequence 86, Appli
32	41	71.9	106	3	US-09-205-231-84	Sequence 84, Appli
33	41	71.9	106	3	US-09-205-231-86	Sequence 86, Appli
34	41	71.9	125	2	US-08-553-501A-55	Sequence 55, Appli
35	41	71.9	125	2	US-08-553-501A-57	Sequence 57, Appli
36	41	71.9	125	3	US-09-205-231-55	Sequence 55, Appli
37	41	71.9	125	3	US-09-205-231-57	Sequence 57, Appli
38	41	71.9	126	2	US-08-553-501A-27	Sequence 27, Appli
39	41	71.9	126	2	US-08-765-783A-73	Sequence 73, Appli
40	41	71.9	126	2	US-08-765-783A-77	Sequence 77, Appli
41	41	71.9	126	3	US-08-921-100-73	Sequence 73, Appli
42	41	71.9	126	3	US-08-921-100-77	Sequence 77, Appli
43	41	71.9	126	3	US-08-880-142-73	Sequence 73, Appli
44	41	71.9	126	3	US-08-880-142-77	Sequence 77, Appli
45	41	71.9	126	3	US-08-902-201-73	Sequence 73, Appli

## ALIGNMENTS

RESULT 1  
US-09-257-069-8  
; Sequence 8, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; CURRENT FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-8

Query Match 100.0%; Score 57; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYLP 11  
Db 1 RASENIYSYLP 11

RESULT 2  
US-09-257-069-4  
; Sequence 4, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; CURRENT FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-4

Query Match 100.0%; Score 57; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 11  
| | | | | | | | | |  
DB 24 RASENIYSYL 34

## RESULT 3

US-08-881-037-68  
; Sequence 68, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-68

Query Match 87.7%; Score 50; DB 3; Length 94;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
| | | | | | | | | |  
DB 24 RASENIYSYL 33

## RESULT 4

US-08-881-037-32  
; Sequence 32, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-32

Query Match 87.7%; Score 50; DB 3; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
| | | | | | | | | |  
DB 16 RASENIYSYL 25

## RESULT 5

US-08-881-037-33  
; Sequence 33, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-33

Query Match 87.7%; Score 50; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 16 RASENIYSYL 25

RESULT 6
US-08-881-037-34
; Sequence 34, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Klick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-35

Query Match 87.7%; Score 50; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 16 RASENIYSYL 25

RESULT 7
US-08-881-037-35
; Sequence 35, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Klick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-35

Query Match 87.7%; Score 50; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 16 RASENIYSYL 25

RESULT 8
US-08-881-037-69
; Sequence 69, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Klick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-34

Query Match 87.7%; Score 50; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 16 RASENIYSYL 25
```

```

; US-08-881-037-34
; US-08-881-037-35
; US-08-881-037-69
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; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-881-037-69

Query Match 87.7%; Score 50; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||  
Db 24 RASENIYSYL 33

RESULT 9  
US-08-881-037-70  
; Sequence 70, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Klick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.

; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 70:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-881-037-70

Query Match 87.7%; Score 50; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||  
Db 24 RASENIYSYL 33

RESULT 10  
US-08-881-037-71  
; Sequence 71, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Klick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-881-037-71

Query Match 87.7%; Score 50; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

Db 24 RASENIYSYL 33  
|||||  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-1  
Query Match 87.7%; Score 50; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
Db 24 RASENIYSYL 33  
|||||  
RESULT 13  
US-08-397-411-2  
Sequence 2, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
Db 24 RASENIYSYL 33  
|||||  
RESULT 12  
US-08-397-411-1  
Sequence 1, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
Db 24 RASENIYSYL 33  
|||||  
RESULT 11  
US-08-881-037-72  
Sequence 72, Application US/08881037  
Patent No. 6080588  
GENERAL INFORMATION:  
APPLICANT: Klick, Gary D.  
APPLICANT: Swanson, Patrick C.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-72  
Query Match 87.7%; Score 50; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
Db 24 RASENIYSYL 33  
|||||  
RESULT 12  
US-08-397-411-1  
Sequence 1, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-2

Query Match 87.7%; Score 50; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.034; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
DB 24 RASENIYSYL 33

RESULT 14  
US-08-397-411-5  
Sequence 5, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-5

Query Match 87.7%; Score 50; DB 3; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RASENIYSYL 10  
DB 24 RASENIYSYL 33

RESULT 15  
US-08-681-432-2  
Sequence 2, Application US/08681432  
Patent No. 5800991  
GENERAL INFORMATION:  
APPLICANT: HALEY, Boyd E.  
APPLICANT: KOHLER, Heinz  
APPLICANT: RAJAGOPALAN, Krishnan  
APPLICANT: PAVLINKOVA, Gabriela  
TITLE OF INVENTION: NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY  
TITLE OF INVENTION: COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR  
TITLE OF INVENTION: MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND  
TITLE OF INVENTION: THERAPEUTICS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURN, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/681,432  
FILING DATE: 23-JUL-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/208,822  
FILING DATE: 11-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 028750-132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-681-432-2

Query Match 87.7%; Score 50; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 0.077; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
DB 24 RASENIYSYL 33

RESULT 16  
US-07-958-140-2  
Sequence 2, Application US/07958140  
Patent No. 5489525  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira H.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS  
NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend  
;; STREET: One Market Plaza, Steuart Street Tower  
;; CITY: San Francisco  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94105-1492  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/958,140  
;; FILING DATE: 19921008  
;; CLASSIFICATION: 436  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 15280-77  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 467-9600  
;; TELEFAX: (415) 543-5043  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 243 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-07-958-140-2

Query Match 87.7%; Score 50; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
Db 157 RASENIYSYL 166  
|||||

RESULT 17  
PCT-US93-09166-2  
;; SEQUENCE 2, Application PC/TUS9309166  
;; GENERAL INFORMATION:  
;; APPLICANT: Pastan, Ira H.  
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend  
;; STREET: One Market Plaza, Steuart Street Tower  
;; CITY: San Francisco  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94105-1492  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/09166  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 15280-77  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 467-9600  
;; TELEFAX: (415) 543-5043  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 243 amino acids

;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; PCT-US93-09166-2

Query Match 87.7%; Score 50; DB 5; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
Db 157 RASENIYSYL 166  
|||||

RESULT 18  
US-08-888-366-24  
;; SEQUENCE 24, Application US/08888366  
;; Patent No. 5972656  
;; GENERAL INFORMATION:  
;; APPLICANT: Lopez, Osvaldo  
;; APPLICANT: Wylie, Dwane E.  
;; APPLICANT: Wagner, Fred W.  
;; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
;; NUMBER OF SEQUENCES: 39  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Merchant & Gould  
;; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55402  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/888,366  
;; FILING DATE: 03-JUL-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/187,407  
;; FILING DATE: 27-JAN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/990,542  
;; FILING DATE: 14-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/493,299  
;; FILING DATE: 14-MAR-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/324,392  
;; FILING DATE: 14-MAR-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Carter, Charles G.  
;; REGISTRATION NUMBER: 35,093  
;; REFERENCE/DOCKET NUMBER: 8648.39USC1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-332-5300  
;; TELEFAX: 612-332-9081  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-888-366-24

Query Match 80.7%; Score 46; DB 2; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||||

Db 24 RASENIYGL 33

RESULT 19  
US-08-379-057-27  
; Sequence 27, Application US/08379057  
; Patent No. 5876950  
; GENERAL INFORMATION:  
; APPLICANT: Siadak, Anthony W. L.  
; APPLICANT: Hollenbaugh, Diane L.  
; APPLICANT: Gilliland, Lisa K.  
; APPLICANT: Gordon, Marcia L.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Aruffo, Alejandro A.  
; TITLE OF INVENTION: Monoclonal Antibodies Specific For  
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bristol-Myers Squibb Company  
; STREET: 3005 First Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,057  
; FILING DATE: 26-JAN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poor, Brian W.  
; REGISTRATION NUMBER: 32,928  
; REFERENCE/DOCKET NUMBER: ON0133-  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 727-3670  
; TELEFAX: (206) 727-3601  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-379-057-27

Query Match 77.2%; Score 44; DB 2; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYGL 10  
Db 24 RASETIYGL 33

RESULT 21  
US-08-379-057-12  
; Sequence 12, Application US/08379057  
; Patent No. 5876950  
; GENERAL INFORMATION:  
; APPLICANT: Siadak, Anthony W. L.  
; APPLICANT: Hollenbaugh, Diane L.  
; APPLICANT: Gilliland, Lisa K.  
; APPLICANT: Gordon, Marcia L.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Aruffo, Alejandro A.  
; TITLE OF INVENTION: Monoclonal Antibodies Specific For  
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bristol-Myers Squibb Company  
; STREET: 3005 First Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,057  
; FILING DATE: 26-JAN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poor, Brian W.  
; REGISTRATION NUMBER: 32,928  
; REFERENCE/DOCKET NUMBER: ON0133-  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 727-3670  
; TELEFAX: (206) 727-3601  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-379-057-27

Query Match 77.2%; Score 44; DB 2; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYGL 10  
Db 24 RASETIYGL 33

RESULT 20  
US-08-379-057-28  
; Sequence 28, Application US/08379057  
; Patent No. 5876950  
; GENERAL INFORMATION:  
; APPLICANT: Siadak, Anthony W. L.  
; APPLICANT: Hollenbaugh, Diane L.  
; APPLICANT: Gilliland, Lisa K.  
; APPLICANT: Gordon, Marcia L.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Aruffo, Alejandro A.  
; TITLE OF INVENTION: Monoclonal Antibodies Specific For  
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bristol-Myers Squibb Company  
; STREET: 3005 First Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,057  
; FILING DATE: 26-JAN-1995  
; CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-379-057-12

Query Match 77.2%; Score 44; DB 2; Length 128;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 44 RASETIYSYL 53

RESULT 22
US-09-406-532-8
; Sequence 8, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(11)
; OTHER INFORMATION: 1588 light chain CDR 1
; US-09-406-532-8

Query Match 75.4%; Score 43; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.053;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 1 RASENIYSFV 10

RESULT 23
US-09-406-532-4
; Sequence 4, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; US-09-406-532-4

; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-406-532-4

Query Match 75.4%; Score 43; DB 4; Length 107;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 24 RASENIYSFV 33

RESULT 24
US-08-553-501A-62
; Sequence 62, Application US/08553501A
; Patent No. 5856135
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/553,501A
; APPLICATION NUMBER: US/08/553,501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-553-501A-62

Query Match 71.9%; Score 41; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

```

Db 1 RASENIYSNL 10

RESULT 25

US-08-765-783A-81

Sequence 81, Application US/08765783A

Patent No. 5994524

GENERAL INFORMATION:

APPLICANT: Matsushima, Kouji

APPLICANT: Matsumoto, Yoshihiro

APPLICANT: Yamada, Yoshiki

APPLICANT: Sato, Koh

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Yamazaki, Tatsumi

TITLE OF INVENTION: Reshaped Human Antibody to

TITLE OF INVENTION: Interleukin-8

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,783A

FILING DATE: 07-MAR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 35029-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-1500

TELEFAX: 202-822-0168

TELEX:

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-765-783A-81

Query Match 71.9%; Score 41; DB 2; Length 11;

Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

Db 1 RASENIYSYL 10

RESULT 26

US-09-205-231-62

Sequence 62, Application US/09205231

Patent No. 6121423

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: HIRATA, Yuichi

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

US-09-205-231-62

Query Match 71.9%; Score 41; DB 3; Length 11;

Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

Db 1 RASENIYSNL 10

RESULT 27

US-09-416-557-81

Sequence 81, Application US/09416557

Patent No. 6245894

GENERAL INFORMATION:

APPLICANT: Matsushima, Kouji

APPLICANT: Matsumoto, Yoshihiro

APPLICANT: Yamada, Yoshiki

APPLICANT: Sato, Koh

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Yamazaki, Tatsumi

TITLE OF INVENTION: Reshaped Human Antibody to

TITLE OF INVENTION: Interleukin-8

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

US-09-416-557-81

Query Match 71.9%; Score 41; DB 3; Length 11;

Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10

Db 1 RASENIYSNL 10

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/416.557  
FILING DATE: 12-October-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765.783  
FILING DATE: 7-March-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-416-557-81

Query Match 71.9%; Score 41; DB 4; Length 11;  
Best Local Similarity 90.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENITSYL 10  
Db 1 RASEIITSYL 10

## RESULT 28

US-08-553-501A-87  
Sequence 87, Application US/08553501A  
Patent No. 5856135  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553.501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399

TELEX: 904136  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-553-501A-87

Query Match 71.9%; Score 41; DB 2; Length 98;  
Best Local Similarity 90.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENITSYL 10  
Db 24 RASENITSNL 33

## RESULT 29

US-09-205-231-87  
Sequence 87, Application US/09205231  
Patent No. 6121423  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205.231  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/553.501  
FILING DATE: 20-FEB-1996  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-205-231-87

Query Match 71.9%; Score 41; DB 3; Length 98;  
Best Local Similarity 90.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||  
Db 24 RASENIYSNL 33

## RESULT 30

US-08-553-501A-84  
; Sequence 84, Application US/08553501A  
; Patent No. 5856135  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,501A  
; FILING DATE: 20-FEB-1996  
; CLASSIFICATION: 536  
; INFORMATION FOR SEQ ID NO: 84:  
; APPLICATION NUMBER: WO PCT/JP94/00859  
; FILING DATE: 30-MAY-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-129787  
; FILING DATE: 31-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-553-501A-84

Query Match 71.9%; Score 41; DB 2; Length 106;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||  
Db 24 RASENIYSNL 33

## RESULT 31

US-08-553-501A-86  
; Sequence 86, Application US/08553501A  
; Patent No. 5856135  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6

NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-553-501A-86

Query Match 71.9%; Score 41; DB 2; Length 106;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||  
Db 24 RASENIYSNL 33

## RESULT 32

US-09-205-231-84  
; Sequence 84, Application US/09205231  
; Patent No. 6121423  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/205,231

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501  
FILING DATE: 20-FEB-1996  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-205-231-84

Query Match 71.9%; Score 41; DB 3; Length 106;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
Db 24 RASENIYSNL 33

RESULT 33  
US-09-205-231-86  
Sequence 86, Application US/09205231  
Patent No. 6121423  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,231  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501  
FILING DATE: 20-FEB-1996  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-205-231-86

Query Match 71.9%; Score 41; DB 3; Length 106;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
Db 24 RASENIYSNL 33

RESULT 34  
US-08-553-501A-55  
Sequence 55, Application US/08553501A  
Patent No. 5856135  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-501A-55

Query Match 71.9%; Score 41; DB 2; Length 125;  
Best Local Similarity 90.0%; Pred. No. 1.8;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASENIYSYL 10  
| | | | | | | |  
Db 43 RASENIYSNL 52

RESULT 35  
US-08-553-501A-57  
; Sequence 57, Application US/08553501A  
; Patent No. 5856135  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,501A  
; FILING DATE: 20-FEB-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP94/00859  
; FILING DATE: 30-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-129787  
; FILING DATE: 31-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 125 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-553-501A-57

Query Match 71.9%; Score 41; DB 2; Length 125;  
Best Local Similarity 90.0%; Pred. No. 1.8;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASENIYSYL 10  
| | | | | | | |  
Db 43 RASENIYSNL 52

RESULT 36  
US-09-205-231-55  
; Sequence 55, Application US/09205231  
; Patent No. 6121423  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: HIRATA, Yuichi

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/205,231  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,501  
; FILING DATE: 20-FEB-1996  
; APPLICATION NUMBER: WO PCT/JP94/00859  
; FILING DATE: 30-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-129787  
; FILING DATE: 31-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 125 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-205-231-55

Query Match 71.9%; Score 41; DB 3; Length 125;  
Best Local Similarity 90.0%; Pred. No. 1.8;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASENIYSYL 10  
| | | | | | | |  
Db 43 RASENIYSNL 52

RESULT 37  
US-09-205-231-57  
; Sequence 57, Application US/09205231  
; Patent No. 6121423  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,231  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501  
FILING DATE: 20-FEB-1996  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA: JP 5-129787  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-205-231-57

Query Match 71.9%; Score 41; DB 3; Length 125;  
Best Local Similarity 90.0%; Pred. No. 1.8;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
Db 43 RASENTSYNL 52

RESULT 38  
US-08-553-501A-27  
Sequence 27, Application US/08553501A  
Patent No. 5856135  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA: JP 5-129787  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-501A-27

Query Match 71.9%; Score 41; DB 2; Length 126;  
Best Local Similarity 90.0%; Pred. No. 1.8;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
Db 44 RASENTSYNL 53

RESULT 39  
US-08-765-783A-73  
Sequence 73, Application US/08765783A  
Patent No. 5994524  
GENERAL INFORMATION:  
APPLICANT: Matsushima, Kouji  
APPLICANT: Matsumoto, Yoshihiro  
APPLICANT: Yamada, Yoshiki  
APPLICANT: Sato, Koh  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to  
TITLE OF INVENTION: Interleukin-8  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,783A  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal

FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1..19  
OTHER INFORMATION:  
US-08-765-783A-73

Query Match 71.9%; Score 41; DB 2; Length 126;  
Best Local Similarity 90.0%; Pred. No. 1.8;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||  
Db 43 RASEIIYSYL 52

QY 1 RASENIYSYL 10  
|||  
Db 43 RASEIIYSYL 52  
Search completed: July 18, 2003, 15:11:50  
Job time: 13.76 secs

RESULT 40  
US-08-765-783A-77  
Sequence 77, Application US/08765783A

Patent No. 5994524

GENERAL INFORMATION:

APPLICANT: Matsushita, Kouji

APPLICANT: Matsumoto, Yoshinhiro

APPLICANT: Yamada, Yoshiki

APPLICANT: Sato, Koh

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Yamazaki, Tatsumi

TITLE OF INVENTION: Reshaped Human Antibody to

TITLE OF INVENTION: Interleukin-8

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,783A

FILING DATE: 07-MAR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 35029-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-1500

TELEFAX: 202-822-0168

TELEX:

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Signal Sequence

LOCATION: 1..19

OTHER INFORMATION:

US-08-765-783A-77

Query Match 71.9%; Score 41; DB 2; Length 126;

Best Local Similarity 90.0%; Pred. No. 1.8;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:09:56 ; Search time 28.38 Seconds

(without alignments)  
46.031 Million cell updates/sec

Title: US-10-007-790-8  
Perfect score: 57  
Sequence: 1 RASENTSYSLP 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA: \*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCRT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
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5: /cgn2\_6/ptodata/1/pubppaa/PCRTUS\_PUBCOMB.pep:\*  
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10: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep1:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep2:\*  
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17: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	50	87.7	12	US-10-322-142-7
2	50	87.7	101	US-10-096-246-18
3	50	87.7	106	US-10-096-246-15
4	50	87.7	107	US-10-322-142-32
5	45	78.9	108	US-10-096-246-19
6	45	78.9	259	US-10-207-655-13
7	43	75.4	110	US-10-096-246-16
8	41	71.9	11	US-09-730-857-81
9	41	71.9	126	US-09-730-857-73
10	41	71.9	127	US-09-730-857-77
11	38	66.7	88	US-09-905-243-33
12	38	66.7	108	US-09-848-798-41
13	38	66.7	241	US-08-779-457-50
14	38	66.7	253	US-09-880-748-936
15	38	66.7	12	US-08-844-215-12
16	36.5	64.0	107	US-08-844-215-12

17	36	63.2	110	US-10-096-246-14	Sequence 14, Appl
18	36	63.2	333	US-09-829-482-3	Sequence 3, Appl
19	36	63.2	468	US-10-236-433-14	Sequence 14, Appl
20	36	63.2	562	US-09-815-242-5565	Sequence 5565, Ap
21	36	63.2	567	US-09-815-242-12320	Sequence 12320, A
22	36	63.2	567	US-09-815-242-12952	Sequence 12952, A
23	36	63.2	617	US-09-815-242-13228	Sequence 13228, A
24	35	61.4	11	US-10-091-300-57	Sequence 57, Appl
25	35	61.4	30	US-09-956-206A-9	Sequence 9, Appl
26	35	61.4	59	US-09-864-761-47508	Sequence 47508, A
27	35	61.4	107	US-09-977-283A-75	Sequence 75, Appl
28	35	61.4	107	US-09-977-283A-76	Sequence 76, Appl
29	35	61.4	107	US-09-977-283A-77	Sequence 77, Appl
30	35	61.4	107	US-10-091-300-37	Sequence 37, Appl
31	35	61.4	108	US-10-194-975-94	Sequence 94, Appl
32	35	61.4	108	US-10-096-246-17	Sequence 17, Appl
33	35	61.4	127	US-09-977-283A-5	Sequence 5, Appl
34	35	61.4	127	US-09-977-283A-7	Sequence 7, Appl
35	35	61.4	127	US-09-977-283A-17	Sequence 17, Appl
36	35	61.4	127	US-09-977-283A-17	Sequence 17, Appl
37	35	61.4	237	US-10-194-975-109	Sequence 109, App
38	34	59.6	107	US-09-863-693-25	Sequence 25, Appl
39	34	59.6	107	US-10-143-437-25	Sequence 25, Appl
40	34	59.6	121	US-09-864-761-45718	Sequence 45718, A
41	34	59.6	121	US-09-864-761-45718	Sequence 45718, A
42	34	59.6	138	US-09-945-301-10	Sequence 10, Appl
43	34	59.6	179	US-09-823-829-8	Sequence 8, Appl
44	34	59.6	179	US-09-823-829-8	Sequence 8, Appl
45	34	59.6	239	US-09-880-748-1882	Sequence 1882, Ap

#### ALIGNMENTS

RESULT 1  
US-10-322-142-7  
; Sequence 7, Application US/10322142  
; Publication No. US20030113322A1  
; GENERAL INFORMATION:  
; APPLICANT: BEG, CEDRIC  
; APPLICANT: BRIANT-LONGUET, LAURENCE  
; APPLICANT: CERUTTI, MARTINE  
; APPLICANT: CHARDES, THIERRY  
; APPLICANT: DEVAUCHELLE, GERARD  
; APPLICANT: DEVAUX, CHRISTIAN  
; APPLICANT: GRANIER, CLAUDE  
; APPLICANT: MAMAS, CLAUDE  
; APPLICANT: OLIVE, DANIEL  
; TITLE OF INVENTION: CDR-H1-DERIVED PETIDE CB11, PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: MADE THEREFROM AND METHODS OF TREATING DISORDERS IN  
; TITLE OF INVENTION: MAMMALS  
; FILE REFERENCE: 1129-R-02  
; CURRENT APPLICATION NUMBER: US/10/322,142  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 60/341,349  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/374,754  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-322-142-7  
Query Match 87.7%; Score 50; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0052;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||  
DB 3 RASENIYSYL 12

## RESULT 2

US-10-096-246-18  
; Sequence 18, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-18

Query Match 87.7%; Score 50; DB 15; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||  
DB 17 RASENIYSYL 26

## RESULT 3

US-10-096-246-15  
; Sequence 15, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-15

Query Match 87.7%; Score 50; DB 15; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.056;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||  
DB 24 RASENIYSYL 33

## RESULT 4

US-10-322-142-32  
; Sequence 32, Application US/10322142  
; Publication No. US20030113322A1  
; GENERAL INFORMATION:

APPLICANT: BES, CEDRIC  
APPLICANT: BRIANT-LONGUET, LAURENCE  
APPLICANT: CERUTTI, MARTINE  
APPLICANT: CHARDES, THIERRY  
APPLICANT: DEVAUCHELLE, GERARD  
APPLICANT: DEVAUX, CHRISTIAN  
APPLICANT: GRANIER, CLAUDE  
APPLICANT: MAMAS, CLAUDE  
APPLICANT: OLIVE, DANIEL  
APPLICANT: PAU, BERNARD

TITLE OF INVENTION: CDR-H1-DERIVED PETIDE CELL, PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: MADE THEREFROM AND METHODS OF TREATING DISORDERS IN  
; FILE REFERENCE: 1129-R-02  
; CURRENT APPLICATION NUMBER: US/10/322,142  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 60/341,349  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/374,754  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL  
US-10-322-142-32

Query Match 87.7%; Score 50; DB 15; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.056;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||  
DB 24 RASENIYSYL 33

## RESULT 5

US-10-096-246-19  
; Sequence 19, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-19

Query Match 78.9%; Score 45; DB 15; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.48;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||  
DB 24 RASENIYSYL 33

## RESULT 6

US-10-207-655-13

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; Sequence 13, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(259)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD37 SCFV
US-10-207-655-13

Query Match          78.9%; Score 45; DB 15; Length 259;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
   |||||
Db 44 RTSSENVSYL 53

RESULT 7
US-10-096-246-16
; Sequence 16, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
; TITLE OF INVENTION: SCFV Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NBL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-16

Query Match          75.4%; Score 43; DB 15; Length 110;
Best Local Similarity 90.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
   |||||
Db 24 RASVNIYSYL 33

RESULT 8
US-09-730-857-81
; Sequence 81, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
```

```
; Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-09-730-857-81

Query Match          71.9%; Score 41; DB 10; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
   |||||
Db 1 RASENIYSYL 10

RESULT 9
US-09-730-857-73
; Sequence 73, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/730,857  
FILING DATE: 07-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/416,557  
FILING DATE: 1999-10-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1...19  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-730-857-73

Query Match 71.9%; Score 41; DB 10; Length 126;  
Best Local Similarity 90.0%; Pred. No. 3.1;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASENTSYL 10  
Db 43 RASENTSYL 52

RESULT 10  
US-09-730-857-77  
Sequence 77, Application US/09730857  
Patent No. US20020082396A1  
GENERAL INFORMATION:  
APPLICANT: Matsushima, Kouji  
Matsumoto, Yoshihiro  
Yamada, Yoshiki  
Sato, Koh  
Tsuchiya, Masayuki  
Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/730,857  
FILING DATE: 07-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/416,557  
FILING DATE: 1999-10-12  
ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1...19  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-09-730-857-77

Query Match 71.9%; Score 41; DB 10; Length 126;  
Best Local Similarity 90.0%; Pred. No. 3.1;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASENTSYL 10  
Db 43 RASENTSYL 52

RESULT 11  
US-09-730-857-27  
Sequence 27, Application US/09730857  
Patent No. US20020082396A1  
GENERAL INFORMATION:  
APPLICANT: Matsushima, Kouji  
Matsumoto, Yoshihiro  
Yamada, Yoshiki  
Sato, Koh  
Tsuchiya, Masayuki  
Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/730,857  
FILING DATE: 07-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/416,557  
FILING DATE: 1999-10-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1...20  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 27;  
US-09-730-857-27

Query Match 71.9%; Score 41; DB 10; Length 127;  
Best Local Similarity 90.0%; Pred. No. 3.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||:|||||  
Db 44 RASEIIYSYL 53

RESULT 12  
US-09-905-243-33  
Sequence 33, Application US/09905243  
Patent No. US20020062009A1  
GENERAL INFORMATION:  
APPLICANT: Taylor, Alexander H  
TITLE OF INVENTION: Monoclonal Antibodies with Reduced  
FILE REFERENCE: P50770  
CURRENT APPLICATION NUMBER: US/09/905,243  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 09/300,970  
PRIOR FILING DATE: 1999-04-28  
NUMBER OF SEQ. ID NOS: 97  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 88  
TYPE: PRT  
ORGANISM: Pan troglodytes  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (24)...(34)  
OTHER INFORMATION: CDRI  
NAME/KEY: DOMAIN  
LOCATION: (50)...(66)  
OTHER INFORMATION: CDRII  
US-09-905-243-33

Query Match 66.7%; Score 38; DB 10; Length 88;  
Best Local Similarity 70.0%; Pred. No. 7.6;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||:|||||  
Db 24 RASGCIYNLY 33

RESULT 13  
US-09-848-798-41  
Sequence 41, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 41  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 110  
US-09-848-798-41

Query Match 66.7%; Score 38; DB 12; Length 108;  
Best Local Similarity 80.0%; Pred. No. 9.5;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|||:|||||  
Db 23 RASONISSYL 32

RESULT 14  
US-08-779-457-50  
Sequence 50, Application US/08779457  
Publication No. US20020193571A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
APPLICANT: Chiang, Nancy Y.  
APPLICANT: Kyung, Jin Kim  
APPLICANT: Matthews, William  
APPLICANT: Rodrigues, Maria L.  
TITLE OF INVENTION: MSX RECEPTOR AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,457  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667197  
FILING DATE: 06/20/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-779-457-50

Query Match 66.7%; Score 38; DB 8; Length 241;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||: |||:  
Db 158 RASOGITNYL 167

RESULT 15  
US-09-880-748-936  
; Sequence 936, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: P5523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 936  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-936

Query Match 66.7%; Score 38; DB 12; Length 253;  
Best Local Similarity 70.0%; Pred. No. 24;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||: |||:  
Db 169 RASOGITNYL 178

RESULT 16  
US-08-844-215-12  
; Sequence 12, Application US/08844215  
; Publication No. US20020016445A1  
; GENERAL INFORMATION:  
; APPLICANT: PERSSON, MATS AXEL  
; APPLICANT: ALLANDER, TOBIAS ERIK  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/844,215  
; FILING DATE: 17-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/635,109  
; FILING DATE: 19-APR-1996  
; ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 80146.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-844-215-12

Query Match 64.0%; Score 36.5; DB 8; Length 107;  
Best Local Similarity 81.8%; Pred. No. 18;  
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 1 RASENIYSYL 10  
|||: |||:  
Db 23 RASOGITNYL 33

RESULT 17  
US-10-096-246-14  
; Sequence 14, Application US/10096246  
; Publication No. US2003010060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo  
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (vee)  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-14

Query Match 63.2%; Score 36; DB 15; Length 110;  
Best Local Similarity 80.0%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
|||: |||:  
Db 24 RASENIYRL 33

RESULT 18  
US-09-829-482-3  
; Sequence 3, Application US/09829482  
; Patent No. US20020001843A1  
; GENERAL INFORMATION:  
; APPLICANT: LIGHTNER, JONATHAN EDWARD  
; TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD VERSION 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/829,482  
FILING DATE: 10-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/852615  
FILING DATE: MAY 7, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MAJARIAN, WILLIAM R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1083-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-829-482-3

Query Match 63.2%; Score 36; DB 10; Length 333;  
Best Local Similarity 70.0%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RASENIYSTLP 11  
: : : : :  
Db 190 SSISIVSYLP 199

RESULT 19  
US-10-236-433-14  
Sequence 14, Application US/10236433  
Publication No. US20030100025A1  
GENERAL INFORMATION:  
APPLICANT: O'Connor, Michael B.  
APPLICANT: Gilbert, Lawrence I.  
TITLE OF INVENTION: Insecticide Targets  
FILE REFERENCE: 09531-070001  
CURRENT APPLICATION NUMBER: US/10/236,433  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/318,006  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: 60/317,890  
PRIOR FILING DATE: 2001-09-07  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Drosophila  
US-10-236-433-14

Query Match 63.2%; Score 36; DB 15; Length 468;  
Best Local Similarity 54.5%; Pred. No. 1,1e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENIYSTLP 11  
: : : : :  
Db 28 RGMGNLYNLP 38

RESULT 20  
US-09-815-242-5565  
Sequence 5565, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5565  
LENGTH: 562  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-815-242-5565

Query Match 63.2%; Score 36; DB 10; Length 562;  
Best Local Similarity 54.5%; Pred. No. 1,3e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENIYSTLP 11  
: : : : :  
Db 34 QSTGIVSYLP 44

RESULT 21  
US-09-815-242-12320  
Sequence 12320, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931

;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12320  
;; LENGTH: 567  
;; TYPE: PRT  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-12330

Query Match 63.2%; Score 36; DB 10; Length 567;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENTSYLP 11  
DB 34 QSTSGIVSYLP 44

RESULT 22  
US-09-815-242-12952  
;; Sequence 12952, Application US/09815242  
;; Patent No. US20020061569A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Kari L.  
;; APPLICANT: Zykkind, Judith W.  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John D.  
;; APPLICANT: Carr, Grant J.  
;; APPLICANT: Yamamoto, Robert T.  
;; APPLICANT: Xu, H. Howard  
;; TITLE OF INVENTION: Identification of Essential Genes in  
;; TITLE OF INVENTION: Prokaryotes  
;; FILE REFERENCE: ELITRA.01A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12952  
;; LENGTH: 567  
;; TYPE: PRT  
;; ORGANISM: Staphylococcus aureus  
US-09-815-242-12952

Query Match 63.2%; Score 36; DB 10; Length 567;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENTSYLP 11  
DB 34 QSTSGIVSYLP 44

RESULT 23  
US-09-815-242-13228  
;; Sequence 13228, Application US/09815242  
;; Patent No. US20020061569A1

;; GENERAL INFORMATION:  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Kari L.  
;; APPLICANT: Zykkind, Judith W.  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John D.  
;; APPLICANT: Carr, Grant J.  
;; APPLICANT: Yamamoto, Robert T.  
;; APPLICANT: Xu, H. Howard  
;; TITLE OF INVENTION: Identification of Essential Genes in  
;; TITLE OF INVENTION: Prokaryotes  
;; FILE REFERENCE: ELITRA.01A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 13228  
;; LENGTH: 617  
;; TYPE: PRT  
;; ORGANISM: Streptococcus pneumoniae  
US-09-815-242-13228

Query Match 63.2%; Score 36; DB 10; Length 617;  
Best Local Similarity 54.5%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENTSYLP 11  
DB 34 QVAGVSYLP 44

RESULT 24  
US-10-091-300-57  
;; Sequence 57, Application US/10091300  
;; Publication No. US20030108545A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rockwell, Patricia  
;; APPLICANT: Goldstein, Neil I.  
;; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular  
;; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist  
;; FILE REFERENCE: 11245/46211  
;; CURRENT APPLICATION NUMBER: US/10/091,300  
;; CURRENT FILING DATE: 2002-03-04  
;; NUMBER OF SEQ ID NOS: 85  
;; SOFTWARE: WordPerfect 8.0 for Windows  
;; SEQ ID NO 57  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Human  
US-10-091-300-57

Query Match 61.4%; Score 35; DB 15; Length 11;  
Best Local Similarity 70.0%; Pred. No. 2.9;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENTSYLP 10  
DB 1 RASONINNYL 10

```

RESULT 25
US-09-956-206A-9
; Sequence 9, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; CERIANI, ROBERTO L.
; PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,539
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11683
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MITT. ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 276332000101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-956-206A-9
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 61.4%; Score 35; DB 11; Length 30;
Best Local Similarity 70.0%; Pred. No. 8.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
||| |||
Db 10 RASGNINHYL 19

RESULT 26
US-09-864-761-47508
; Sequence 47508, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

```

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; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47508
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL138734.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: P44596, EVALUATE 1.20e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1286316.1, EVALUATE 1.00e-09
; US-09-864-761-47508

Query Match 61.4%; Score 35; DB 10; Length 59;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 NIYSYLP 11
||| |||
Db 38 NIYKYL 44

RESULT 27
US-09-977-283A-75
; Sequence 75, Application US/09977283A
; Publication No. US20030031664A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
; FILE REFERENCE: 0609.4320003
; CURRENT APPLICATION NUMBER: US/09/977,283A

```

;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 08/934,000  
;; PRIOR FILING DATE: 1997-09-19  
;; PRIOR APPLICATION NUMBER: 60/026,356  
;; PRIOR FILING DATE: 1996-09-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 75  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (21)..(121)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (52)..(152)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (71)..(171)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (74)..(174)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (86)..(186)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (93)..(193)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (94)..(194)  
;; OTHER INFORMATION: May be any Amino Acid  
US-09-977-283A-75

Query Match 61.4%; Score 35; DB 12; Length 107;  
Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENITSYL 10  
Db 24 RASGNHNYL 33

RESULT 28  
US-09-977-283A-76  
;; Sequence 76, Application US/09977283A  
;; Publication No. US20030031664A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Reed, Guy L.  
;; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
;; FILE REFERENCE: 0609,4320003  
;; CURRENT APPLICATION NUMBER: US/09/977,283A  
;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 08/934,000  
;; PRIOR FILING DATE: 1997-09-19  
;; PRIOR APPLICATION NUMBER: 60/026,356  
;; PRIOR FILING DATE: 1996-09-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 76  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (74)..(174)  
;; OTHER INFORMATION: May be any Amino Acid  
US-09-977-283A-76

Query Match 61.4%; Score 35; DB 12; Length 107;

Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RASENITSYL 10  
Db 24 RASGNHNYL 33

RESULT 29  
US-09-977-283A-77  
;; Sequence 77, Application US/09977283A  
;; Publication No. US20030031664A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Reed, Guy L.  
;; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
;; FILE REFERENCE: 0609,4320003  
;; CURRENT APPLICATION NUMBER: US/09/977,283A  
;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 08/934,000  
;; PRIOR FILING DATE: 1997-09-19  
;; PRIOR APPLICATION NUMBER: 60/026,356  
;; PRIOR FILING DATE: 1996-09-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 77  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (9)..(9)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (17)..(117)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (18)..(118)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (21)..(121)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (52)..(152)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (56)..(156)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (70)..(170)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (71)..(171)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (72)..(172)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (74)..(174)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (76)..(176)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (86)..(186)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (93)..(193)  
;; OTHER INFORMATION: May be any Amino Acid  
;; NAME/KEY: MISC\_FEATURE  
;; LOCATION: (94)..(194)  
;; OTHER INFORMATION: May be any Amino Acid  
US-09-977-283A-77

Query Match 61.4%; Score 35; DB 12; Length 107;  
Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASEN1SYL 10  
||| |::||  
Db 24 RASGN1HNYL 33

RESULT 30  
US-10-091-300-37

; Sequence 37, Application US/10091300  
; Publication No. US20030108545A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular  
; FILE REFERENCE: 11245/46211  
; CURRENT APPLICATION NUMBER: US/10/091,300  
; CURRENT FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 37  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Human  
US-10-091-300-37

Query Match 61.4%; Score 35; DB 15; Length 107;  
Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASEN1SYL 10  
||| |::||  
Db 24 RASGN1HNYL 33

RESULT 31  
US-10-194-975-94

; Sequence 94, Application US/10194975  
; Publication No. US20030039649A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: Super Humanized Antibodies  
; FILE REFERENCE: 501231.01  
; CURRENT APPLICATION NUMBER: US/10/194,975  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 94  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-194-975-94

Query Match 61.4%; Score 35; DB 15; Length 108;  
Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASEN1SYL 10  
||| |::||  
Db 24 RASGN1HNYL 33

RESULT 32  
US-10-096-246-17

; Sequence 17, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor  
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (vee)  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-17

Query Match 61.4%; Score 35; DB 15; Length 108;  
Best Local Similarity 70.0%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASEN1SYL 10  
||| |::||  
Db 24 RASGN1HNYL 33

RESULT 33  
US-09-977-283A-5

; Sequence 5, Application US/09977283A  
; Publication No. US20030031664A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Guy L.  
; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
; FILE REFERENCE: 0609.4320003  
; CURRENT APPLICATION NUMBER: US/09/977,283A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 08/934,000  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/026,356  
; PRIOR FILING DATE: 1996-09-20  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
; NAME/KEY: MISC FEATURE  
; LOCATION: (-12)..(-12)  
; OTHER INFORMATION: May be either Gly or Ala  
US-09-977-283A-5

Query Match 61.4%; Score 35; DB 12; Length 127;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASEN1SYL 10  
||| |::||  
Db 44 RASGN1HNYL 53

RESULT 34  
US-09-977-283A-7

; Sequence 7, Application US/09977283A  
; Publication No. US20030031664A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Guy L.  
; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
; FILE REFERENCE: 0609.4320003  
; CURRENT APPLICATION NUMBER: US/09/977,283A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 08/934,000

;; PRIOR FILING DATE: 1997-09-19  
;; PRIOR APPLICATION NUMBER: 60/026,356  
;; PRIOR FILING DATE: 1996-09-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 7  
;; LENGTH: 127  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
US-09-977-283A-7

Query Match 61.4%; Score 35; DB 12; Length 127;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
||| ||: ||  
Db 44 RASGNHNYL 53

RESULT 35  
US-09-977-283A-9  
;; Sequence 9, Application US/09977283A  
;; Publication No. US20030031664A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Reed, Guy L.  
;; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
;; FILE REFERENCE: 0609.4320003  
;; CURRENT APPLICATION NUMBER: US/09/977,283A  
;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 08/934,000  
;; PRIOR FILING DATE: 1997-09-19  
;; PRIOR APPLICATION NUMBER: 60/026,356  
;; PRIOR FILING DATE: 1996-09-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 127  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
US-09-977-283A-9

Query Match 61.4%; Score 35; DB 12; Length 127;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
||| ||: ||  
Db 44 RASGNHNYL 53

RESULT 36  
US-09-977-293A-17  
;; Sequence 17, Application US/09977283A  
;; Publication No. US20030031664A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Reed, Guy L.  
;; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
;; FILE REFERENCE: 0609.4320003  
;; CURRENT APPLICATION NUMBER: US/09/977,283A  
;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 08/934,000  
;; PRIOR FILING DATE: 1997-09-19  
;; PRIOR APPLICATION NUMBER: 60/026,356  
;; PRIOR FILING DATE: 1996-09-20  
;; NUMBER OF SEQ ID NOS: 81  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 17  
;; LENGTH: 127

;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
US-09-977-283A-17

Query Match 61.4%; Score 35; DB 12; Length 127;  
Best Local Similarity 70.0%; Pred. No. 41;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
||| ||: ||  
Db 44 RASGNHNYL 53

RESULT 37  
US-10-194-975-109  
;; Sequence 109, Application US/10194975  
;; Publication No. US20030039649A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Foote, Jefferson  
;; TITLE OF INVENTION: Super Humanized Antibodies  
;; FILE REFERENCE: 501231.01  
;; CURRENT APPLICATION NUMBER: US/10/194,975  
;; CURRENT FILING DATE: 2002-10-10  
;; PRIOR APPLICATION NUMBER: US 60/305,111  
;; PRIOR FILING DATE: 2001-07-12  
;; NUMBER OF SEQ ID NOS: 122  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 109  
;; LENGTH: 237  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: humanized chimeric D1.3 antibody  
US-10-194-975-109

Query Match 61.4%; Score 35; DB 15; Length 237;  
Best Local Similarity 70.0%; Pred. No. 81;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
||| ||: ||  
Db 47 RASGNHNYL 56

RESULT 38  
US-09-863-693-25  
;; Sequence 25, Application US/09863693  
;; Patent No. US20020062010A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ARATHOON, R.  
;; CARTER, P.J.  
;; MERCHANT, A.M.  
;; PRESTA, L.G.  
;; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES  
;; HAVING HETEROMULTIMERIC AND COMMON COMPONENTS  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/863,693  
;; FILING DATE: 23-May-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/070,166  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Conley, Deirdre L.  
REGISTRATION NUMBER: 36,487  
REFERENCE/DOCKET NUMBER: P1099R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-2066  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-863-693-25  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
  
Query Match 59.6%; Score 34; DB 10; Length 107;  
Best Local Similarity 70.0%; Pred. No. 52;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 RASENTSYL 10  
Db 24 RASEGIYHWL 33  
  
RESULT 39  
US-10-143-437-25  
Sequence 25, Application US/10143437  
Publication No. US20030078385A1  
GENERAL INFORMATION:  
APPLICANT: ARATHOON, R.  
CARTER, P.J.  
MERCHANT, A.M.  
PRESTA, L.G.  
TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES  
HAVING HETEROMULTIMERIC AND COMMON COMPONENTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/143,437  
FILING DATE: 10-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/863,693  
FILING DATE: 23-May-2001  
APPLICATION NUMBER: 09/070,166  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Conley, Deirdre L.  
REGISTRATION NUMBER: 36,487  
REFERENCE/DOCKET NUMBER: P1099R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-2066  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-10-143-437-25  
Query Match 59.6%; Score 34; DB 15; Length 107;  
Best Local Similarity 70.0%; Pred. No. 52;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 RASENTSYL 10  
Db 24 RASEGIYHWL 33  
  
RESULT 40  
US-09-864-761-45718  
Sequence 45718, Application US/09864761  
Patent No. US20020046763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 45718  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC009487.3  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.79

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.98  
 OTHER INFORMATION: EST HUMAN HIT: BE897487.1, EVALUE 1.00e-52  
 OTHER INFORMATION: SWISSPROT HIT: P14196, EVALUE 2.50e-01  
 US-09-864-761-45718

Query Match 59.6%; Score 34; DB 10; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASENIIYS 8  
 |||||  
 Db 69 ASENIIYS 75

Search completed: July 18, 2003, 15:35:56  
 Job time : 29.38 secs



Db 24 RASENTSYL 33  
|||||

## RESULT 3

S20810 Ig kappa chain V region (hybridoma C8) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C/Accession: S20810

R:Hogbenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.

Submitted to the EMBL Data Library, September 1990

A/Description: Nucleotide sequences of the variable region cDNAs encoding a murine anti

A/Reference number: S20809

A/Accession: S20810

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-101 <HOO>

A/Cross-references: EMBL:X54693; NID:G50251; PIDN:CAA38509.1; PID:G50252

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 50; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
|||||

Db 17 RASENTSYL 26  
|||||

## RESULT 4

B47329 Ig kappa chain V region (PR1) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-Sep-1993 #sequence\_revision 17-Jul-1994 #text\_change 21-Jan-2000

C/Accession: B47329

R/Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.

Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993

A/Title: A recombinant immunotoxin that is active on prostate cancer cells and that is c

A/Reference number: A47329; MUID:93133825; PMID:8421689

A/Accession: B47329

A/Status: preliminary

A/Molecule type: mRNA; protein

A/Residues: 1-106 <BRI>

A/Experimental source: BALB/c

A/Note: sequence modified after extraction from NCBI backbone

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S31488

R/Bespalov, I.A.; Shlyanov, P.A.; Lukashovich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov,

C/Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 50; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
|||||

Db 24 RASENTSYL 33  
|||||

## RESULT 5

S24290 Ig kappa chain V region (J334/32) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Jun-2000

C/Accession: S24290

R/Moncharmont, B.

Submitted to the EMBL Data Library, September 1991

A/Description: Cloning and sequencing of the cDNA coding for the variable regions of the

A/Reference number: S24287

A/Accession: S24290

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-107 <MON>

A/Cross-references: EMBL:X62704; NID:G51693; PIDN:CAA44580.1; PID:G13333967

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
|||||

Db 24 RASENTSYL 33  
|||||

## RESULT 6

KVMS49 Ig kappa chain V region (M149) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 16-Aug-1996

C/Accession: A01919

R/Appella, E.; Alvarez, V.L.

Mol. Immunol. 17, 1507-1513, 1980

A/Title: Amino acid sequence of the variable region of M149 mouse myeloma light chain: c

A/Reference number: A01919; MUID:82057806; PMID:6795447

A/Accession: A01919

A/Molecule type: protein

A/Residues: 1-108 <APP>

A/Experimental source: strain BALB/c

A/Note: this chain was isolated from a myeloma protein

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: #status predicted

Query Match 87.7%; Score 50; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
|||||

Db 24 RASENTSYL 33  
|||||

## RESULT 7

S31488 Ig kappa chain precursor V region (P11) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S31488

R/Bespalov, I.A.; Shlyanov, P.A.; Lukashovich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov,

C/Keywords: heterotetramer; immunoglobulin

F:16-110/Domain: immunoglobulin homology <IMM>

A/Accession: S31488

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <BES>

A/Cross-references: EMBL:X69859; NID:G50929; PIDN:CAA49493.1; PID:G50930

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:16-110/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 50; DB 2; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10  
|||||

Db 44 RASENTSYL 53  
|||||

```
RESULT 8
S11245
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S11245
R:Wellman, A.A.; Meares, C.F.
Nucleic Acids Res. 18, 5281, 1990
A:Title: Sequences of the Lym-1 antibody heavy and light chain variable regions.
A:Reference number: S11244; MUID:90384832; PMID:2119497
A:Accession: S11245
A:Molecule type: mRNA
A:Residues: 1-134 <MBL>
A:Cross-references: EMBL:X53484
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:/37-11/Domain: immunoglobulin homology <IMM>

Query Match          75.4%; Score 43; DB 2; Length 134;
Best Local Similarity 90.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 45 RASVNIYSYL 54

RESULT 9
S22024
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S22024
R:Caultfield, M.J.
submitted to the EMBL Data Library, September 1991
A:Description: Nucleotide sequences of the mRNA/cDNA encoding a pathogenic anti-erythro
A:Reference number: S22023
A:Accession: S22024
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-81 <CAU>
A:Cross-references: EMBL:X60425; NID:G51028; PIDN:CAA42956.1; PID:G1333923
C:Genetics:
A:introns: 65/3; 72/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          71.9%; Score 41; DB 2; Length 81;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 1 RASENIYSNL 10

RESULT 10
PL0080
Ig kappa chain V region (E4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: PL0080
R:Neek, K.; Hasemann, C.; Pollak, B.; Alkan, S.S.; Bralt, M.; Siaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A:Title: Structural characterization of antidiabetic antibodies: evidence that Ab2s are
A:Reference number: PL0080; MUID:89094248; PMID:2492056
A:Accession: PL0080
A:Molecule type: mRNA
A:Residues: 1-107 <MBE>
A:Cross-references: GB:X58596; GB:Y00794; NID:G51574; PIDN:CAA41471.1; PID:G938255
A:Experimental source: strain BALB/c
```

```
A:Note: 106-leu is translated from the codon CUN
A:Note: the sequence shown here is from the V kappa region of an antidiabetic monoclonal
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:/16-90/Domain: immunoglobulin homology <IMM>

Query Match          71.9%; Score 41; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 24 RPSENIYSEL 33

RESULT 11
S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed ag
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234 <DB1>
A:Cross-references: EMBL:X13187; NID:G51784; PIDN:CAA31579.1; PID:G51785
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:/1-20/Domain: signal sequence #status predicted <SIG>
F:/21-224/Product: Ig kappa chain #status predicted <MAT>
F:/36-110/Domain: immunoglobulin homology <IMM>

Query Match          71.9%; Score 41; DB 2; Length 234;
Best Local Similarity 90.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
Db 44 RASENIYSNL 53

RESULT 12
AC0429
2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) [imported] - Yersinia pestis
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 11-Jan-2002
C:Accession: AC0429
R:Perkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AC0429
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-656 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92759.1; PID:G15981454; GSPDB:GN00175
C:Genetics:
A:Gene: cpdB
C:Superfamily: 2',3'-cyclic-nucleotide 2'-phosphodiesterase; 2',3'-cyclic-nucleotide 2'-p
C:Keywords: phosphoric diester hydrolase

Query Match          71.9%; Score 41; DB 2; Length 656;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10
:|:|:|:|:|
```

Db 366 KASDNMYSTL 375

RESULT 13

IG kappa chain V region (K-25) - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 21-Jan-2000

C/Accession: A01951

R/Jatton, J.C.

Biochem. J. 147, 235-247, 1975

A/Title: Comparison of the amino acid sequences of the variable domains of two homogenized

A/Reference number: A90281; MUID:76039436; PMID:241319

A/Accession: A01951

A/Molecule type: Protein

A/Residues: 1-108 <JAT>

A/Note: Residues 109-139 of the constant region are identical with the corresponding res

C/Comment: This chain was obtained from antibody to type III pneumococci and was isolate

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap

C/KeyWords: heterotrimer

C/Accession: PH0880

F/16-90/Domain: immunoglobulin homology <IMM>

F/23-88/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 70.2%; Score 40; DB 1; Length 108;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSTL 10

Db 24 QASQBIYSTL 33

RESULT 14

IG kappa chain V region (SCH) - human (Fragment)

N/Alternate names: myeloma protein

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 09-May-1997

C/Accession: PH0880

R/Mahmimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0880

A/Molecule type: protein

A/Residues: 1-65 <MAN>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/KeyWords: heterotrimer; immunoglobulin

F/1-23/Region: framework 1

F/24-34/Region: complementarity-determining 1

F/35-49/Region: framework 2

F/50-56/Region: complementarity-determining 2

F/57-65/Region: framework 3

Query Match

Best Local Similarity 68.4%; Score 39; DB 2; Length 65;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSTL 10

Db 24 RASQNYTFL 33

RESULT 15

IG kappa chain V region - human (Fragment)

C/Species: Homo sapiens (man)

C/Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000

C/Accession: S52793

R/Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougencot, B.; Ranco, P.; Denoroy, L.; Deret,

submitted to the EMBL Data Library, March 1995

A/Description: light chain V region gene usage restriction and peculiarities in myeloma-

A/Reference number: S52789

A/Accession: S52793

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-129 <ROC>

A/Cross-references: EMBL:X65997; NID:G758600; PIDN:CAA59989.1; PID:G758601

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/KeyWords: heterotrimer; immunoglobulin

F/38-112/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 68.4%; Score 39; DB 2; Length 129;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSTL 10

Db 46 RASQNIYSTL 55

RESULT 16

2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) precursor - Yersinia enterocoli

C/Species: Yersinia enterocolitica

C/Date: 19-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C/Accession: S52695

R/Truelsen, K.S.

submitted to the EMBL Data Library, March 1995

A/Reference number: S52695

A/Accession: S52695

A/Molecule type: DNA

A/Residues: 1-652 <TRU>

A/Cross-references: EMBL:X65742; NID:G747912; PIDN:CAA59745.1; PID:G747913

C/Comment: In E. coli the enzyme is bifunctional, catalyzing two consecutive reactions c

netically distinguishable active sites for two corresponding substrates can be identifier

C/Genetics:

C/Superfamily: 2',3'-cyclic-nucleotide 2'-phosphodiesterase; 2',3'-cyclic-nucleotide 2'-i

C/KeyWords: multifunctional enzyme; periplasmic space; phosphoric diester hydrolase

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-652/Product: 2',3'-cyclic-nucleotide 2'-phosphodiesterase #status predicted <MAT>

F/26-600/Domain: 2',3'-cyclic-nucleotide 2'-phosphodiesterase homology <CPDB>

F/30-123/Domain: phosphodiesterase core homology <PBC>

Query Match

Best Local Similarity 68.4%; Score 39; DB 1; Length 652;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASENISTYL 10

Db 364 ASDNMYSTL 372

RESULT 17

DNA-binding protein - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Sep-1999

C/Accession: S41479

R/Wu, L.C.; Mak, C.H.; Dear, N.; Boehm, T.; Foroni, L.; Rabbits, T.H.

Nucleic Acids Res. 21, 5067-5073, 1993

A/Title: Molecular cloning of a zinc finger protein which binds to the heptamer of the s

A/Reference number: S41479; MUID:94077706; PMID:8255760

A/Accession: S41479

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-767 <WUL>

A/Cross-references: EMBL:L07911; NID:G349300; PIDN:AAA40039.1; PID:G349301

C/Superfamily: HIV-BP2 enhancer-binding protein

Query Match

Best Local Similarity 68.4%; Score 39; DB 2; Length 767;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 11  
|:|:|:|:|  
Db 610 RSEENLFSLP 620

## RESULT 18

T42717  
DNA-binding protein Rc - mouse  
N:Alternate names: Ig kappa chain gene enhancer Recognition component  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T42717  
R:Wu, L.C.; Liu, Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Li, Z.; Yu, C.Y.  
Genomics 35, 415-424, 1996  
A:Title: The mouse DNA binding protein Rc for the kappa B motif of transcription and for  
a family of large transcriptional proteins  
A:Reference number: Z22238; MUID:97001141; PMID:8812474  
A:Accession: T42717  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2282 <MUL>  
A:Cross-references: EMBL:L46815; NID:G1377885; PID:G1377886; PIDN:AAB40884.1  
A:Experimental source: strain BALB/c; clone T1; thymocyte, brain  
C:Genetics:  
A:Gene: Rc  
C:Function:  
A:Description: binds V(D)J recombination signal sequence and kappa B motif  
C:Superfamily: HIV-BP2 enhancer-binding protein  
C:Keywords: DNA recombination; transcription factor

Query Match 68.4%; Score 39; DB 2; Length 2282;

Best Local Similarity 54.5%; Pred. No. 97;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 11  
|:|:|:|:|  
Db 2125 RSEENLFSLP 2135

## RESULT 19

T38457  
putative sensory transduction histidine kinase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T38457  
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z21749  
A:Accession: T38457  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2310 <MUR>  
A:Cross-references: EMBL:Z98978; PIDN:CAB11683.1; GSPDB:GN00066; SPDB:SPAC27E2.09  
A:Experimental source: strain 972h-; cosmid c27E2  
C:Genetics:  
A:Gene: SPDB:SPAC27E2.09  
A:Map position: 1

Query Match 68.4%; Score 39; DB 2; Length 2310;

Best Local Similarity 60.0%; Pred. No. 99;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASENIVSYL 11  
|:|:|:|:|  
Db 876 SSSNVYDYL 885

## RESULT 20

A64079  
2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) precursor - Haemophilus influ  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 21-Jan-2000

C:Accession: A64079  
R:Rieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: A64079  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-657 <TIGR>  
A:Cross-references: GB:U32740; GB:L42023; NID:G1573572; PIDN:AAC22242.1; PID:G1573573; T3  
C:Comment: In E. coli the enzyme is bifunctional, catalyzing two consecutive reactions c  
netically distinguishable active sites for two corresponding substrates can be identified  
C:Superfamily: 2',3'-cyclic-nucleotide 2'-phosphodiesterase; 2',3'-cyclic-nucleotide 2'-i  
C:Keywords: multifunctional enzyme; periplasmic space; phosphoric diester hydrolase  
F,1-28/Domain: signal sequence #status predicted <SIG>  
F,29-657/Product: 2',3'-cyclic-nucleotide 2'-phosphodiesterase #status predicted <MUT>  
F,32-605/Domain: 2',3'-cyclic-nucleotide 2'-phosphodiesterase core homology <CPDB>  
F,35-128/Domain: phosphodiesterase core homology <PFC>

Query Match 66.7%; Score 38; DB 1; Length 657;  
Best Local Similarity 60.0%; Pred. No. 40;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|:|:|:|:|  
Db 368 KATDNNISYL 377

## RESULT 21

A20969  
Ig kappa chain precursor V-J-C regions - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 21-Jan-2000  
C:Accession: A20969; A25448  
R:McCartney-Francis, N.; Skurla Jr., R.M.; Mage, R.G.; Bernstein, K.E.  
Proc. Natl. Acad. Sci. U.S.A. 81, 1794-1798, 1984  
A:Title: Kappa-chain allotypes and isotypes in the rabbit: cDNA sequences of clones encod  
ing type expression.  
A:Reference number: A20969; MUID:84170388; PMID:6424124  
A:Accession: A20969  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-229 <MCC>  
A:Cross-references: GB:K01359; NID:G165373; PIDN:AAA1334.1; PID:G165374  
R:Akimenko, M.A.; Mariame, B.; Rougeon, F.  
Proc. Natl. Acad. Sci. U.S.A. 83, 5180-5183, 1986  
A:Title: Evolution of the immunoglobulin kappa light chain locus in the rabbit: evidence  
A:Reference number: A94110; MUID:86259753; PMID:3088570  
A:Contents: Ig kappa-1 chain, 69 allotype, J-K1.2 segment  
A:Accession: A25448  
A:Molecule type: DNA  
A:Residues: 111-123 <AKI>  
A:Cross-references: GB:M14067; GB:M14062; GB:M14063; GB:M14064; GB:M14065; GB:M14066; NIT  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F,143-212/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 37; DB 2; Length 229;  
Best Local Similarity 80.0%; Pred. No. 20;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
|:|:|:|:|  
Db 38 QASENIYSYL 47

## RESULT 22

D97750  
hypothetical protein RC0404 [imported] - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii

C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
 C/Accession: D97750  
 R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R  
 Science 293, 2093-2098, 2001  
 A>Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
 A/Reference number: A97700; MUID:21442074; PMID:11557893  
 A/Accession: D97750  
 A/Status: Preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-230 <KIR>  
 A/Cross-references: GB:AE006914; PIDN:AAU02942.1; PID:G15619471; GSPDB:GN00173  
 C/Genetics:  
 A/Gene: RC0404

Query Match 64.9%; Score 37; DB 2; Length 230;  
 Best Local Similarity 54.5%; Pred. No. 20;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 ||:|||||  
 Db 220 RINGNLYSYFP 230

RESULT 23  
 S08054  
 hypothetical protein 4 - maize mitochondrion plasmid S-1  
 C/Species: mitochondrion Zea mays (maize)  
 C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 02-Jun-2000  
 C/Accession: S08054  
 R/Pallard, W.; Sederoff, R.R.; Levings III, C.S.  
 EMB0 J. 4, 1125-1128, 1985  
 A>Title: Nucleotide sequence of the S-1 mitochondrial DNA from the S cytoplasm of maize.  
 A/Reference number: S07183  
 A/Accession: S08054  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-252 <PAI>  
 A/Cross-references: EMBL:X02451  
 C/Genetics:  
 A/Genome: mitochondrion  
 C/Superfamily: Zea mays mitochondrion 28.8K hypothetical protein  
 C/Keywords: mitochondrion

Query Match 64.9%; Score 37; DB 2; Length 252;  
 Best Local Similarity 60.0%; Pred. No. 22;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 10  
 ||:|||||  
 Db 26 RATDNLVSHL 35

RESULT 24  
 C32058  
 mcbC protein - Escherichia coli plasmid pmcCB17  
 C/Species: Escherichia coli  
 C/Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 08-Oct-1999  
 C/Accession: C32058  
 R/Gentiloud, O.; Moreno, F.; Kotler, R.  
 J. Bacteriol. 171, 1126-1135, 1989  
 A>Title: DNA sequence, products, and transcriptional pattern of the genes involved in p  
 A/Reference number: A32058; MUID:89123111; PMID:2644225  
 A/Accession: C32058  
 A/Molecule type: DNA  
 A/Residues: 1-272 <GEN>  
 A/Cross-references: GB:M24253; NID:G341145; PIDN:AAA72743.1; PID:G522292  
 C/Genetics:  
 A/Genome: plasmid

Query Match 64.9%; Score 37; DB 2; Length 272;  
 Best Local Similarity 54.5%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 ||:|||||  
 Db 144 QAGTNYHYLP 154

RESULT 25  
 S53040  
 probable membrane protein YMR010w - Yeast (Saccharomyces cerevisiae)  
 N/Alternate names: hypothetical protein YMR270.13  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 19-Apr-2002  
 C/Accession: S53040  
 R/Devlin, K.; Churcher, C.M.  
 submitted to the EMBL Data Library, March 1995  
 A/Reference number: S53028  
 A/Accession: S53040  
 A/Molecule type: DNA  
 A/Residues: 1-405 <DEV>  
 A/Cross-references: EMBL:Z48613; NID:G728645; PID:G728658; GSPDB:GN00013; MIPS:YMR010w  
 A/Experimental source: strain AB972  
 C/Genetics:  
 A/Gene: MIPS:YMR010w  
 A/Cross-references: SGD:S0004612  
 A/Map position: 13R  
 C/Superfamily: Saccharomyces cerevisiae probable membrane protein YMR010w  
 C/Keywords: transmembrane protein  
 F:79-95/Domain: transmembrane #status predicted <TM1>  
 F:107-123/Domain: transmembrane #status predicted <TM2>  
 F:224-240/Domain: transmembrane #status predicted <TM3>  
 F:259-275/Domain: transmembrane #status predicted <TM4>  
 F:303-319/Domain: transmembrane #status predicted <TM5>

Query Match 64.9%; Score 37; DB 2; Length 405;  
 Best Local Similarity 66.7%; Pred. No. 37;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SENIYSYLP 11  
 ||:|||||  
 Db 28 SDRLYSYLP 36

RESULT 26  
 T45676  
 hypothetical protein F14P22.150 - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 28-Jul-2000  
 C/Accession: T45676  
 R/D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;  
 submitted to the Protein Sequence Database, January 2000  
 A/Reference number: Z23011  
 A/Accession: T45676  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-597 <DAN>  
 A/Cross-references: EMBL:AL137082  
 A/Experimental source: cultivar Columbia; BAC clone F14P22  
 C/Genetics:  
 A/Map position: 3  
 A/Insertions: 53/2; 299/3; 328/3; 351/3; 380/3; 409/3; 427/3; 458/2; 496/3; 546/1  
 A/Note: F14P22.150  
 C/Superfamily: Arabidopsis thaliana hypothetical protein F14P22.170

Query Match 64.9%; Score 37; DB 2; Length 597;  
 Best Local Similarity 70.0%; Pred. No. 56;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASENISYLP 11  
 ||:|||||  
 Db 261 ASSDIYSYCP 270

RESULT 27  
 T30544

major surface glycoprotein - Pneumocystis carinii (fragment)  
C/Species: Pneumocystis carinii  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 15-Jun-2001  
C/Accession: T30544  
R/Ref: Turner, R.E.; Sorial, V.; Klyvington, D.; Angus, C.W.; Kovacs, J.A.  
Infect. Immun. 66, 4268-4273, 1998  
A/Title: Characterization of major surface glycoprotein genes of human Pneumocystis carinii  
A/Reference number: Z17905; MUID:98380374; PMID:9712777  
A/Accession: T30544  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 11008 <MEI>  
A/Cross-references: EMBL:AF03212; NID:g3560520; PID:g3560521; PID:AA034975.1  
C/Genetic: MSG  
A/Genes: MSG  
C/Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 64.9%; Score 37; DB 2; Length 1008;  
Best Local Similarity 54.5%; Pred. No. 97;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASNIYSYLP 11  
Db 248 KSESDCTEYLP 258

RESULT 28  
S03968  
Ig kappa chain V-J region (34-2B) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
C/Accession: S03968  
R/Ref: Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
Eur. J. Immunol. 20, 771-777, 1990  
A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
A/Reference number: S03965; MUID:90269328; PMID:2347362  
A/Accession: S03968  
A/Molecule type: mRNA  
A/Residues: 1-107 <REI>  
A/Cross-references: EMBL:X51856; NID:g55403; PID:CAA36149.1; PID:g930233  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 63.2%; Score 36; DB 2; Length 107;  
Best Local Similarity 70.0%; Pred. No. 14;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASNIYSYLP 10  
Db 24 RASNIYIWL 33

RESULT 29  
H90386  
hypothetical protein SS02176 [imported] - Sulfolobus solfataricus  
C/Species: Sulfolobus solfataricus  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C/Accession: H90386  
R/Ref: Singh, R.K.; Cafalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.  
arXiv: R.A.; Ragan, M.A.; Seneen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A/Description: Sulfolobus solfataricus complete genome.  
A/Reference number: A99139  
A/Accession: H90386  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-184 <KUR>  
A/Cross-references: GB:AE006641; NID:g13815473; PID:AAK42351.1; GSPDB:GN00155  
C/Genetic: SSO2176  
A/Genes: SSO2176

Query Match 63.2%; Score 36; DB 2; Length 184;  
Best Local Similarity 77.8%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SENIYSYLP 11  
Db 155 SPITISYLP 163

RESULT 30  
AB0719  
Probable pertussis-like toxin chain (EC 2.4.2.-) [imported] - Salmonella enterica subsp.  
C/Species: Salmonella enterica subsp. enterica serovar Typh  
A/Note: this species has also been called Salmonella typh  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
C/Accession: AB0719  
R/Ref: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Croft, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar  
A/Reference number: AB0502; PMID:11677608  
A/Accession: AB0719  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-242 <PAR>  
A/Cross-references: GB:AL513382; PID:CAD02123.1; PID:g16502957; GSPDB:GN00176  
C/Genetic: STY1890  
A/Genes: STY1890  
C/Keywords: glycosyltransferase; pentosyltransferase

Query Match 63.2%; Score 36; DB 2; Length 242;  
Best Local Similarity 63.6%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RASNIYSYLP 11  
Db 98 RADNIFYSLP 108

RESULT 31  
D64588  
probable DNA helicase - Helicobacter pylori (strain 26895)  
C/Species: Helicobacter pylori  
C/Date: 30-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 06-Feb-1998  
C/Accession: D64588  
R/Ref: Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, S.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.  
Nature 388, 539-547, 1997  
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.  
A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A/Reference number: A64520; MUID:97394467; PMID:9252185  
A/Accession: D64588  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-274 <TOM>  
A/Cross-references: GB:AE000511; TIGR:HP0548

Query Match 63.2%; Score 36; DB 2; Length 274;  
Best Local Similarity 62.5%; Pred. No. 37;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 ENIYSYLP 11  
Db 72 ENIYKYIP 79

RESULT 32  
A45094  
glycogenin glucosyltransferase (EC 2.4.1.186) - rabbit  
N/Alternate names: glycogen synthase 38K chain; glycogenin

C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 11-Jun-1999  
 C/Accession: A45094; S06482; S02470  
 R/Vikupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; Depooll-Roach, A.A.; Roach, P.J.  
 J. Biol. Chem. 267, 25759-25763, 1992  
 A>Title: Rabbit skeletal muscle glycogenin. Molecular cloning and production of fully fu  
 A/Reference number: A45094; MUID:93100288; PMID:1281472  
 A/Accession: A45094  
 A/Molecule type: mRNA  
 A/Residues: 1-332 <VTS>  
 A/Cross-references: GB:U01791; NID:g165512; PIDN:AAA31404.1; PID:g165513  
 A/Experimental source: skeletal muscle  
 A/Note: Sequence is inconsistent with the nucleotide translation  
 A/Note: sequence extracted from NCBI backbone (NCBIP:120846)  
 R/Campbell, D.G.; Cohen, P.  
 Eur. J. Biochem. 185, 119-125, 1989  
 A>Title: The amino acid sequence of rabbit skeletal muscle glycogenin.  
 A/Reference number: S06482; MUID:90032666; PMID:2806254  
 A/Accession: S06482  
 A/Molecule type: protein  
 A/Residues: 1-87, 'S', 89-96, 'L', 98-332 <CAM>  
 R/Pitcher, J.; Smythe, C.; Campbell, D.G.; Cohen, P.  
 Eur. J. Biochem. 169, 497-502, 1987  
 A>Title: Identification of the 38-kDa subunit of rabbit skeletal muscle glycogen synthas  
 A/Reference number: S02470; MUID:88082782; PMID:3121316  
 A/Accession: S02470  
 A/Molecule type: protein  
 A/Residues: 9-19;38-44, 'W',90-94;204-207, 'F', 209-210, 'KH', 213-219 <PIT>  
 C/Function:  
 A>Description: catalyzes the alpha-glucosylation of itself on a specific tyrosine residu  
 osyl-glycogenin by UDPglucose to produce glycogen and UDP  
 A/Pathway: glycogen/starch biosynthesis  
 A/Note: required to initiate the synthesis of glycogen  
 C/Superfamily: glycogenin  
 C/Keywords: acetylated amino end; glycogen/starch biosynthesis; glycoprotein; glycosyltr  
 F/2/Modified site: acetylated amino end (Thr) #status experimental  
 F/14/Binding site: carbohydrate (Tyr) (covalent) #status experimental

Query Match 63.2%; Score 36; DB 1; Length 332;  
 Best Local Similarity 70.0%; Pred. No. 46;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASENISYLP 11  
 Db 189 SSISISYLP 198

RESULT 33  
 JC4695  
 glycogenin glucosyltransferase (EC 2.4.1.186) - human  
 N/Alternate names: glycogenin  
 N/Contains: glycogen(starch) synthase, glycogenin subunit  
 C/Species: Homo sapiens (man)  
 C/Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 11-Jun-1999  
 C/Accession: JC4695; G01948; S45141  
 R/Barbetti, F.; Rocchi, M.; BossoLasco, M.; Cordera, R.; Sbraccia, P.; Cons  
 Biochem. Biophys. Res. Commun. 220, 72-77, 1996  
 A>Title: The human skeletal muscle glycogenin gene: cDNA, tissue expression, and chromos  
 A/Reference number: JC4695; MUID:96176958; PMID:8602861  
 A/Accession: JC4695  
 A/Molecule type: mRNA  
 A/Residues: 1-333 <BAR>  
 A/Cross-references: GB:U4431; NID:g1174166; PIDN:AAB0014.1; PID:g1174167  
 A/Experimental source: skeletal muscle  
 R/Rodriguez, I.R.  
 submitted to the EMBL Data Library, July 1995  
 A/Reference number: G08914  
 A/Accession: G01948  
 A/Status: translated from GB/EMBL/DBD  
 A/Molecule type: mRNA  
 A/Residues: 1-333 <ROD>  
 A/Cross-references: EMBL:U15125; NID:g9763399; PIDN:AAB09752.1; PID:g976400  
 R/Leffers, H.; Wiemann, S.; Anorge, W.

submitted to the EMBL Data Library, June 1994  
 A>Description: Cloning and sequencing of a cDNA encoding human glycogenin.  
 A/Reference number: S45140  
 A/Accession: S45141  
 A/Molecule type: mRNA  
 A/Residues: 1-203, 'KMSQEPHYICPLGNSQLMHSRLYPKNGR', 'NDGNRRRLIWEQIPITSRGNTLTSSR', 'NTAFEC  
 A/Cross-references: EMBL:X79537; NID:g496894; PIDN:CAA56073.1; PID:g496895  
 C/Genetics:  
 A/Gene: GDB:GYG  
 A/Cross-references: GDB:1326953  
 A/Map position: 3q24-3q25.1  
 C/Function:  
 A>Description: catalyzes the alpha-glucosylation of itself on a specific tyrosine residu  
 osyl-glycogenin by UDPglucose to produce glycogen and UDP  
 A/Pathway: glycogen/starch biosynthesis  
 A/Note: required to initiate the synthesis of glycogen  
 C/Superfamily: glycogenin  
 C/Keywords: acetylated amino end; glycogen/starch biosynthesis; glycoprotein; glycosyltr  
 F/2/Modified site: acetylated amino end (Thr) (in mature form) #status predicted  
 F/19/Binding site: carbohydrate (Tyr) (covalent) #status predicted

Query Match 63.2%; Score 36; DB 1; Length 333;  
 Best Local Similarity 70.0%; Pred. No. 46;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASENISYLP 11  
 Db 190 SSISISYLP 199

RESULT 34  
 B89900  
 proline-tRNA ligase [imported] - Staphylococcus aureus (strain N315)  
 C/Species: Staphylococcus aureus  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 C/Accession: B89900  
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; I  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
 A/Reference number: A89758; MUID:21311952; PMID:1148146  
 A/Accession: B89900  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-567 <KUR>  
 A/Cross-references: GB:BA000018; PID:g13701063; PIDN:BA842358.1; GSPDB:GN00149  
 A/Experimental source: strain N315  
 C/Genetics:  
 A/Gene: proS  
 C/Superfamily: proline-tRNA ligase

Query Match 63.2%; Score 36; DB 2; Length 567;  
 Best Local Similarity 54.5%; Pred. No. 81;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENISYLP 11  
 Db 34 QSTSGISYLP 44

RESULT 35  
 F97184  
 DNA modification methyltransferase [imported] - Clostridium acetobutylicum  
 C/Species: Clostridium acetobutylicum  
 C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 C/Accession: F97184  
 R/Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 J. Bacteriol. 183, 4823-4838, 2001  
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
 A/Reference number: A96900; MUID:21359325; PMID:21359325  
 A/Accession: F97184

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-581 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK80265.1; PID:g15025315; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2309

Query Match 63.2%; Score 36; DB 2; Length 581;  
Best Local Similarity 54.5%; Pred. No. 84;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RASENTSYLP 11  
: |||||  
Db 530 KLGENTYVYP 540

RESULT 36  
A82358  
vitamin B12 receptor VC0156 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: A82358  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10552301  
A:Accession: A82358  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-611 <HEI>  
A:Cross-references: GB:AE004105; GB:AE003852; NID:99654551; PIDN:AAFP3332.1; GSPDB:GN001  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0156  
A:Map position: 1  
C:Superfamily: vitamin B12 receptor; tonB-dependent receptor amino-terminal homology; tc

Query Match 63.2%; Score 36; DB 2; Length 611;  
Best Local Similarity 77.8%; Pred. No. 88;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENTSY 9  
: |||||  
Db 242 RAYENTYQY 250

RESULT 37  
A95031  
prolyl-tRNA synthetase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C:Accession: A95031  
R:Reitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple, nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Lotz, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: A95031  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-617 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AAK74442.1; PID:g14971734; GSPDB:GN00164; TIGR:SP4  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0264  
C:Superfamily: proline-tRNA ligase

Query Match 63.2%; Score 36; DB 2; Length 617;

Best Local Similarity 54.5%; Pred. No. 89;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 RASENTSYLP 11  
: |||||  
Db 34 QVSAGVSYLP 44

RESULT 38  
C97902  
proline-tRNA ligase (EC 6.1.1.15) [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 03-Jun-2002  
C:Accession: C97902  
R:Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; DeHoff, B.S.; E e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McHenry, S.; M y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: C97902  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-617 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAK99047.1; PID:g15457791; GSPDB:GN00174  
C:Genetics:  
A:Gene: pros  
C:Superfamily: proline-tRNA ligase  
C:Keywords: ligase

Query Match 63.2%; Score 36; DB 2; Length 617;  
Best Local Similarity 54.5%; Pred. No. 89;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENTSYLP 11  
: |||||  
Db 34 QVSAGVSYLP 44

RESULT 39  
F90257  
hypothetical protein SS01053 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: F90257  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-v Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to Genbank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: F90257  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-637 <KUR>  
A:Cross-references: GB:AE006641; NID:g13814241; PIDN:AAK41317.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: SS01053

Query Match 63.2%; Score 36; DB 2; Length 637;  
Best Local Similarity 71.4%; Pred. No. 92;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 NITYSLP 11  
: |||||  
Db 591 NVYSYLP 597

RESULT 40  
A32935  
protein P1 - Entamoeba histolytica (fragment)  
C:Species: Entamoeba histolytica

C;Date: 20-Dec-1989 #sequence\_revision 20-Dec-1989 #text\_change 24-Feb-1995  
 C;Accession: A32935  
 R;Tamich, E.; Hortsman, R.D.; Knobloch, J.; Arnold, H.H.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 5118-5122, 1989  
 A;Title: Genomic DNA differences between pathogenic and nonpathogenic Entamoeba histolytic  
 A;Reference number: A32935; MUID:89296955; PMID:2544890  
 A;Accession: A32935  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-639 <TAN>

Query Match 63.2%; Score 36; DB 2; Length 639;  
 Best Local Similarity 45.5%; Pred. No. 93;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RASENYSYLP 11  
 DB 419 RVEDNVIDYTP 429

Search completed: July 18, 2003, 15:10:45  
 Job time : 15.3 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:20 ; Search time 6.82 Seconds  
(without alignments)  
66.897 Million cell updates/sec

Title: US-10-007-790-8  
Perfect score: 57  
Sequence: 1 RASENTSYLP 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	50	87.7	108 1	KVSD_MOUSE
2	40	70.2	108 1	KV07_RABIT
3	39	68.4	652 1	CN16_YEREN
4	38	66.7	657 1	CN16_HAEN
5	37	64.9	256 1	YMS4_MALZE
6	37	64.9	272 1	MCBC_ECOLI
7	37	64.9	405 1	YMP0_YEAST
8	36	63.2	332 1	GLYG_MOUSE
9	36	63.2	332 1	GLYG_RABIT
10	36	63.2	332 1	GLYG_RAT
11	36	63.2	349 1	GLYG_HUMAN
12	36	63.2	639 1	APRP_ENTHI
13	35	61.4	108 1	KV1V_HUMAN
14	35	61.4	115 1	KVSC_MOUSE
15	35	61.4	549 1	G6PI_BUCAL
16	35	61.4	579 1	SYP_CHLMT
17	35	61.4	581 1	SYP_CHLTR
18	35	61.4	640 1	APRN_ENTHI
19	35	61.4	647 1	CN16_ECOLI
20	35	61.4	647 1	CN16_SALT
21	35	61.4	813 1	YTOJ_CAEEL
22	34	59.6	53 1	ATP8_DROSI
23	34	59.6	108 1	KVIN_HUMAN
24	34	59.6	120 1	CY21_RHOCE
25	34	59.6	377 1	CARA_NEIGO
26	34	59.6	377 1	CARA_NEIMA
27	34	59.6	377 1	CARA_NEIMB
28	34	59.6	489 1	C302_DROME
29	34	59.6	662 1	UL06_HSV6U
30	34	59.6	662 1	UL06_HSV6Z
31	34	59.6	1335 1	RRPO_FKXV
32	34	59.6	53 1	ATP8_DROME
33	33	57.9	53 1	ATP8_DROYA

34	33	57.9	107 1	KV1D_HUMAN	P01596 homo sapien
35	33	57.9	108 1	KV1H_HUMAN	P01600 homo sapien
36	33	57.9	114 1	CY21_RHOPA	P00090 rhodopsin
37	33	57.9	117 1	KV6H_MOUSE	P01641 mus musculus
38	33	57.9	121 1	CY22_RHOCE	P81154 rhodopsin
39	33	57.9	188 1	YVDE_LACLC	P22347 lactococcus
40	33	57.9	268 1	EFTS_BUCAL	P57326 buchnera ap
41	33	57.9	347 1	FMA1_PORGI	P13793 porphyromon
42	33	57.9	347 1	FMB1_PORGI	P33980 porphyromon
43	33	57.9	434 1	VG05_VARV	P32995 variola vir
44	33	57.9	478 1	GYRB_CYTAU	Q91C00 cytophaga a
45	33	57.9	478 1	GYRB_CYTHU	Q91C01 cytophaga h

## ALIGNMENTS

```

RESULT 1
ID KVSD_MOUSE STANDARD; PRT; 108 AA.
AC P01636;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 149.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=82057806; PubMed=6795447;
RA Appella E., Alvarez V.L.;
RT "Amino acid sequence of the variable region of M149 mouse myeloma
RT light chain: comparison with the nucleotide sequence of K2 and K3
RT clones."
RL Mol. Immunol. 17:1507-1513(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01919; KYMS49.
DR HSSP; P01607; 1RET.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 78 FRAMEWORK-3.
FT DOMAIN 6 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 97 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108
SQ SEQUENCE 108 AA; 12030 MW; 0B5244D2B410D84C CRC64;

Query Match 87.7%; Score 50; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYLP 10
| | | | | | | | | |
Db 24 RASENTSYLP 33

RESULT 2
ID KV07_RABIT STANDARD; PRT; 108 AA.
AC P01686;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Ig kappa chain V region K-25.  
 OS *Oryctolagus cuniculus* (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CC NCBI\_TaxID=9986;  
 RN (1)  
 RP MEDLINE=76039436; PubMed=241319;  
 RA Jaton J.-C.;  
 RT "Comparison of the amino acid sequences of the variable domains of  
 RT two homogeneous rabbit antibodies to type III pneumococcal  
 RT polysaccharide.";  
 RL Biochem. J. 147:235-247(1975).  
 CC -1- MISCELLANEOUS: RESIDUES 109-139 OF THE CONSTANT REGION ARE  
 CC IDENTICAL WITH THE CORRESPONDING RESIDUES OF RABBIT 4135 KAPPA  
 CC CHAIN.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III  
 CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.  
 DR PIR; A01951; KVR82K.  
 DR HSP; P80362; IWT.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SMO0406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 86 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 1143 MW; C16F0687550D1B6B CRC64;  
 Query Match 70.2%; Score 40; DB 1; Length 108;  
 Best Local Similarity 70.0%; Pred. No. 1.4;  
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASENIYSYL 10  
 Db 24 QASOBISYL 33

RESULT 3  
 CN16\_YEREN STANDARD; PRT; 652 AA.  
 ID ID CN16\_YEREN STANDARD; PRT; 652 AA.  
 AC P53052;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor (EC 3.1.4.16).  
 GN CPDB.  
 OS *Yersinia enterocolitica*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC *Yersinia*.  
 OX NCBI\_TaxID=630;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 51871 / WA-314 / Serotype O:8;  
 RA Truetsch K.S.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS BIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE  
 CC REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE  
 CC AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.  
 CC -1- CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O =  
 CC nucleoside 3'-phosphate.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.  
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 CC -----  
 DR EMBL; X85742; CA59745.1; -.  
 DR HSP; P07024; 2USH.  
 DR InterPro: IPR002224; 5\_nucleotidase.  
 DR InterPro: IPR004843; M-peptidase.  
 DR InterPro: IPR004844; S/T phosphatase.  
 DR Pfam; PF00149; Metallophos; 1.  
 DR Pfam; PF02872; 5\_nucleotidase; 1.  
 DR PROSITE; PS00785; 5\_NUCLEOTIDASE\_1; 1.  
 DR PROSITE; PS00786; 5\_NUCLEOTIDASE\_2; 1.  
 KW Hydrolyase; Multifunctional enzyme; Periplasmic; signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 652 2',3'-CYCLIC-NUCLEOTIDE 2'-  
 FT PHOSPHODIESTERASE.  
 SQ SEQUENCE 652 AA; 71491 MW; 8781369575794B17 CRC64;  
 Query Match 68.4%; Score 39; DB 1; Length 652;  
 Best Local Similarity 77.8%; Pred. No. 14;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASENISYSL 10  
 Db 364 ASDNYSYL 372

RESULT 4  
 CN16\_HAEIN STANDARD; PRT; 657 AA.  
 ID ID CN16\_HAEIN STANDARD; PRT; 657 AA.  
 AC P4764;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor (EC 3.1.4.16).  
 GN CPDB OR H10583.  
 OS *Haemophilus influenzae*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC *Haemophilus*.  
 OX NCBI\_TaxID=727;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Rd / KM20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghegan N.S.M.,  
 RA Gnehm C.U., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*  
 RT Rd.";  
 RL Science 269:496-512(1995).  
 CC -1- FUNCTION: THIS BIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE  
 CC REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE  
 CC (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O =  
 CC nucleoside 3'-phosphate.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.  
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CC -----
DR EMBL: U32740; AAC22242.1; -.
DR TIGR: H10583; -.
DR InterPro: IPR002224; 5_nucleotidase.
DR InterPro: IPR004843; M_ppestrase.
DR InterPro: IPR004844; S/T_phosphatase.
DR Pfam: PF00149; Metallophos; 1.
DR Pfam: PF02872; 5_nucleotidase; 1.
DR PROSITE: PS00785; 5_NUCLEOTIDASE_1; 1.
DR PROSITE: PS00786; 5_NUCLEOTIDASE_2; 1.
DR HydroLase: Multifunctional enzyme; Periplasmic; Signal;
KW Complete proteome.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 657 2',3'-CYCLIC-NUCLEOTIDE 2'-
FT CHAIN 27 657 PHOSPHODIESTERASE.
SQ SEQUENCE 657 AA; 72763 MW; 201CAAB15014499 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 657;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10
DB 368 KATDMYSYL 377

RESULT 5
YMS4_MAIZE STANDARD; PRT; 256 AA.
ID YMS4_MAIZE STANDARD; PRT; 256 AA.
AC P10580;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 29 kDa protein in mitochondrial S-1 DNA (URF 4).
OS Zea mays (Maize).
OG Mitochondrion.
OC Plasmid S-1.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN NCBI_TaxID=4577;
RP SEQUENCE FROM N.A.
RA Pallard M., Sedgeroff R.R., Levings C.S. III;
RT "Nucleotide sequence of the S-1 mitochondrial DNA from the S cytoplasm
of maize."
RL EMBO J. 4:1125-1128 (1985).
CC -!- MISCELLANEOUS: THE MITOCHONDRIA FROM THE S MALE-STERILE CYTOPLASM
OF MAIZE CONTAIN UNIQUE DNA-PROTEIN COMPLEXES, DESIGNATED S-1 AND
S-2. THESE COMPLEXES CONSIST OF DOUBLE-STRANDED LINEAR DNAs WITH
PROTEINS COVALENTLY ATTACHED TO THE 5' TERMINI.
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CC -----
DR EMBL: X02451; -; NOT_ANNOTATED_CDS.
DR MAIZEDB: 69620; -.
KW Hypothetical protein; Mitochondrion; Plasmid.
SQ SEQUENCE 256 AA; 29338 MW; B1D6DB31E402D175 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 256;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYL 10
DB 30 RATDNLTYSHL 39

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RESULT 6
MCBC_ECOLI STANDARD; PRT; 272 AA.
ID MCBC_ECOLI STANDARD; PRT; 272 AA.
AC P23185;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Microcin B17 processing protein mbcB.
GN MCBC.
OS Escherichia coli.
OG Plasmid IncFII pmcCB17.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN NCBI_TaxID=562;
RP SEQUENCE FROM N.A.
RX MEDLINE=8912311; PubMed=264425;
RA Genilloud O., Moreno F., Kolter R.;
RT "DNA sequence, products, and transcriptional pattern of the genes
involved in production of the DNA replication inhibitor microcin
B17."
RL J. Bacteriol. 171:1126-1135 (1989).
CC -!- FUNCTION: NECESSARY TO PROCESS THE INACTIVE MICROCIN B17 (MCBA)
CC PRECURSOR INTO THE ACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: TO R.LEGUMINOSARUM TRXB WHICH IS INVOLVED IN THE
CC PROCESSING OF TRIFOLIOTOXIN.
CC -----
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CC -----
DR EMBL: M24253; AAA72743.1; -.
DR PIR: C32058; C32058.
KW Antibiotic; Plasmid.
SQ SEQUENCE 272 AA; 30753 MW; 956E1744338C051D CRC64;

Query Match 64.9%; Score 37; DB 1; Length 272;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENTSYL 11
DB 144 QAGTNYHYLP 154

RESULT 7
YMP0_YEAST STANDARD; PRT; 405 AA.
ID YMP0_YEAST STANDARD; PRT; 405 AA.
AC O03687;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 46.9 kDa protein in PUBLI-HXT2 intergenic region.
GN YMR010W OR YMR8270.13.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN NCBI_TaxID=4932;
RP SEQUENCE FROM N.A.
RC STRAIN=5288c / AB972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC -----  
 CC EMBL/248613; CA88526.1; -  
 CC SGD; S0004612; YMR010W.  
 CC Hypothetical protein; Transmembrane.  
 CC FT TRANSMEM 32 72 POTENTIAL.  
 CC FT TRANSMEM 77 97 POTENTIAL.  
 CC FT TRANSMEM 104 124 POTENTIAL.  
 CC FT TRANSMEM 179 199 POTENTIAL.  
 CC FT TRANSMEM 224 244 POTENTIAL.  
 CC FT TRANSMEM 255 275 POTENTIAL.  
 CC FT TRANSMEM 300 320 POTENTIAL.  
 CC FT SEQUENCE 405 AA; 46872 MW; AF019859073E134E CRC64;

Query Match 64.9%; Score 37; DB 1; Length 405;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SENIYSTLP 11  
 Db 28 SDTLYSTLP 36

RESULT 8  
 GLYG\_MOUSE STANDARD; PRT; 332 AA.  
 ID GLYG\_MOUSE  
 AC Q9R062;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Glycogenin-1 (EC 2.4.1.186).  
 GN GYG OR GYG1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=20011289; PubMed=10542328;  
 RA van Mäanen M.-H., Fournier P.A., Palmer T.N., Abraham L.J.;  
 RT "Characterization of mouse glycogenin-1 cDNA and promoter region.";  
 RL Biochim. Biophys. Acta 1447:284-290(1999).  
 CC -1- FUNCTION: SELF-GLYCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, TO  
 CC FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR  
 CC GLYCOGEN SYNTHASE.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +  
 CC GLUCOSYLGlycogenin.  
 CC -1- COFACTOR: SELF-GLYCOSYLATION IS DEPENDENT ON THE PRESENCE OF  
 CC DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.  
 CC -1- PATHWAY: Glycogen biosynthesis.  
 CC -1- SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.  
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE, HEART, IN A LESSER EXTENT IN  
 CC KIDNEY, LUNG AND BRAIN.  
 CC -1- PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM  
 CC UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10  
 CC RESIDUES ATTACHED TO TYR-194.  
 CC -1- SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.

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CC -----  
 CC EMBL/AF114031; AAD48901.1; -

DR MGD; MG1:1351614; GYG1.  
 DR InterPro: IPR002495; GT 8.  
 DR Pfam: PF01501; Glyco\_transf 8; 1.  
 KW Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;  
 KW Glycoprotein.  
 FT INIT\_MET 0 0 BY SIMILARITY.  
 FT ACT\_SITE 85 85 BY SIMILARITY.  
 FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
 FT MOD\_RES 43 43 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 FT CARBOHYD 194 194 O-LINKED (GLC...) (BY SIMILARITY).  
 SQ SEQUENCE 332 AA; 37271 MW; 8DA0F1A875552F40 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 332;  
 Best Local Similarity 70.0%; Pred. No. 25;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASENTYSTLP 11  
 Db 189 SSISYSTLP 198

RESULT 9  
 GLYG\_RABBIT STANDARD; PRT; 332 AA.  
 ID GLYG\_RABBIT  
 AC P13280;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Glycogenin-1 (EC 2.4.1.186).  
 GN GYG OR GYG1.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=93100288; PubMed=1281472;  
 RA Viskupic E., Cao Y., Zhang W., Cheng C., Depauli-Roach A.A.,  
 RA Roach P.J.;  
 RT "Rabbit skeletal muscle glycogenin. Molecular cloning and production  
 RT of fully functional protein in Escherichia coli.";  
 RL J. Biol. Chem. 267:25759-25763(1992).  
 RN (2)  
 RP SEQUENCE.  
 RC STRAIN=New Zealand white; TISSUE=Skeletal muscle;  
 RX MEDLINE=90032666; PubMed=2806254;  
 RA Campbell D.G., Cohen P.;  
 RT "The amino acid sequence of rabbit skeletal muscle glycogenin.";  
 RL Eur. J. Biochem. 185:119-125(1989).  
 RN (3)  
 RP SEQUENCE OF 34-47, 181-201, 209-226 AND 307-324.  
 RC TISSUE=Liver;  
 RX MEDLINE=89325337; PubMed=2526735;  
 RA Smythe C., Villar-Palasi C., Cohen P.;  
 RT "Structural and functional studies on rabbit liver glycogenin.";  
 RL Eur. J. Biochem. 183:205-209(1989).  
 RN (4)  
 RP SEQUENCE OF 34-47, AND PHOSPHORYLATION.  
 RX MEDLINE=89374676; PubMed=3151442;  
 RA Lomako J., Whelan W.J.;  
 RT "The occurrence of serine phosphate in glycogenin: a possible  
 RT regulatory site.";  
 RL BioFactors 1:261-264(1988).  
 RN (5)  
 RP CHARACTERIZATION.  
 RX MEDLINE=94192798; PubMed=8143846;  
 RA Alonso M.D., Lomako J., Lomako W.M., Whelan W.J.;  
 RT "Tyrosine-194 of glycogenin undergoes autocatalytic glucosylation but  
 RT is not essential for catalytic function and activity.";  
 RL FEBS Lett. 342:38-42(1994).  
 RN (6)  
 RP CHARACTERIZATION.

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RX MEDLINE=95289736; PubMed=7771798;
RA Cao Y., Steinhilber L.K., Roach P.J.;
RT "Mechanism of glycogenin self-glycosylation.";
RL Arch. Biochem. Biophys. 319:293-298(1995).
RN [7]
RP CHARACTERIZATION, AND MUTAGENESIS OF LYS-85.
RX MEDLINE=9160387; PubMed=10049511;
RA Lin A., Mu J., Yang J., Roach P.J.;
RT "Self-glycosylation of glycogenin, the initiator of glycogen
RT biosynthesis, involves an inter-subunit reaction.";
RL Arch. Biochem. Biophys. 363:163-170(1999)
CC -1- FUNCTION: SELF-GLYCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, TO
CC FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
CC GLYCOSYL SYNTHASE.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
CC glucosylglycogenin.
CC -1- COFACTOR: SELF-GLYCOSYLATION IS DEPENDENT ON THE PRESENCE OF
CC DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SUBUNIT: HOMODIMER TIGHTLY COMPLEXED TO THE 86 KDA CATALYTIC
CC SUBUNIT OF GLYCOSYL SYNTHASE.
CC -1- PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM
CC UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10
CC RESIDUES ATTACHED TO TYR-194.
CC -1- SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
CC -----
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CC -----
DR EMBL: L01791; AAA13404.1; -.
DR PIR: S06482; S06482.
DR InterPro: IPR002495; GT_8.
DR Pfam: PF01501; Glyco_transf_8; 1.
KW Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
KW Glycoprotein.
FT INIT MET 0 0
FT ACT SITE 85 85
FT MOD RES 1 1 ACETYLATION.
FT CARBOHYD 194 194 PHOSPHORYLATION (BY PKA) (IN VITRO).
FT MUTAGEN 85 85 O-LINKED (GLC. . .)
FT CONFLICT 38 38 K->O: LOSS OF ACTIVITY.
FT CONFLICT 88 88 T->L (IN REF. 4).
FT CONFLICT 97 97 C->S (IN REF. 2).
FT CONFLICT 97 97 C->L (IN REF. 2).
SQ SEQUENCE 332 AA; 37266 MW; DD64F6DE6CC5A8PA CRC64;

Query Match 63.2%; Score 36; DB 1; Length 332;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Heart;
RX MEDLINE=99318015; PubMed=10391131;
RA Pak B.J., Sangaralingham S.J., Pang S.C.;
RT "Molecular cloning and developmental expression of rat glycogenin in
RT cardiac tissue.";
RL Mol. Cell. Biochem. 194:117-123(1999).
CC -1- FUNCTION: SELF-GLYCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, TO
CC FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
CC GLYCOSYL SYNTHASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
CC glucosylglycogenin.
CC -1- COFACTOR: SELF-GLYCOSYLATION IS DEPENDENT ON THE PRESENCE OF
CC DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE
CC (BY SIMILARITY).
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SUBUNIT: HOMODIMER TIGHTLY COMPLEXED TO THE 86 KDA CATALYTIC
CC SUBUNIT OF GLYCOSYL SYNTHASE (BY SIMILARITY).
CC -1- PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM
CC UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10
CC RESIDUES ATTACHED TO TYR-194 (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF021343; AAB81219.1; -.
DR EMBL: U06130; AAB53334.1; -.
DR InterPro: IPR002495; GT_8.
DR Pfam: PF01501; Glyco_transf_8; 1.
KW Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
KW Glycoprotein.
FT INIT MET 0 0 BY SIMILARITY.
FT ACT SITE 85 85 BY SIMILARITY.
FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).
FT CARBOHYD 194 194 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT O-LINKED (GLC. . .) (BY SIMILARITY).
SQ SEQUENCE 332 AA; 37247 MW; 41F19CA7F09BPF059 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 332;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 2 ASENITYSLP 11
DB 189 SSISITYSLP 198

RESULT 10
GLYG_RAT STANDARD; PRT; 332 AA.
AC 008730;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogenin-1 (EC 2.4.1.186).
GN GYG OR GYG1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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QY 2 ASENITYSLP 11
DB 189 SSISITYSLP 198

RESULT 11
GLYG_HUMAN STANDARD; PRT; 349 AA.
AC P46976; Q9UNV0;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogenin-1 (EC 2.4.1.186).
GN GYG OR GYG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM GN-1).
RC TISSUE=Skeletal muscle;
RX MEDLINE=96176958; PubMed=8602861;
RA Barbetti F., Rocchi M., Bossolaco M., Cordera R., Sbraccia P.,

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RA Fine11 P., Consalez G.G.;  
 RT "The human skeletal muscle glycogenin gene: cDNA, tissue expression  
 RT and chromosomal localization.";  
 RL Biochem. Biophys. Res. Commun. 220:72-77 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM GN-1).  
 RX MEDLINE=96299648; PubMed=8661012;  
 RA Lomako J., Mazuruk K., Lomako W.M., Alonso M.D., Whelan W.J.,  
 RA Rodriguez I.R.;  
 RT "The human intron-containing gene for glycogenin maps to chromosome 3,  
 RT band q24.";  
 RL Genomics 33:519-522 (1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM GN-1S).  
 RC TISSUE=Skin;  
 RA Leffers H., Wiemann S., Ansoerge W.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM GN-1).  
 RX MEDLINE=99326495; PubMed=10395894;  
 RA van Maanen M.-H., Fournier P.A., Palmer T.N., Abraham L.J.;  
 RT "Characterization of the human glycogenin-1 gene: identification of a  
 RT muscle-specific regulatory domain.";  
 RL Gene 234:217-226 (1999).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM GN-1L), AND ALTERNATIVE SPLICING.  
 RX MEDLINE=20184741; PubMed=10721716;  
 RA Zhai L., Mu J., Zong H., Depauli-Roach A.A., Roach P.J.;  
 RT "Structure and chromosomal localization of the human glycogenin-2 gene  
 RT Gg2.";  
 RL Gene 242:229-235 (2000).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM GN-1).  
 RC TISSUE=Placenta;  
 RA Strauberg R.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM, TO  
 CC FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR  
 CC GLYCOGEN SYNTHASE.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +  
 CC GLYCOSYLGlycogenin.  
 CC -1- COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF  
 CC DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.  
 CC -1- PATHWAY: Glycogen biosynthesis.  
 CC -1- SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOPFORMS: GN-1L (SHOWN HERE), GN-1 AND GN-  
 CC 1S, ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- PPM: SELF-GLUCOSYLATION BY THE TRANSFER OF GLUCOSE RESIDUES FROM  
 CC UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLUCAN OF AROUND 10  
 CC RESIDUES ATTACHED TO TYR-194.  
 CC -1- SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.  
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
 CC FRAMESHIFT IN POSITION 203.  
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 CC -----  
 CC EMBL: U44131, AAB00114.1, -;  
 CC EMBL: U31525, AAB09752.1, -;  
 CC EMBL: X79537, CAAS6073.1, ALT\_FRAME.  
 CC EMBL: AF065481, AAD31084.1, -;  
 CC EMBL: AF065476, AAD31084.1, JOINED.  
 CC EMBL: AF065477, AAD31084.1, JOINED.  
 CC EMBL: AF065478, AAD31084.1, JOINED.  
 CC EMBL: AF065479, AAD31084.1, JOINED.  
 CC EMBL: AF065480, AAD31084.1, JOINED.  
 CC EMBL: AF087942, AAD52093.1, -;  
 CC EMBL: BC000033, AAH00033.1, -;

DR Genew, HGNC:4699; GYG.  
 DR MIM: 603942; -;  
 DR InterPro: IPR002495; GT 8.  
 DR Pfam: PF01501; Glyco\_transf\_8; 1.  
 DR KX Transferrase; Glycogen biosynthesis; Acetylation; Phosphorylation;  
 KW Glycoprotein; Alternative splicing.  
 FT INIT MET 0  
 FT ACT SITE 85 85  
 FT MOD\_RES 1 1  
 FT MOD\_RES 43 43  
 FT CARBOHYD 194 194  
 FT VARSPLIC 203 292  
 FT VARSPLIC 276 292  
 SO SEQUENCE 349 AA; 39252 MW; C41BCFF54C8AF09 CRC64;  
 Query Match 63.2%; Score 36; DB 1; Length 349;  
 Best Local Similarity 70.0%; Pred. No. 26;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 ASENIYSYLP 11  
 Db 189 SSISITSYLP 198  
 RESULT 12  
 APRP\_ENTHI STANDARD; PRT; 639 AA.  
 AC P20302;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Antigenic protein p1 (Pathogenic protein 1) (Fragment).  
 OS Entamoeba histolytica.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_TaxID=5759;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HM-1; IMSS;  
 RX MEDLINE=89296955; PubMed=2544890;  
 RA Tannich E., Horstmann R.D., Knobloch J., Arnold H.H.;  
 RT "Genomic DNA differences between pathogenic and nonpathogenic  
 RT Entamoeba histolytica.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5118-5122 (1989).  
 CC -1- SIMILARITY: 88% IDENTITY WITH PROTEIN FROM NON-PATHOGENIC  
 CC STRAIN.  
 CC PIR: A32935; A32935.  
 DR PIR; A32935; A32935.  
 KW Antigen.  
 KM NON TER 1  
 FT SEQUENCE 639 AA; 72086 MW; 4752187AB956AEB5 CRC64;  
 Qy 1 RASENIYSYLP 11  
 Db 419 RVEDNVYDTP 429  
 Query Match 63.2%; Score 36; DB 1; Length 639;  
 Best Local Similarity 45.5%; Pred. No. 49;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 RESULT 13  
 KXIV\_HUMAN STANDARD; PRT; 108 AA.  
 AC P04430;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-1 region BAN.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

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RX MEDLINE=86174817; PubMed=3083240;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (Al) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KAHUEN.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
KM Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 FRAMEWORK-2.
FT DOMAIN 4 49 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 6 57 FRAMEWORK-3.
FT DOMAIN 7 88 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 8 97 FRAMEWORK-4.
FT DOMAIN 9 98 BY SIMILARITY.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 108;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10
DB 24 RASQSVINYV 33

RESULT 14
KVSC_MOUSE STANDARD; PRT; 115 AA.
ID 21-JUL-1986 (Rel. 01, Created)
AC P01635;
RT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region K2 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=8015999; PubMed=6767723;
RA Nishioaka Y., Leder P.;
RT "Organization and complete sequence of identical embryonic and
RT plasmacytoma kappa V-region genes."
RL J. Biol. Chem. 255:3691-3694(1980).
CC -I- MISCELLANEOUS: THE GENE WAS ISOLATED AND SEQUENCED SEPARATELY FROM
CC TWO DIFFERENT SOURCES, EMBRYOS AND CULTURED PLASMACYTOMA CELLS
CC THAT SECRETE THE SIMILAR KAPPA CHAIN MOPC 149.
CC
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CC -----
CC EMBL; V00778; CA24155.1; -.
DR PIR; A01918; KWSK2.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION K2.
FT DOMAIN 21 43 FRAMEWORK-1.

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FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12581 MW; 4F41E3D40C539DEC CRC64;

Query Match 61.4%; Score 35; DB 1; Length 115;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10
DB 44 RASGNHNYL 53

RESULT 15
G6PI_BUCAL STANDARD; PRT; 549 AA.
ID 16-OCT-2001 (Rel. 40, Created)
AC P57636;
RT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR BU573.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. ARS."
RL Nature 407:81-86(2000).
CC -I- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -I- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -I- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC
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CC -----
CC EMBL; AP00119; BAB13263.1; -.
DR HSSP; O9N1E2; IHOX.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI_1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KM Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 386 386 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
SQ SEQUENCE 549 AA; 63435 MW; 8DF547CE08382244 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 549;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 SENIYSYL 10
DB 517 SQNINYVL 524

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RESULT 16
SYN CHLNU STANDARD; PRT; 579 AA.
ID SYN CHLNU
AC G9PK01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (PRORS).
GN PROS OR TC0672.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=83560;
RN [1]
RP STRAIN=NOPN / N199;
RC MEDLINE=20150255; PubMed=10684935;
RX Read T.D., Brunham R.C., Shen C., Gail S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Baas S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gaim M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP +
CC diphosphate + L-prolyl-tRNA(Pro).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; AE002334; AAF39493.1; -.
DR TIGR; TC0672; -.
DR InterPro; IPR002106; AAcRNA_ligase1.
DR InterPro; IPR004154; HGTp anticodon.
DR InterPro; IPR004500; ProS fam II.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR002316; tRNA-synt_pro.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR Pfam; PF03129; HGTp anticodon; 1.
DR PRINTS; PR01046; tRNAsynthPRO.
DR TIGRFAMs; TIGR00409; proS fam II; 1.
DR PROSITE; PS50862; AA tRNA_LIGASE II; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 579 AA; 65780 MW; 73EBDF5BF54BF06A CRC64;

Query Match 61.4%; Score 35; DB 1; Length 579;
Best Local Similarity 54.5%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENTSYLTP 11
Db 34 KTSKGIYSYTP 44

RESULT 17
SYN CHLNR STANDARD; PRT; 581 AA.
ID SYN CHLNR
AC P36431; O84398;
DT 01-JUN-1994 (Rel. 29, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (PRORS).

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GN PROS OR CT193.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP STRAIN=E/UW-5/CX;
RC MEDLINE=94320787; PubMed=8045424;
RX Schmeil D.H., Wyrick P.B.;
RA "another putative heat-shock gene and aminoacyl-tRNA synthetase gene
RT are located upstream from the grpE-like and dnaK-like genes in
RT Chlamydia trachomatis."
RL Gene 145:57-63(1994).
RN [2]
RP STRAIN=D/UW-3/CX;
RC MEDLINE=9900809; PubMed=9784136;
RX Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatubov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP +
CC diphosphate + L-prolyl-tRNA(Pro).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; L25105; AAA23161.1; -.
DR EMBL; AE001312; AAC67990.1; -.
DR InterPro; IPR002106; AAcRNA_ligase1.
DR InterPro; IPR004154; HGTp anticodon.
DR InterPro; IPR004500; ProS fam II.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR002316; tRNA-synt_pro.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR Pfam; PF03129; HGTp anticodon; 1.
DR PRINTS; PR01046; tRNAsynthPRO.
DR TIGRFAMs; TIGR00409; proS fam II; 1.
DR PROSITE; PS50862; AA tRNA_LIGASE II; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 581 AA; 65653 MW; 08815CF98633F259 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 581;
Best Local Similarity 54.5%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENTSYLTP 11
Db 34 KTSKGIYSYTP 44

RESULT 18
APRN ENTHI STANDARD; PRT; 640 AA.
ID APRN ENTHI
AC P20301;
DT 01-FEB-1991 (Rel. 17, Created)

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DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Antigenic protein NP1 (Non-pathogenic protein 1) (Fragment).  
 OS Entamoeba histolytica.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_TaxID=5759;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SAW 1734;  
 RX MEDLINE=89296955; PubMed=2544890;  
 RA Tammich E., Horstmann R.D., Knobloch J., Arnold H.H.;  
 RT "Genomic DNA differences between pathogenic and nonpathogenic  
 Entamoeba histolytica."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5118-5122(1989).  
 CC -1- SIMILARITY: 88% IDENTITY WITH PROTEIN FROM PATHOGENIC  
 CC STRAIN.  
 DR PIR; B32935; B32935.  
 KW Antigen.  
 FT NON\_TER  
 SQ SEQUENCE 640 AA; 72352 MW; 15BEEDA0C06F7BC CRC64;  
 QY 1 RASENITYSLP 11  
 DB 420 QVENYDYTP 430  
 RESULT 19  
 ID CN16\_ECOLI STANDARD; PRT; 647 AA.  
 AC P08331;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 2',3'-CYCLIC-nucleotide 2'-phosphodiesterase precursor (EC 3.1.4.16).  
 GN CPDB OR B4213.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86139859; PubMed=3005231;  
 RA Liu J., Burns D.M., Beacham I.R.;  
 RT "Isolation and sequence analysis of the gene (cpdB) encoding  
 periplasmic 2',3'-cyclic phosphodiesterase."  
 RL J. Bacteriol. 165:1002-1010(1986).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=95334362; PubMed=7610040;  
 RA Burtland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,  
 RT "Analysis of the Escherichia coli genome VI: DNA sequence of the  
 RT region from 92.8 through 100 minutes."  
 RL Nucleic Acids Res. 23:2105-2119(1995).  
 RN (3)  
 RP SEQUENCE OF 1-20 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=91042419; PubMed=2172762;  
 RA Liu J., Beacham I.R.;  
 RT "Transcription and regulation of the cpdB gene in Escherichia coli  
 RT K12 and Salmonella typhimurium L72: evidence for modulation of  
 RT constitutive promoters by cyclic AMP-CRP complex."  
 RL Mol. Gen. Genet. 222:161-165(1990).  
 RN (4)  
 RP SEQUENCE OF 20-31.  
 RC STRAIN=K12 / EMG2;  
 RX MEDLINE=97443975; PubMed=9296646;  
 RA Link A.J., Robison K., Church G.M.;

RT "Comparing the predicted and observed properties of proteins encoded  
 RT in the genome of Escherichia coli K-12."  
 RL Electrophoresis 18:1259-1313(1997).  
 CC -1- FUNCTION: THIS BIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE  
 CC REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE  
 CC AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.  
 CC -1- CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O =  
 CC nucleoside 3'-phosphate.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic.  
 CC -1- MISCELLANEOUS: TWO KINETICALLY DISTINGUISHABLE ACTIVE SITES FOR  
 CC TWO CORRESPONDING SUBSTRATES CAN BE IDENTIFIED.  
 CC -1- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.  
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 CC -----  
 DR EMBL: M13464; AAA33597.1; -;  
 DR EMBL: U14003; AAA97109.1; -;  
 DR EMBL: AE00492; AAC77170.1; -;  
 DR EMBL: X54008; CAA37954.1; -;  
 DR PIR; A26398; ESECPC.  
 DR HSSP: P07024; 2USH.  
 DR EcGene: EGI0160; cpdB.  
 DR InterPro: IPR002224; 5\_nucleotidase.  
 DR InterPro: IPR004843; M-peptidase.  
 DR InterPro: IPR004844; S/T\_phosphatase.  
 DR Pfam: PF00149; Metallophos; 1.  
 DR Pfam: PF02872; 5\_nucleotidase; 1.  
 DR PROSITE: PS00785; 5\_NUCLEOTIDASE\_1; 1.  
 DR PROSITE: PS00786; 5\_NUCLEOTIDASE\_2; 1.  
 KW Hydroxylase; Multifunctional enzyme; Periplasmic; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 19  
 FT CHAIN 20 647  
 FT 2',3'-CYCLIC-NUCLEOTIDE 2'-  
 FT PHOSPHODIESTERASE.  
 FT A->G (IN REF. 1).  
 FT CONFLICT 316 316 GKPIDPMAMFLVATNNRAYGKFA -> ASRLIRTPCSWL  
 FT CONFLICT 528 552 PPTIALTGQIC (IN REF. 1).  
 FT  
 SQ SEQUENCE 647 AA; 70832 MW; 4B2EDC3563473827 CRC64;  
 QY 1 RASENITYSLP 10  
 DB 358 KSADNMYSTL 367  
 RESULT 20  
 ID CN16\_SALTY STANDARD; PRT; 647 AA.  
 AC P26265;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 2',3'-CYCLIC-nucleotide 2'-phosphodiesterase precursor (EC 3.1.4.16).  
 GN CPDB OR STM4403.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=602;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SSGC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McCalland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.,  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT LT2";  
 RL Nature 413:852-856(2001).  
 RN [2]  
 RP SEQUENCE OF 1-251 FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE=91042419; PubMed=2172762;  
 RA Liu J., Beacham I.R.,  
 RT "Transcription and regulation of the *cpdB* gene in *Escherichia coli*  
 RT K12 and *Salmonella typhimurium* LT2: evidence for modulation of  
 RT constitutive promoters by cyclic AMP-CRP complex.";  
 RL Mol. Genet. 222:161-165(1990).  
 CC -1- FUNCTION: THIS BIFUNCTIONAL ENZYME CATALYZES TWO CONSECUTIVE  
 CC REACTIONS CONVERTING 2',3'-CYCLIC-NUCLEOTIDE TO 3'-NUCLEOTIDE  
 CC AND THEN 3'-NUCLEOTIDE TO NUCLEIC ACID AND PHOSPHATE.  
 CC -1- CATALYTIC ACTIVITY: Nucleoside 2',3'-cyclic phosphate + H(2)O =  
 CC nucleoside 3'-phosphate.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic.  
 CC -1- MISCELLANEOUS: TWO KINETICALLY DISTINGUISHABLE ACTIVE SITES FOR  
 CC TWO CORRESPONDING SUBSTRATES CAN BE IDENTIFIED.  
 CC -1- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.  
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 CC -----  
 DR EMBL: AE008906; AL23223.1; -  
 DR EMBL: X54009; CA37956.1; -  
 DR PIR: S11915; S11915.  
 DR StyGene; SG10065; cpdB.  
 DR InterPro; IPR002224; 5\_nucleotidase.  
 DR Pfam; PF02872; 5\_nucleotidase; 1.  
 DR PROSITE; PS00785; 5\_NUCLEOTIDASE\_1; 1.  
 DR PROSITE; PS00786; 5\_NUCLEOTIDASE\_2; 1.  
 KM Hydroxylase; Multifunctional enzyme; Periplasmic; Signal;  
 KM Complete proteome.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 647 2',3'-CYCLIC-NUCLEOTIDE  
 FT 2'-PHOSPHODIESTERASE.  
 FT FT CONFLICT 51 89 G -> A (IN REF. 2)  
 FT FT CONFLICT 84 89 GYMAA -> RLYCG (IN REF. 2)  
 FT FT CONFLICT 96 98 DVH -> GIQ (IN REF. 2)  
 FT FT CONFLICT 133 133 A -> G (IN REF. 2)  
 FT FT CONFLICT 174 174 I -> N (IN REF. 2)  
 SQ SEQUENCE 647 AA; 70516 MW; E97FE7D6681DB34 CRC64;  
 Query Match 61.4%; Score 35; DB 1; Length 647;  
 Best Local Similarity 50.0%; Pred. No. 76;  
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RASEN1SYL 10  
 Db 358 KSADM1SYL 367  
 RESULT 21  
 ID YTOJ CAEBL STANDARD; PRT; 813 AA.  
 AC Q19673;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical tyrosinase-like protein F21C3.2 in chromosome I.  
 GN F21C3.2  
 OS *Caenorhabditis elegans*.  
 SC *Caenorhabditis elegans*.  
 EC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;

OC Rhabdilitidae; Pelodierinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA McMurtry A.,  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP REVISIONS.  
 RA Jones S.J.M.,  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: Binds 2 copper ions per subunit (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Z71261; CA95805.1; -  
 DR WormPep; F21C3.2; CE17689.  
 DR InterPro; IPR003582; SHKT.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00264; tyrosinase; 1.  
 DR PRINTS; PR00092; TYROSINASE.  
 DR SMART; SMO0254; SHKT; 4.  
 DR PROSITE; PS00497; TYROSINASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00498; TYROSINASE\_2; 1.  
 KM Hypothetical protein; Oxidoreductase; Monooxygenase; Copper.  
 FT METAL 282 282  
 FT METAL 291 291 COPPER A (BY SIMILARITY).  
 FT METAL 401 401 COPPER B (BY SIMILARITY).  
 FT METAL 405 405 COPPER B (BY SIMILARITY).  
 FT METAL 428 428 COPPER B (BY SIMILARITY).  
 SQ SEQUENCE 813 AA; 91226 MW; D151CE52A2625A91 CRC64;  
 Query Match 61.4%; Score 35; DB 1; Length 813;  
 Best Local Similarity 55.6%; Pred. No. 96;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 SEN1SYL 11  
 Db 487 TDMLYSYAP 495  
 RESULT 22  
 ID ATP8 DROSI STANDARD; PRT; 53 AA.  
 AC P50270; O9ME70;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).  
 GN ATP8 OR ATP8 OR ATP8B.  
 OS *Drosophila simulans* (Fruit fly).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93374296; PubMed=8365657;  
 RA Kaneo M., Saita Y., Matsura E.T., Chigusa S.I.,  
 RT "Evolution of the mitochondrial ATPase 6 gene in *Drosophila*:  
 RT unusually high level of polymorphism in *D. melanogaster*.";  
 RL Genet. Res. 61:195-204(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NC48, TT00, HM00, HM09, and NC37;

RA Ballard J.W.O.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT  
 (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPase COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  
 H(+) (Out).  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.  
 CC -1- SIMILARITY: BELONGS TO THE ATPase PROTEIN 8 FAMILY.  
 CC  
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DR EMBL; S64977; AAD1957.1; -.  
 DR EMBL; AF200838; AAF77358.1; -.  
 DR EMBL; AF200833; AAF77292.1; -.  
 DR EMBL; AF200834; AAF77306.1; -.  
 DR EMBL; AF200835; AAF77319.1; -.  
 DR EMBL; AF200837; AAF77332.1; -.  
 DR EMBL; AF200837; AAF77343.1; -.  
 DR FlyBase; FBgn0012876; Dsln[mt:ATPase8.  
 DR InterPro; IPR001421; ATPase8\_mit.  
 DR Pfam; PF00895; ATP-synt 8; 1.  
 DR Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.  
 FT CONFLICT 26 M -> I (IN REF. 1).  
 FT CONFLICT 32 34 IPN -> MPD (IN REF. 1).  
 SQ SEQUENCE 53 AA; 6364 MW; 45D2C68EE47491E3 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 53;  
 Best Local Similarity 66.7%; Pred. No. 8.6;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SENIYSTLP 11  
 Db 25 SMNYSYIP 33

RESULT 23  
 KVIN\_HUMAN STANDARD; PRT; 108 AA.  
 AC F01606;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 1g kappa chain V-1 region OU.  
 OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 RT chains.";  
 RL Science 169:56-59 (1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN.  
 CC PIR: A01872; KIHUOU.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SMO0406; IGV; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 59.6%; Score 34; DB 1; Length 108;  
 Best Local Similarity 70.0%; Pred. No. 18;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENIYSTLP 10  
 Db 24 RASZTISSTLP 33

RESULT 24  
 CY21\_RHOCE STANDARD; PRT; 120 AA.  
 ID CY21\_RHOCE  
 AC P81153;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome C2, iso-1 (C552).  
 OS Rhodospirillum rubrum (Rhodocycla centennaria).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;  
 NC Rhodospirillum  
 NC NBI\_TaxID=34018;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 43720;  
 RX MEDLINE=98323574; PubMed=9659396;  
 RA Samy B., Fitch J., Meyer T.E., Cusanovich M.A., van Beeumen J.J.;  
 RT "Purification and primary structure analysis of two cytochrome c2  
 RT isozymes from the purple phototrophic bacterium Rhodospirillum  
 RT rubrum.";  
 RL Biochim. Biophys. Acta 1384:345-355 (1998).  
 CC -1- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,  
 CC PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR  
 CC TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION  
 CC PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN  
 CC AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA. THE REDOX  
 CC POTENTIAL OF THIS CYTOCHROME IS 316 MV.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.  
 DR HSSP; P00083; ICRY.  
 DR InterPro; IPR000345; Cyt\_c\_heme\_bind.  
 DR InterPro; IPR003088; Cyt\_C1.  
 DR InterPro; IPR002327; Cyt\_C1AB.  
 DR Pfam; PF00034; Cytochrome c; 1.  
 DR PRINTS; PR00604; CYTCRMEC1AB.  
 DR ProDom; PD000375; Cyt\_C1AB; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; 1.  
 DR PROSITE; PS00190; CYTOCHROME C; 1.  
 KW Electron transport; Photosynthesis; Heme.  
 KW Electron transport; Photosynthesis; Heme.  
 FT BINDING 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT BINDING 15 15 HEME (COVALENT).  
 FT BINDING 18 18 HEME (COVALENT).  
 FT BINDING 19 19 IRON (HEME AXIAL LIGAND).  
 FT METAL 98 98 IRON (HEME AXIAL LIGAND).  
 FT METAL 98 98 IRON (HEME AXIAL LIGAND).  
 SQ SEQUENCE 120 AA; 12818 MW; BBE05414A003E6BF CRC64;

Query Match 59.6%; Score 34; DB 1; Length 120;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SENIYSTLP 11  
 Db 65 AENIMAYLP 73

RESULT 25  
 CARA\_NEIGO STANDARD; PRT; 377 AA.  
 ID CARA\_NEIGO

AC Q50983; Q509598;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain).  
 GN CARA.  
 OS Neisseria gonorrhoeae.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=485;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MS11;  
 RA Ridel T., Bobberger H.J., Pandit J., Meyer T.F.;  
 RT "The Neisseria gonorrhoeae carA gene: Generation of mutants and implication of pyrimidine biosynthesis for the infection of epithelial cells";  
 RT Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CH811;  
 RX MEDLINE=95291461; PubMed=7773412;  
 RA Lawson F.S., Billores F.M., Dillon J.A.;  
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria gonorrhoeae includes a large, variable intergenic sequence which is also present in other Neisseria species.";  
 RL Microbiology 141:1183-1191(1995).  
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.  
 CC -1- PATHWAY: Arginine biosynthesis.  
 CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE CARA FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.  
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 CC -----  
 DR EMBL: Z54242; CA91011.1; -;  
 DR EMBL: U11295; AAA74995.1; -;  
 DR HSSP: P00907; 1A9X.  
 DR InterPro: IPR002474; CPSase\_sm\_chain.  
 DR InterPro: IPR001317; CPS GATase.  
 DR InterPro: IPR000991; GATase 1.  
 DR Pfam: PF00988; CPSase\_sm\_chain; 1.  
 DR Pfam: PF00117; GATase; 1.  
 DR PRINTS: PR00099; CPSGATASE.  
 DR PRINTS: PR00096; GATASE.  
 DR PROSITE: PS00442; GATASE TYPE I; 1.  
 KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;  
 KW Glutamine amidotransferase.  
 FT DOMAIN 1 187  
 FT DOMAIN 188 377  
 FT ACT\_SITE 266 266  
 FT ACT\_SITE 63 63  
 FT CONFLICT 74 77 SVVA -> TVLP (IN REF. 2).  
 FT CONFLICT 127 127 MISSING (IN REF. 2).  
 FT CONFLICT 205 208 MLAS -> ISP (IN REF. 2).  
 FT CONFLICT 237 238 NG -> QR (IN REF. 2).  
 FT CONFLICT 248 248 G -> A (IN REF. 2).  
 FT CONFLICT 345 345 S -> F (IN REF. 2).  
 FT CONFLICT 364 364 S -> F (IN REF. 2).  
 SQ SEQUENCE 377 AA; 40515 MW; BD54P6F6S056BCA2 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 377;  
 Best Local Similarity 60.0%; Pred. No. 66;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 RASENYSYL 10  
 Db 93 RASESLHDYL 102

RESULT 26  
 CARA\_NEIMA STANDARD; PRT; 377 AA.  
 ID CARA\_NEIMA  
 AC Q50983;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain).  
 GN CARA OR NMA0608.  
 OS Neisseria meningitidis (serogroup A).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65639;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=20222556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S., Jagsels K., Leacher S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrall B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";  
 RL Nature 404:502-506(2000).  
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.  
 CC -1- PATHWAY: Arginine biosynthesis.  
 CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CARA FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.  
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 CC -----  
 DR EMBL: AL162753; CAB83898.1; -;  
 DR HSSP: P00907; ICE8.  
 DR InterPro: IPR002474; CPSase\_sm\_chain.  
 DR InterPro: IPR001317; CPS GATase.  
 DR InterPro: IPR000991; GATase 1.  
 DR Pfam: PR00988; CPSase\_sm\_chain; 1.  
 DR Pfam: PF00117; GATase; 1.  
 DR PRINTS: PR00099; CPSGATASE.  
 DR PRINTS: PR00096; GATASE.  
 DR PROSITE: PS00442; GATASE TYPE I; 1.  
 KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;  
 KW Glutamine amidotransferase; Complete proteome.  
 FT DOMAIN 1 186  
 FT DOMAIN 187 377  
 FT ACT\_SITE 266 266  
 FT ACT\_SITE 63 63  
 FT CONFLICT 74 77 SVVA -> TVLP (IN REF. 2).  
 FT CONFLICT 127 127 MISSING (IN REF. 2).  
 FT CONFLICT 205 208 MLAS -> ISP (IN REF. 2).  
 FT CONFLICT 237 238 NG -> QR (IN REF. 2).  
 FT CONFLICT 248 248 G -> A (IN REF. 2).  
 FT CONFLICT 345 345 S -> F (IN REF. 2).  
 FT CONFLICT 364 364 S -> F (IN REF. 2).  
 SQ SEQUENCE 377 AA; 40605 MW; 1C641580B26272 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 377;  
 Best Local Similarity 60.0%; Pred. No. 66;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENITSYL 10  
 |||:|:|  
 Db 93 RASESLHDYL 102

## RESULT 27

OC CARA NEIMB STANDARD; PRT; 377 AA.  
 ID CARA NEIMB  
 AC 09JXX4;  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain).  
 GN CARA OR NMB1849.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 NCBI\_TaxID=491;  
 RX MEDLINE=20175755; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B., Cotton M.D., Uuterkack T.R., Khouiri H., Qin H., Vamathevan J., Smith H.O., Fraser C.M., Moxon E.R., Rappapoli R., Venter J.C.;  
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain M58.";  
 RL Science 287:1809-1815(2000).  
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.  
 CC -1- PATHWAY: Arginine biosynthesis.  
 CC -1- SUBUNIT: Composed of two chains, the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CARA FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.  
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 CC -----  
 CC EMBL; AE002535; AAF42183.1; -.  
 DR HSSP; P00907; ICSO.  
 DR TIGR; NMB1849; -.  
 DR InterPro; IPR002474; CPSase\_sm\_chain.  
 DR InterPro; IPR001317; CPS\_GATase.  
 DR InterPro; IPR000991; GATase\_1.  
 DR Pfam; PF00988; CPSase\_sm\_chain; 1.  
 DR Pfam; PF00117; GATase; 1.  
 DR PRINTS; PR00099; CPSGATASE.  
 DR PRINTS; PR00096; GATASE.  
 DR PROSITE; PS00442; GATASE\_TYPE\_I; 1.  
 KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase;  
 KM Glutamine amidotransferase; Complete proteome.  
 FT DOMAIN 1 186 CPSASE.  
 FT ACT\_SITE 266 266 GLUTAMINE AMIDOTRANSFERASE.  
 SQ SEQUENCE 377 AA; 40587 MW; 36733FC080681670 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 377;  
 Best Local Similarity 60.0%; Pred. No. 66;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENITSYL 10  
 |||:|:|  
 Db 93 RASESLHDYL 102

## RESULT 28

OC DROSOPHILA MELANOGASTER (FRUIT FLY).  
 ID DROSOPHILA MELANOGASTER (FRUIT FLY).  
 AC 09NGX9; 09VZJ0;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Cytochrome P450 302a1, mitochondrial precursor (EC 1.14.-.-) (disembodied protein).  
 GN DIB OR CYP302A1 OR CG12028.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Abail J.F., Aspavanti A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotier P., Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P., Dea Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorelli J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalaal M., Kalush F., Karpen G.H., Ke Z., Kensington J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclebo J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Szallasi Z., Taylor C., Turner R., Venter L., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye Y., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC SEQUENCE FROM N.A.  
 RP CHAVEZ V.M., Marques G., Kobayashi K., Delbecq J.P., Burr J., Natzie J.E., O'Connor M.B.;  
 RT "The Drosophila disembodied gene controls late embryonic morphogenesis and codes for a cytochrome P450 enzyme that regulates embryonic ecdysone levels.";  
 RT Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: REGULATES EMBRYONIC ECDYSONE LEVELS.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +

```
CC oxidized flavoprotein + H(2)O.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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DR EMBL: AE003480; AAF47831.2; -  
DR EMBL: AF237560; AAF60174.1; -  
DR HSSP: P14779; IJPZ.  
DR FlyBase: FBgn0000449; dib.  
DR InterPro: IPR001128; Cytochrome\_P450.  
DR Pfam: PF00067; P450; 1.  
DR PRINTS: PR00385; P450.  
DR PROSITE: PS00086; CYTOCHROME\_P450; 1.  
KM Oxidoreductase; Monooxygenase; Membrane; Heme; Mitochondrion;  
KM Transit peptide.  
FT TRANSIT 1 ?  
FT CHAIN 1 ?  
FT BINDING 434 434 MITOCHONDRION (POTENTIAL).  
FT CONFLICT 186 186 CYTOCHROME\_P450\_302A1.  
FT CONFLICT 205 205 HEME (BY SIMILARITY).  
FT CONFLICT 252 252 C -> S (IN REF. 2).  
FT CONFLICT 255 255 S -> G (IN REF. 2).  
FT CONFLICT 327 327 L -> M (IN REF. 2).  
FT CONFLICT 394 394 R -> K (IN REF. 2).  
FT CONFLICT 394 394 A -> R (IN REF. 2).  
SQ SEQUENCE 489 AA; 55573 MW; AE15A97E79E502B CRC64;

Query Match 59.6%; Score 34; DB 1; Length 489;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NIYSYLP 11  
Db 35 NLNLYLP 41

RESULT 29  
UL06 HSV6U STANDARD; PRT; 662 AA.  
AC P52453;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Varion protein U76.  
GN U76 OR HDLFI.  
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Roseolovirus.  
OX NCBI\_TaxID=10370;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95027704; Pubmed=7941342;  
RA Nicholas J.;  
RT "Nucleotide sequence analysis of a 21-kbp region of the genome of  
RT human herpesvirus-6 containing homologues of human cytomegalovirus  
RT major immediate-early and replication genes.";  
RL Virology 204:738-750(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95266321; Pubmed=7747482;  
RA Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,  
RA Martin M.E., Efethathion S., Craxton M., Macaulay H.A.;  
RT "The DNA sequence of human herpesvirus-6: structure, coding content,  
RT and genome evolution.";  
RL Virology 209:29-51(1995).  
CC -1- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA  
CC PACKAGING.

```
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,  
CC EBV-1 56, EBV BBRL1, HCMV UL104, AND VZV 54.  
CC -----  
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DR EMBL: U13194; AAA68467.1; -  
DR EMBL: X83413; CAAS8368.1; -  
DR InterPro: IPR002660; Herpes\_UL6.  
DR Pfam: PF01763; Herpes\_UL6; 1.  
DR ProDom: PD003210; Herpes\_UL6; 1.  
SQ SEQUENCE 662 AA; 77234 MW; 95D555757B3A7F99 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 662;  
Best Local Similarity 66.7%; Pred. No. 1,2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SENIYSLP 11  
Db 53 SKMLSYLP 61

RESULT 30  
UL06 HSV6Z STANDARD; PRT; 662 AA.  
AC P52454;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Varion protein U76.  
GN U76 OR CB3L.  
OS Human herpesvirus (type 6 / strain Z29) (HHV6).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Roseolovirus.  
OX NCBI\_TaxID=36351;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96195263; Pubmed=8634027;  
RA Lindquister G.J., Inoue N., Allen R.D., Castelli J.W.,  
RA Stamey F.R., Dambaugh T.R., O'Brian J.J., Danovich R.M.,  
RA Frenkel N., Pellet P.E.;  
RT "Restriction endonuclease mapping and molecular cloning of the human  
RT herpesvirus 6 variant B strain Z29 genome.";  
RL Arch. Virol. 141:367-379(1996).  
CC -1- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA  
CC PACKAGING.  
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,  
CC EBV-1 56, EBV BBRL1, HCMV UL104, AND VZV 54.  
CC -----  
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DR EMBL: AF157706; AAB06359.1; -  
DR InterPro: IPR002660; Herpes\_UL6.  
DR Pfam: PF01763; Herpes\_UL6; 1.  
DR ProDom: PD003210; Herpes\_UL6; 1.  
SQ SEQUENCE 662 AA; 77199 MW; 5126392A37C67B90 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 662;  
Best Local Similarity 66.7%; Pred. No. 1,2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SENIYSLP 11

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Db          53 SKNLSYLP 61

RESULT 31
RPO_FKMW    STANDARD; PRT; 1335 AA.
ID_RPO_FKMW
AC P22168;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replication protein (152 kDa protein) (ORF 1) [contains: RNA-
OS directed RNA polymerase (EC 2.7.7.48); Probable helicase].
OS Foxtail mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12179;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374015; PubMed=1840610;
RA Bancroft J.B., Rouleau M., Johnston R., Prins L., Mackie G.A.;
RT "The entire nucleotide sequence of foxtail mosaic virus RNA.";
RL J. Gen. Virol. 72:2173-2181(1991).
CC -1- FUNCTION: RNA-replication. The central part of this protein
CC possibly functions as an ATP-binding helicase.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(n).
CC -----
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CC -----
DR EMBL; M62730; AAA43826.1; -
DR PIR; J01258; J01258.
DR InterPro; IPR001788; RNA_dep_RNApol2.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNApol2; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferrase.
FT NP_BIND 603 610 ATP (POTENTIAL).
SQ SEQUENCE 1335 AA; 152317 MW; D2BCBBA932F49DB9 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 1335;
Best Local Similarity 62.5%; Pred. No. 2,4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 4 ENIYSYLP 11
Db 131 DTIVSYLP 138

RESULT 32
ATP8_DROME STANDARD; PRT; 53 AA.
ID_ATP8_DROME
AC P03932;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTATP8 OR ATP8 OR ATPASE8.
OS Drosophila melanogaster (fruit fly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83245048; PubMed=6408489;

```

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RA de Bruijn M.H.L.;
RT "Drosophila melanogaster mitochondrial DNA, a novel organization and
RT genetic code.";
RL Nature 304:234-241(1983).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (1n) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J01404; AAB59241.1; -
DR EMBL; U37541; AAC47814.1; -
DR PIR; A93307; PWPF8.
DR Pfam; PF0013573; mt_ATPase8.
DR InterPro; IPR001421; ATPase8_mt.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SQ SEQUENCE 53 AA; 6364 MW; 45D2C68AA437FC23 CRC64;

Query Match 57.9%; Score 33; DB 1; Length 53;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SENIYSYLP 11
Db 25 STIVSYLP 33

RESULT 33
ATP8_DROVA STANDARD; PRT; 53 AA.
ID_ATP8_DROVA
AC P03933;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTATP8 OR ATP8 OR ATPASE8.
OS Drosophila yakuba (fruit fly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=2317.6 Ivory Coast;
RX MEDLINE=86089137; PubMed=3001325;
RA Clary D.O., Wolstenholme D.R.;
RT "The mitochondrial DNA molecular of Drosophila yakuba: nucleotide
RT sequence, gene organization, and genetic code.";
RL J. Mol. Evol. 22:252-271(1985).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246544; PubMed=6306579;
RA Clary D.O., Wolstenholme D.R.;
RT "Nucleotide sequence of a segment of Drosophila mitochondrial DNA
RT that contains the genes for cytochrome c oxidase subunits II and III
RT and ATPase subunit 6.";
RL Nucleic Acids Res. 11:4211-4227(1983).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (1n) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBCELLULAR LOCATION: Membrane-bound.

```

CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.  
CC -----  
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CC -----  
DR EMBL: X03240; CAA26988.1; -;  
DR EMBL: X00924; CAA25441.1; -;  
DR PIR: A93477; PMF88Y.  
DR PIR: D25797; D25797.  
DR FLYBase: FBgn0013178; Dyak\mt:ATPase8.  
DR InterPro: IPR001421; ATPase8\_mit.  
DR Pfam: PF00895; ATP-synt\_8\_1.  
KW Hydrogen ion transport; Cc(0); Mitochondrion; Transmembrane.  
SQ SEQUENCE 53 AA; 6337 MW; 6741C69A7B57EP9B CRC64;  
  
QY Query Match 57.9%; Score 33; DB 1; Length 53;  
Best Local Similarity 66.7%; Pred. NO. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Db 3 SENIYSTLP 11  
25 SINYSTYP 33  
  
RESULT 34  
ID KVIH HUMAN STANDARD; PRT; 107 AA.  
AC P01556;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region CAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75075135; PubMed=4216454;  
RA Milstein C.P.; Deverson E.V.;  
RT "primary structure of kappa light chain from a human myeloma  
RT protein."  
RL Eur. J. Biochem. 49:377-391 (1974).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
CC MARKER.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA-PROTEIN.  
DR PIR: A01864; KIHUAR.  
DR HSSP: P80362; 1WTL.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
KW Immunoglobulin V region; Glycoprotein.  
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;  
  
QY Query Match 57.9%; Score 33; DB 1; Length 107;  
Best Local Similarity 70.0%; Pred. NO. 27;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Db 1 RASENIYSTL 10  
24 RASQISSTYL 33  
  
RESULT 35  
ID KVIH HUMAN  
AC P01556;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Matanabe S.; Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
DR PIR: A01868; KIHUHU.  
DR HSSP: P80362; 1WTL.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A616D8D0618 CRC64;  
  
QY Query Match 57.9%; Score 33; DB 1; Length 108;  
Best Local Similarity 70.0%; Pred. NO. 28;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Db 1 RASENIYSTL 10  
24 RASQISSTYL 33  
  
RESULT 36  
ID CY21 RHOPA STANDARD; PRT; 114 AA.  
AC P00050;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cytochrome C2.  
OS Rhodopseudomonas palustris (strain ATCC 17001 / 2.1.6).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Bradyrhizobium group; Rhodopseudomonas.  
OX NCBI\_TaxID=1076;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79199667; PubMed=221822;  
RA Ambler R.P.; Daniel M.; Hermoso J.; Meyer T.E.; Bartsch R.G.;  
RA Kamen M.D.;  
RT "Cytochrome c2 sequence variation among the recognised species of  
RT purple nonsulfur photosynthetic bacteria."  
RL Nature 278:659-660 (1979).  
RN [2]  
RP SEQUENCE. AND BLOCKAGE OF N-TERMINUS.  
RA Ambler R.P.; Meyer T.E.; Murray S.;  
RL Submitted (DEC-1974) to the PIR data bank.  
CC -1- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,  
CC PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR

TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION  
 PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN  
 AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.

CC PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN  
 CC AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.  
 CC PIR; A00082; CCRFP2.  
 DR HSP; P00094; 1C2R.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR003088; Cyt\_C1.  
 DR InterPro; IPR002327; Cyt\_C1AB.  
 DR Pfam; PF00034; Cytochrome\_c; 1.  
 DR PRINTS; PR00604; CYTOCHROME\_C1.  
 DR ProDom; PD000375; Cyt\_C1AB; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
 KW Electron transport; Photosynthesis; Heme.  
 KM MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT BINDING 13 13 HEME (COVALENT).  
 FT BINDING 16 16 HEME (COVALENT).  
 FT METAL 17 17 IRON (HEME AXIAL LIGAND).  
 FT METAL 93 93 IRON (HEME AXIAL LIGAND).  
 SQ SEQUENCE 114 AA; 12208 MW; 13657331CDD4464 CRC64;

Query Match 57.9%; Score 33; DB 1; Length 114;  
 Best Local Similarity 75.0%; Pred. No. 29;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ENIYSYLP 11  
 DB 61 ENIAYLP 68

RESULT 37  
 KVSH\_MOUSE STANDARD; PRT; 117 AA.  
 ID KVSH\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01641;  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 1g kappa chain V-V region MOPC 173B precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81064681; PubMed=6777049;  
 RA Max E.E., Seidman J.G., Miller H., Leder P.;  
 RT "Variation in the crossover point of kappa immunoglobulin gene V-J  
 recombination: evidence from a cryptic gene.";  
 RL Cell 21:793-799(1980).  
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 CC -----  
 CC EMBL; K00880; AAA39031.1; -.  
 DR PIR; A01924; KVM53B.  
 DR HSP; P01607; 1REI.  
 DR InterPro; IPR003006; 1g\_MHC.  
 DR InterPro; IPR003596; 1g\_V.  
 DR Pfam; PF00047; 1g; 1.  
 DR SMART; SMO0406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 KM SIGNAL 1 22  
 FT CHAIN 23 117 IG KAPPA CHAIN V-V REGION MOPC 173B.  
 FT DOMAIN 23 45 FRAMEWORK-1.  
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 57 71 FRAMEWORK-2.  
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 79 110 FRAMEWORK-3.  
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 45 110 BY SIMILARITY.  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 12954 MW; 24B3D4B9AC2E4D6C CRC64;

Query Match 57.9%; Score 33; DB 1; Length 117;  
 Best Local Similarity 60.0%; Pred. No. 30;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASENIYSYL 10  
 DB 46 RASQDHGHL 55

RESULT 38  
 CY22\_RHOCE STANDARD; PRT; 121 AA.  
 ID CY22\_RHOCE STANDARD; PRT; 121 AA.  
 AC P81154;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c2, iso-2 (C552).  
 OS Rhodospirillum rubrum (Rhodocycla rubra).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;  
 OC Rhodospirillum.  
 NCBI\_TaxID=34018;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 43720;  
 RX MEDLINE=98323574; PubMed=9659396;  
 RA Samyn B., Fitch J., Weyer T.E., Guseanovich M.A., van Beunnen J.J.;  
 RT "Purification and primary structure analysis of two cytochrome c2  
 isozymes from the purple phototrophic bacterium Rhodospirillum  
 rubrum.";  
 RT Biochim. Biophys. Acta 1384:345-355 (1998).  
 RL Biochim. Biophys. Acta 1384:345-355 (1998).  
 CC -1- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,  
 PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR  
 TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION  
 PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN  
 AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA. THE REDOX  
 POTENTIAL OF THIS CYTOCHROME IS 293 mV.  
 CC -----  
 CC -1- SIMILARITY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.  
 CC -----  
 CC HSP; P00083; 1CRY.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR003088; Cyt\_C1.  
 DR InterPro; IPR002327; Cyt\_C1AB.  
 DR Pfam; PF00034; Cytochrome\_c; 1.  
 DR PRINTS; PR00604; CYTOCHROME\_C1.  
 DR ProDom; PD000375; Cyt\_C1AB; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
 KW Electron transport; Photosynthesis; Heme.  
 KM BINDING 15 15 HEME (COVALENT).  
 FT BINDING 18 18 HEME (COVALENT).  
 FT METAL 19 19 IRON (HEME AXIAL LIGAND).  
 FT METAL 98 98 IRON (HEME AXIAL LIGAND).  
 SQ SEQUENCE 121 AA; 13035 MW; 889393C3C6022430A CRC64;

Query Match 57.9%; Score 33; DB 1; Length 121;  
 Best Local Similarity 75.0%; Pred. No. 31;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ENIYSYLP 11  
 DB 66 ENIAYLP 73

RESULT 39  
 YVDE\_LACLC STANDARD; PRT; 168 AA.  
 ID YVDE\_LACLC STANDARD; PRT; 168 AA.  
 AC P22347;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yvde homolog (Fragment).

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OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCDO 763;
RX MEDLINE=91241789; PubMed=1674656;
RA Nardi M., Chopin M.-C., Chopin A., Cals M.M., Gripon J.-C.;
RT "Cloning and DNA sequence analysis of an X-prolyl dipeptidyl
  aminopeptidase gene from Lactococcus lactis subsp. lactis NCDO 763.";
RL Appl. Environ. Microbiol. 57:45-50(1991).
CC -1- SIMILARITY: TO E.COLI YCUL.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
  frameshift in position 165.
CC -----
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CC -----
CC EMBL; M35865; AAA25208.1; ALT_FRAME.
CC DR Hypothetical protein.
CC FT NON TER 188 188
SQ SEQUENCE 188 AA; 21148 MW; 381784FP912354DB CRC64;

Query Match 57.9%; Score 33; DB 1; Length 188;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SENIYSYLP 11
   :|:|:|:|
Db 50 TENIKYLP 58

RESULT 40
EFTS_BUCAI STANDARD; PRT; 268 AA.
ID PF5732;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Elongation factor Ts (EF-Ts).
TSP OR BU232.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
  symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigerobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
  Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: ASSOCIATES WITH THE EF-TU GDP COMPLEX AND INDUCES THE
  EXCHANGE OF GDP TO GTP, IT REMAINS BOUND TO THE AMINOACYL-TRNA.
CC EF-TU GTP COMPLEX UP TO THE GTP HYDROLYSIS STAGE ON THE RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE EF-TS FAMILY.
CC -----
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CC -----
CC EMBL; AP001118; BAB12947.1; -.

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DR HSSP; P02997; 1EFU.
DR InterPro; IPR001816; EF_TS.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PR00627; UBA; 1.
DR Pfam; PF00889; EF_TS; 1.
DR TIGRfam; TIGR00116; tsf; 1.
DR PROSITE; PS01126; EF_TS_1; 1.
DR PROSITE; PS01127; EF_TS_2; 1.
KM Elongation factor; Protein biosynthesis; Complete proteome.
FT SITE 81 84
   INVOLVED IN MG++ ION DISLOCATION FROM EF-
   TU (BY SIMILARITY).
SQ SEQUENCE 268 AA; 30266 MW; DCD46DA293BDB064 CRC64;

Query Match 57.9%; Score 33; DB 1; Length 268;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 ENIYSYL 10
   ||:|:|
Db 142 ENIFSYL 148

Search completed: July 18, 2003, 15:07:18
Job time : 7.82 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:40 ; Search time 28.38 Seconds  
(without alignments)  
79.863 Million cell updates/sec

Title: US-10-007-790-8  
Perfect score: 57  
Sequence: 1 RASENTSYLP 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	87.7	234	11	Q8VCP0 mus musculus
2	41	71.9	656	16	Q82B89 Q82B89 yersinia pe
3	40	70.2	1628	4	Q9HCL7 Q9HCL7 homo sapien
4	40	70.2	2406	4	Q9BZS0 Q9BZS0 homo sapien
5	39	68.4	2282	11	Q61479 Q61479 mus musculus
6	39	68.4	2310	3	Q14002 Q14002 schizosacch
7	38	66.7	474	2	Q9FNU3 Q9FNU3 mytilus ed
8	38	66.7	1678	13	Q8UW88 Q8UW88 oryzias lat
9	37	64.9	214	10	Q9XEV5 Q9XEV5 oryza sativ
10	37	64.9	230	8	Q921L6 Q921L6 rickettsia
11	37	64.9	256	6	Q9MTC3 Q9MTC3 zea mays (m
12	37	64.9	478	2	Q9FAU4 Q9FAU4 microscilla
13	37	64.9	597	10	Q9M2G0 Q9M2G0 arabidopsis
14	37	64.9	602	10	Q8W0Z9 Q8W0Z9 arabidopsis
15	37	64.9	833	12	Q69403 Q69403 pseudorabie
16	37	64.9	1008	3	Q74672 Q74672 pneumocysti

17	36	63.2	88	2	Q9XSH7 Q9XSH7 helicobacte
18	36	63.2	184	17	Q97WNS Q97WNS sulfolobus
19	36	63.2	237	11	Q9DAA4 Q9DAA4 mus musculus
20	36	63.2	242	16	Q826A4 Q826A4 salmonele
21	36	63.2	434	12	Q8V506 Q8V506 monkeypox v
22	36	63.2	459	17	Q8U483 Q8U483 pyrococcus
23	36	63.2	460	3	Q9Y761 Q9Y761 kluyveromyc
24	36	63.2	545	17	Q975A8 Q975A8 sulfolobus
25	36	63.2	567	16	Q99UK9 Q99UK9 staphylococ
26	36	63.2	581	16	Q97G07 Q97G07 clostridium
27	36	63.2	611	16	Q9KV19 Q9KV19 vibrio chol
28	36	63.2	617	16	Q97SRI Q97SRI streptococ
29	36	63.2	637	17	Q97Z76 Q97Z76 sulfolobus
30	36	63.2	1067	16	Q92FQ3 Q92FQ3 listeria in
31	36	63.2	1068	16	Q8YAO9 Q8YAO9 listeria mo
32	36	63.2	1114	5	Q05352 Q05352 entamoeba h
33	35	61.4	109	11	Q920B6 Q920B6 mus musculus
34	35	61.4	120	17	Q9HLG1 Q9HLG1 thermoplas
35	35	61.4	140	10	Q9AST6 Q9AST6 arabidopsis
36	35	61.4	180	17	P95293 P95293 methanobac
37	35	61.4	200	9	Q96GQ3 Q96GQ3 roseophag
38	35	61.4	270	5	Q962N2 Q962N2 plasmodium
39	35	61.4	298	11	Q9QYF0 Q9QYF0 mus musculus
40	35	61.4	357	16	Q83275 Q83275 treponema p
41	35	61.4	369	3	Q9Y7Y5 Q9Y7Y5 schizosacch
42	35	61.4	421	5	Q9U6S0 Q9U6S0 strongyloce
43	35	61.4	441	12	Q9YVJ2 Q9YVJ2 melanooplus
44	35	61.4	467	11	Q9D489 Q9D489 mus musculus
45	35	61.4	470	5	Q05351 Q05351 entamoeba h

#### ALIGNMENTS

RESULT 1  
ID Q8VCP0 PRELIMINARY; PRT; 234 AA.  
AC Q8VCP0;  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 21, Last annotation update)  
DE Hypothetical 25.7 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019474; AAH19474.1; -  
DR InterPro; IPR003597; IG.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; igf\_2.  
DR SMART; SM00409; IGF\_2.  
DR SMART; SM00407; IGF1; 1.  
DR SMART; SM00406; IGF; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 87.7%; Score 50; DB 11; Length 234;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENTSYLP 10  
DB 44 RASENTSYLP 53

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RESULT 2
Q8ZB89          PRELIMINARY;      PRT;      656 AA.
AC  Q8ZB89
DT  01-MAR-2002 (TEMBLrel. 20, Created)
DT  01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE  2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16).
GN  CPDB OR YP03330.
OS  Yersinia pestis.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Yersinia.
OX  NCBI_TaxID=632;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CO-92 / BIOVAR ORIENTALIS;
RA  MEDLINE=21470413; PubMed=11586360;
RA  Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA  Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA  Baker S., Baaham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA  Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA  Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA  Leather S., Moulé S., Oyston P.C.F., Quail M., Rutherford K.,
RA  Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT  "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL  Nature 413:523-527(2001).
DR  EMBL: AJ14157; CAC92759.1; -
DR  InterPro: IPR002224; 5_nucleotidase.
DR  InterPro: IPR004843; M-pestase.
DR  InterPro: IPR004844; S/T_phosphatase.
DR  Pfam: PF02872; 5_nucleotidase; 1.
DR  PRINTS: PRO1607; APYRASEFAMILY.
DR  PROSITE: PS00785; 5_NUCLEOTIDASE_1; 1.
DR  PROSITE: PS00785; 5_NUCLEOTIDASE_2; 1.
KW  Hydrolyase; Complete proteome.
SQ  SEQUENCE 656 AA; 72095 MW; FEF21AF90E9DF13F CRC64;

Query Match          71.9%; Score 41; DB 16; Length 656;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY  1 RASENIYSYL 10
Db  366 KASDNMYSYL 375

RESULT 3
Q9HCL7          PRELIMINARY;      PRT;      1628 AA.
AC  Q9HCL7
DT  01-MAR-2001 (TEMBLrel. 16, Created)
DT  01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT  01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE  KIAA1555 protein (Fragment).
GN  KIAA1555.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=20450683; PubMed=10997877;
RA  Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.;
RT  "Prediction of the coding sequences of unidentified human genes.
RT  XVIII. The complete sequences of 100 new cDNA clones from brain which
RT  code for large proteins in vitro.";
RL  DNA Res. 7:273-281(2000).
DR  EMBL: AB046775; BAB13381.1; -
DR  HSSP: P15822; 1BBO.
DR  InterPro: IPR000822; Znf_C2H2.
DR  Pfam: PF00096; Zf-C2H2; 2.
DR  SMART: SM00355; Znf_C2H2; 2.

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DR  PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
DR  PROSITE: PS00157; ZINC_FINGER_C2H2_2; 2.
KW  DNA-binding; Metal-binding; Zinc-finger.
FT  NON TER
SQ  SEQUENCE 1628 AA; 174427 MW; 4E23A34360A3D939 CRC64;

Query Match          70.2%; Score 40; DB 4; Length 1628;
Best Local Similarity 63.6%; Pred. No. 84;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  1 RASENIYSYL 11
Db  2171 RTEENIFSHLP 2181

RESULT 4
Q9BZ50          PRELIMINARY;      PRT;      2406 AA.
AC  Q9BZ50
DT  01-JUN-2001 (TEMBLrel. 17, Created)
DT  01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT  01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE  Kappa B and V(D)J recombination signal sequences binding protein.
GN  KBC.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=BRIN, AND THYMOCYTES;
RX  MEDLINE=21100880; PubMed=1161801;
RA  Hicar M.D., Liu Y., Allen C.E., Wu L.C.;
RT  "Structure of the Human Zinc Finger Protein HIVEP3: Molecular Cloning,
RT  Expression, Exon-Intron Structure, and Comparison with Paralogous
RT  Genes HIVEP1 and HIVEP2.";
RL  Genomics 71:89-100(2001).
DR  EMBL: AF278765; AAK01082.1; -
DR  HSSP: P15822; 1BBO.
DR  InterPro: IPR002034; AIPM/HcIt_synch.
DR  InterPro: IPR000822; Znf_C2H2.
DR  Pfam: PF00096; Zf-C2H2; 5.
DR  SMART: SM00355; Znf_C2H2; 5.
DR  PROSITE: PS00815; AIPM_HOMOCIT_SYNTH_1; UNKNOWN_1.
DR  PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR  PROSITE: PS00157; ZINC_FINGER_C2H2_2; 5.
KW  DNA-binding; Metal-binding; Zinc-finger.
SQ  SEQUENCE 2406 AA; 259381 MW; 7F496F2BBF3AE93F CRC64;

Query Match          70.2%; Score 40; DB 4; Length 2406;
Best Local Similarity 63.6%; Pred. No. 13e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  1 RASENIYSYL 11
Db  2171 RTEENIFSHLP 2181

RESULT 5
Q61479          PRELIMINARY;      PRT;      2282 AA.
AC  Q61479
DT  01-NOV-1996 (TEMBLrel. 01, Created)
DT  01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT  01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE  DNA binding protein RC.
GN  KRC OR RC.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.

```

RC STRAIN=BALE/C; TISSUE=THYMOCYTE;  
RX MEDLINE=97001141; PubMed=8812474;  
RA Wu L.C., Liu Y., Stradmann J., Mak C.H., Lee B., Li Z., Yu C.Y.;  
RT "The mouse DNA binding protein Rc for the kappa B motif of  
RT transcription and for the V(D)J recombination signal sequences  
RT contains composite DNA-protein interaction domains and belongs to a  
RT new family of large transcriptional proteins.";  
RL Genomics 35:415-424(1996).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: I46815; ABA04884.1; -.  
DR HSSP: P15822; 1BBO.  
DR MGD: MGI:106589; K7C.  
DR InterPro: IPR000822; Znf\_C2H2.  
DR Pfam: PF00096; Zf\_C2H2\_5.  
DR PRINTS: PR00048; ZINC\_FINGER.  
DR SMART: SM00355; Znf\_C2H2\_5.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
DR PROSITE: PS0157; ZINC\_FINGER\_C2H2\_2; 5.  
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.  
SQ SEQUENCE 2282 AA; 246919 MW; E4404B8C8C9F7B2C CRC64;

Query Match 68.4%; Score 39; DB 11; Length 2282;  
Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENITYSLP 11  
Db 2125 RSEENLFSLP 2135

RESULT 6  
O14002  
AC 014002 PRELIMINARY; PRT; 2310 AA.  
DT 01-JUN-1998 (TEMBLrel. 06, Created)  
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)  
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
DE Putative sensor-like histidine kinase C27E2.09 (EC 2.7.3.-).  
GN SPAC27E2.09.  
OS Schizosaccharomyces pombe (Fission Yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.  
DR EMBL: Z98978; CAB1683.1; -.  
DR HSSP: P06657; 2CHF.  
DR InterPro: IPR003594; ATPbind\_ATPase.  
DR InterPro: IPR004358; Bact\_sens\_pr\_C.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003018; GAF.  
DR InterPro: IPR003661; His\_kin.  
DR InterPro: IPR004359; His\_kin\_sig.  
DR InterPro: IPR002114; Hpr\_Serp\_site.  
DR InterPro: IPR001610; PAC.  
DR InterPro: IPR000014; PAS domain.  
DR InterPro: IPR001789; Response\_reg.  
DR Pfam: PF01590; GAF\_1.  
DR Pfam: PF02518; HATPase\_C; 1.  
DR Pfam: PF00069; Pkinase\_1.  
DR Pfam: PF00072; response\_reg; 1.  
DR Pfam: PF00512; signal; 1.  
DR PRINTS: PR00344; BCTRLSENSOR.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR ProDom: PD000039; Response\_reg; 1.  
DR SMART: SM00065; GAF\_1.  
DR SMART: SM00387; HATPase\_C; 1.

DR SMART; SM00388; HSKA; 1.  
DR SMART; SM00086; PAC; 1.  
DR SMART; SM00091; PAS; 1.  
DR SMART; SM00448; REC; 1.  
DR TIGRfam: TRG00229; sensory box; 1.  
DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00589; PTS\_HPR\_SER; UNKNOWN\_1.  
KW Hypothetical protein; Sensory transduction; Transferase; Kinase;  
KM Transmembrane.  
FT TRANSMEM 81 101 POTENTIAL.  
FT TRANSMEM 118 138 POTENTIAL.  
FT TRANSMEM 218 238 POTENTIAL.  
FT TRANSMEM 443 463 POTENTIAL.  
FT TRANSMEM 509 529 POTENTIAL.  
FT TRANSMEM 540 560 POTENTIAL.  
FT TRANSMEM 624 644 POTENTIAL.  
FT TRANSMEM 662 682 POTENTIAL.  
FT TRANSMEM 687 707 POTENTIAL.  
FT TRANSMEM 965 985 POTENTIAL.  
FT TRANSMEM 1064 1084 POTENTIAL.  
FT TRANSMEM 1116 1136 POTENTIAL.  
FT TRANSMEM 1164 1184 POTENTIAL.  
FT TRANSMEM 1292 1312 POTENTIAL.  
FT TRANSMEM 1548 1568 POTENTIAL.  
FT TRANSMEM 1578 1598 POTENTIAL.  
FT TRANSMEM 1944 1964 POTENTIAL.  
FT TRANSMEM 976 979 POLY-TYR.  
FT DOMAIN 1108 1111 POLY-LEU.  
SQ SEQUENCE 2310 AA; 264619 MW; 5A49120DB37E299D CRC64;

Query Match 68.4%; Score 39; DB 3; Length 2310;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASENITYSLP 11  
Db 876 SSSNVYDLP 885

RESULT 7  
ID 09FAU3 PRELIMINARY; PRT; 474 AA.  
AC 09FAU3;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
DE DNA gyrase B subunit (Fragment).  
GN GYRB.  
OS Myroides odoratus.  
OC Bacteria; CPB group; Flavobacteriia; Myrioides group; Myrioides.  
OX NCBI\_TaxID=256;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IFO14945;  
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;  
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga like  
RT bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum  
RT maritimum comb. nov. and Haerentibaculum ovolyticus comb. nov., and  
RT two new species.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING  
CC -1- OF DOUBLE-STRANDED DNA.  
CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.  
DR EMBL: AB034239; BAB12497.1; -.  
DR HSSP: P06982; 1AU6.  
DR InterPro: IPR003594; ATPbind\_ATPase.  
DR InterPro: IPR002936; DNAPrim\_toprim.  
DR InterPro: IPR001241; DNA\_topoisomII.  
DR Pfam: PF00204; DNA\_gyraseB; 1.  
DR Pfam: PF02518; HATPase\_C; 1.  
DR Pfam: PF01751; Toprim; 1.  
DR PRINTS: PR00418; TP12FAMILY.  
DR SMART; SM00433; TOP2c; 1.

DR PROSITE; PS00177; TOPOISOMERASE II; 1.  
 KM ATP-binding; Isomerase; Topoisomerase.  
 FT NON\_TER 1  
 FT NON\_TER 474 474  
 SQ SEQUENCE 474 AA; 53012 MW; SE9DA485E2304A81 CRC64;

Query Match 66.7%; Score 38; DB 2; Length 474;  
 Best Local Similarity 87.5%; Pred. No. 53;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SENIYSYL 10  
 DB 165 SENIYSYV 172

## RESULT 8

ID 08UW88 PRELIMINARY; PRT; 1678 AA.  
 AC 08UW88;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Vitellinogenin I.  
 GN OL-VITL.  
 OS Oryzias latipes (Medaka fish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.  
 NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Arai Y., Kim B., Nishikawa T., Shiraiishi H.;  
 RT "vitellinogenin I cDNA in Oryzias latipes";  
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AB064320; BAB79696.1; -  
 DR InterPro; IPR001747; Lipid\_transprt\_N.  
 DR InterPro; IPR001846; VWF\_D\_  
 DR Pfam; PF01347; Vitellinogenin\_N\_1.  
 DR Pfam; PF00094; vwd; 1.  
 DR SMART; SM00216; vwd; 1.  
 SQ SEQUENCE 1678 AA; 185552 MW; 6073384BFF25D27 CRC64;

Query Match 66.7%; Score 38; DB 13; Length 1678;  
 Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 DB 1322 RSAEKYDYDMP 1332

## RESULT 9

ID 09XEV5 PRELIMINARY; PRT; 214 AA.  
 AC 09XEV5;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE Hypothetical 23.5 kDa protein.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Llaça V., Lou A., Young S., Messing J.;  
 RT "Microsytetry in a gene desert region in maize, sorghum, and rice";  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF119222; AAD27682.1; -  
 KM Hypothetical protein.

SQ SEQUENCE 214 AA; 23503 MW; 4CF88225B36FAE4C CRC64;  
 Query Match 64.9%; Score 37; DB 10; Length 214;  
 Best Local Similarity 63.6%; Pred. No. 35;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 DB 167 RASENISSFP 177

## RESULT 10

ID 0921L6 PRELIMINARY; PRT; 230 AA.  
 AC 0921L6;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein RC0404.  
 GN RC0404.  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MALISH 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
 RL Science 293:2093-2098(2001).  
 DR EMBL; AB08604; AA02942.1; -  
 DR InterPro; IPR002725; DUF45.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF01863; DUF45; 1.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 230 AA; 26825 MW; F7547039385EA74 CRC64;

Query Match 64.9%; Score 37; DB 16; Length 230;  
 Best Local Similarity 54.5%; Pred. No. 38;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASENIYSYLP 11  
 DB 220 RINGKNLSYFP 230

## RESULT 11

ID 09MTC3 PRELIMINARY; PRT; 256 AA.  
 AC 09MTC3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE URF 4 (Fragment).  
 OS Zea mays (Maize).  
 OG Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Zea.  
 NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pallard M., Sederoff R.R., Levings C.S. III;  
 RT "Nucleotide sequence of the S-1 mitochondrial Dna from the cytoplasm  
 RT of maize";  
 RL EMBO J. 4:1125-1128(1985).  
 DR EMBL; X02451; CAB57810.1; -  
 KM Mitochondrion.  
 FT NON\_TER 1 1

SQ SEQUENCE 256 AA; 29308 MW; DAFA69F803CAB93 CRC64;  
 Query Match 64.9%; Score 37; DB 8; Length 256;  
 Best Local Similarity 60.0%; Pred. No. 43;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASENIYSYL 10  
 ||:||||:  
 Db 30 RATDNLVSHL 39

RESULT 12  
 Q9FAU4 PRELIMINARY; PRT; 478 AA.  
 AC Q9FAU4;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE DNA gyrase B subunit (Fragment).  
 GN GYRB.  
 OS Microscilla marina.  
 OC Bacteria; CF8 group; Flexibacter group; Microscilla.  
 NC NCB1\_TaxID=1027;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCIMB1400;  
 RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;  
 RT "Phylogenetic analysis and taxonomic study of marine Cytophaga like  
 RT bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum  
 RT multium comb. nov. and Haerentibaculum ovaliticus comb. nov., and  
 RT two new species.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING  
 CC OF DOUBLE-STRANDED DNA.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.  
 DR EMBL; AB034238; BAB12496.1; -.  
 DR HSSP; P06982; 1A6.  
 DR InterPro; IPR001757; ATPase\_E1-E2.  
 DR InterPro; IPR003594; ATPbind\_ATPase.  
 DR InterPro; IPR002936; DNAPrim\_topim.  
 DR InterPro; IPR001241; DNA\_topoisom.  
 DR Pfam; PF00204; DNA\_gyraseB; 1.  
 DR Pfam; PF02518; HATPase\_C; 1.  
 DR Pfam; PF01751; Toprim; 1.  
 DR PRINTS; PR00418; TP12FAMILY.  
 DR SMART; SM00433; TOP2C; 1.  
 DR PROSITE; PS00154; ATPase\_E1\_E2; UNKNOWN\_1.  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; 1.  
 KW ATP-binding; Isomerase; Topoisomerase.  
 FT NON TER 1 1  
 FT NON TER 478 478  
 SQ SEQUENCE 478 AA; 53421 MW; D15062145A1EAD7 CRC64;

Query Match 64.9%; Score 37; DB 2; Length 478;  
 Best Local Similarity 75.0%; Pred. No. 84;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SENIYSYL 10  
 ||:||||:  
 Db 164 SENVSYV 171

RESULT 13  
 Q9M2G0 PRELIMINARY; PRT; 597 AA.  
 AC Q9M2G0;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Hypothetical 66.1 kDa protein.  
 GN F14P22.150.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,  
 RA Lemcke K., Mayer K.F.X., Quettier F., Salanoubat M.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL137082; CAB68194.1; -.  
 DR InterPro; IPR002106; ATRNA\_ligaseII.  
 DR InterPro; IPR005135; Exo\_endo\_phos.  
 DR Pfam; PF03372; Exo\_endo\_phos\_1.  
 DR PROSITE; PS00179; AA\_TRNA\_LIGASE\_II\_1; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 66113 MW; 67301789A3C83151 CRC64;

Query Match 64.9%; Score 37; DB 10; Length 597;  
 Best Local Similarity 70.0%; Pred. No. 11e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASENISYLP 11  
 ||:||||:  
 Db 261 ASSDIYSYCP 270

RESULT 14  
 Q8M0Z9 PRELIMINARY; PRT; 602 AA.  
 AC Q8M0Z9;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE AT3G58560/F14P22.150.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,  
 RA Carrinci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai U., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
 RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RT "Arabidopsis cDNA clones.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF462845; AAL58932.1; -.  
 DR InterPro; IPR002106; ATRNA\_ligaseII.  
 DR InterPro; IPR005135; Exo\_endo\_phos.  
 DR Pfam; PF03372; Exo\_endo\_phos\_1.  
 DR PROSITE; PS00179; AA\_TRNA\_LIGASE\_II\_1; UNKNOWN\_1.  
 SQ SEQUENCE 602 AA; 66761 MW; 233754749BCE74DC CRC64;

Query Match 64.9%; Score 37; DB 10; Length 602;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASENISYLP 11  
 ||:||||:  
 Db 261 ASSDIYSYCP 270

RESULT 15  
 Q69403 PRELIMINARY; PRT; 833 AA.  
 AC Q69403;

DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Helicase.  
 GN ULS.  
 OS Pseudorabies virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxId=10345;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=INDIANA-FUNKHAUSER;  
 RX MEDLINE=94303212; PubMed=8030256;  
 RA Dean H.J., Cheung A.K.;  
 RT "Identification of the pseudorabies virus UL4 and ULS (helicase)  
 RT genes";  
 RL Virology 202:962-967(1994).  
 DR EMBL; L20708; AA50986.1; -;  
 DR InterPro; IPR003840; Herpes\_helicase.  
 DR Pfam; PF02689; Herpes\_Helicase; 1.  
 SQ SEQUENCE 833 AA; 92016 MW; 8DFC78C00B7C9BD CRC64;

Query Match 64.9%; Score 37; DB 12; Length 833;  
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASEN1SYLP 10  
 Db 263 RASEN1LTYL 292

RESULT 16  
 ID 074672 PRELIMINARY; PRT: 1008 AA.  
 AC 074672;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE Major surface glycoprotein (Fragment).  
 GN MSG.  
 OS Pneumocystis carinii f. sp. hominis.  
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;  
 OC Pneumocystis.  
 OX NCBI\_TaxId=42068;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94314421; PubMed=7518806;  
 RA Garbe T.R., Stringer J.R.;  
 RT "Molecular characterization of clustered variants of genes encoding  
 RT major surface antigens of human Pneumocystis carinii";  
 RL Infect. Immun. 62:3092-3101(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98380374; PubMed=9712777;  
 RA Mei Q., Turner R.E., Sorial V., Kivington D., Angus C.W.,  
 RA Kovacs J.A.;  
 RT "Characterization of major surface glycoprotein genes of human  
 RT Pneumocystis carinii and high-level expression of a conserved  
 RT region";  
 RL Infect. Immun. 66:4268-4273(1998).  
 DR EMBL; AF033212; AAC34975.1; -;  
 DR InterPro; IPR003330; MSG.  
 DR Pfam; PF02349; MSG; 7.  
 FT NON TER 1  
 SQ SEQUENCE 1008 AA; 114617 MW; 04DAEB1093B1AF81 CRC64;

Query Match 64.9%; Score 37; DB 3; Length 1008;  
 Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASEN1SYLP 11  
 Db 243 KSHEDCEYLP 258

RESULT 17  
 ID 09X5H7 PRELIMINARY; PRT: 88 AA.  
 AC 09X5H7;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE HELA.  
 GN HELA.  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxId=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43504;  
 RX MEDLINE=99214098; PubMed=10198012;  
 RA McGee D.J., May C.A., Garner R.M., Himpel J.M., Mobley H.L.T.;  
 RT "Isolation of Helicobacter pylori genes that modulate urease  
 RT activity";  
 RL J. Bacteriol. 181:2477-2484(1999).  
 DR EMBL; AF125214; AAD27694.1; -;  
 SQ SEQUENCE 88 AA; 10190 MW; 6C301645517BD2B3 CRC64;

Query Match 63.2%; Score 36; DB 2; Length 88;  
 Best Local Similarity 62.5%; Pred. No. 21;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 EN1SYLP 11  
 Db 72 EN1KYVP 79

RESULT 18  
 ID 097WN5 PRELIMINARY; PRT: 184 AA.  
 AC 097WN5;  
 DT 01-OCT-2001 (TReMBLrel. 18, Created)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
 DE Hypothetical protein SSO2176.  
 GN SSO2176.  
 OS Sulfolobus solfataricus.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxId=2287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
 RX MEDLINE=21332286; PubMed=11427726;  
 RA She Q., Singh R.K., Contaloni F., Zivanovic Y., Allard G.,  
 RA Aayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,  
 RA De Moers A., Erasuo G., Fletcher C., Gordon P.M.K.,  
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
 RA Charlebois R.A., Doelittle W.F., Duguet M., Gaasterland T.,  
 RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;  
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
 DR EMBL; AE006823; AAK42351.1; -;  
 KW Hypothetical protein: Complete proteome.  
 SQ SEQUENCE 184 AA; 21050 MW; 555PF2EBED172D7 CRC64;

Query Match 63.2%; Score 36; DB 17; Length 184;  
 Best Local Similarity 77.8%; Pred. No. 47;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEN1SYLP 11  
 Db 155 SP1SYLP 163

RESULT 19  
 Q9DAA4 PRELIMINARY; PRT; 237 AA.  
 ID Q9DAA4  
 AC Q9DAA4  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2002 (TEMBLrel. 17, Last sequence update)  
 DE 1700016G05RIK protein.  
 GN 1700016G05RIK  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamono N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohcsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY  
 EMBL: AK006028; BAB24373.1; -  
 DR HSP; P00761; IAKS.  
 DR MEROPS; S01.989; -  
 DR MGD; MGI:1914940; 1700016G05RIK.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser-protease\_Try.  
 DR Pfam: PF00089; trypsin\_1  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR HydroLase; Serine protease.  
 SO SEQUENCE 237 AA; 26698 MW; EF9139656B0394A CRC64;

Query Match 63.2%; Score 36; DB 11; Length 237;  
 Best Local Similarity 85.7%; Pred. No. 61;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 NITYSLP 11  
 Db 220 NITYSLP 226

RESULT 20  
 Q8Z6A4 PRELIMINARY; PRT; 242 AA.  
 ID Q8Z6A4  
 AC Q8Z6A4  
 DT 01-MAR-2002 (TEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
 DE Putative pertussis-like toxin subunit (EC 2.4.2.-).  
 GN STY1890.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.  
 NCBI\_Taxid=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18."  
 RL Nature 413:848-852(2001).  
 DR EMBL; AL627271; CAD02123.1; -  
 DR InterPro: IPR003898; Borpert\_toxA.  
 DR Pfam; PF02917; Pertussis\_S1; 1.  
 KM Transferrase; Glycosyltransferase; Hypothetical protein;  
 KW Complete proteome.  
 SO SEQUENCE 242 AA; 27178 MW; 5F121C49B771EA37 CRC64;

Query Match 63.2%; Score 36; DB 16; Length 242;  
 Best Local Similarity 63.6%; Pred. No. 63;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RASENYSYLP 11  
 Db 98 RADNYSYLP 108

RESULT 21  
 Q8V506 PRELIMINARY; PRT; 434 AA.  
 ID Q8V506  
 AC Q8V506  
 DT 01-MAR-2002 (TEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
 DE GSR.  
 GN GSR.  
 OS Monkeypox virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_Taxid=10244;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZAIRE-96-I-16;  
 RX MEDLINE=21592287; PubMed=11734207;  
 RA Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safonov P.F.,  
 RA Ryazankina O.I., Petrov N.A., Gutov V.V., Uvarova E.A.,  
 RA Mikheev M.V., Sisler J.R., Esposto J.J., Jantling P.B., Moss B.,  
 RA Sandakchilev L.S.;  
 RT "Human monkeypox and smallpox viruses: genomic comparison."  
 RL FEBS Lett. 509:66-70(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZAIRE-96-I-16;  
 RA Shchelkunov S.N., Totmenin A.V., Safonov P.F., Gutov V.V.,  
 RA Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,  
 RA Esposto J.J., Moss B., Sisler J.R., Jantling P.B., Sandakchilev L.S.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF380138; AAL40532.1; -  
 SO SEQUENCE 434 AA; 49924 MW; 949D8C594448A93 CRC64;

Query Match 62.5%; Score 36; DB 12; Length 434;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 ENYSYLP 11  
 Db 303 EDVYSYLP 310

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RESULT 22
ID Q8U483; PRELIMINARY; PRT; 459 AA.
AC Q8U483;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Argininosuccinate lyase.
GN PF0208.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VCL / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO10147; AAL80332.1; -
KM Iyase, Complete proteome.
SQ SEQUENCE 459 AA; 51347 MW; 733C8CAF847694D CRC64;

Query Match 63.2%; Score 36; DB 17; Length 459;
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENITSYLP 11
Db 136 KAENVTYLP 146

RESULT 23
ID Q9Y761; PRELIMINARY; PRT; 460 AA.
AC Q9Y761;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Alphan-acetylglucosamine transferase.
GN GNT1.
OS Kluveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGI/2;
MEDLINE=99156950; PubMed=10037760;
RA Guillen E., Abejón C., Hirschberg C.B.;
RT "The genes for the Golgi apparatus N-acetylglucosaminyltransferase and
the UDP-N-acetylglucosamine transporter are contiguous in
Kluveromyces lactis."
RL J. Biol. Chem. 274:6641-6646(1999).
DR EMBL: AF106080; AAD25740.1; -
KM Transferase.
SQ SEQUENCE 460 AA; 53169 MW; 9163B78C47550A2F CRC64;

Query Match 63.2%; Score 36; DB 3; Length 460;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 SENYSLYP 11
Db 266 SEDIYNFLP 274

RESULT 24
ID Q975A8; PRELIMINARY; PRT; 545 AA.
AC Q975A8;

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DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative molybdopterin biosynthesis moa protein.
GN S70504.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=11955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermacidophilic
Crenarchaeon, Sulfolobus tokodaii strain7."
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000982; BAB65499.1; -
DR InterPro: IPR001453; MOCF_biosynth.
DR InterPro: IPR005111; MoaA_C.
DR Pfam: PF00994; MOCF_biosynth. 1.
DR Pfam: PF03454; MoaA_C. 1.
DR Pfam: PF03453; MoaA_N. 1.
DR Pfam: PF002460; MOCF_biosynth. 1.
DR TIGRFAMs: TIGR00177; molyb_syn. 1.
DR PROSITE: PS01079; MOCF_BIOSYNTHESIS_2; UNKNOWN_1.
KM Hypothetical protein: Complete proteome.
SQ SEQUENCE 545 AA; 60835 MW; E21E5B8355F85C27 CRC64;

Query Match 63.2%; Score 36; DB 17; Length 545;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENITSYLP 11
Db 341 KADNRITYLP 351

RESULT 25
ID Q99UK9; PRELIMINARY; PRT; 567 AA.
AC Q99UK9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Prolinase-RNA ligase.
GN PROS OR SAV1263 OR SAI106.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Matsuura A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanemisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -I- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA (AMINO ACID) = AMP +

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CC PYROPHOSPHATE + L-AMINOACYL-TRNA (AMINO ACID).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.  
 DR EMBL: AP003161; BAB57425.1; -.  
 DR EMBL: AP003133; BAB42358.1; -.  
 DR InterPro: IPR002106; AACRNA\_ligaseII.  
 DR InterPro: IPR004154; HGP\_anticonodon.  
 DR InterPro: IPR004500; Profs\_fam\_II.  
 DR InterPro: IPR002314; tRNA-synt\_2b.  
 DR InterPro: IPR002316; tRNA-synt\_pro.  
 DR Pfam: PF03129; HGP\_anticonodon; 1.  
 DR Pfam: PF00587; tRNA-synt\_2b; 1.  
 DR PRINTS: PR01046; TRNASYNTHPRO.  
 DR TIGRFAMs: TIGR00409; profs\_fam\_II\_1.  
 DR PROSITE: PS00179; AA TRNA\_LIGASE\_II\_1; 1.  
 KW ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Complete proteome.  
 SQ SEQUENCE 567 AA; 63859 MW; 7FC2249781B41C0 CRC64;

Query Match 63.2%; Score 36; DB 16; Length 567;  
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENTSYSTP 11  
 DB 34 QSTSGIYSTLP 44

## RESULT 26

Q97GQ7 PRELIMINARY; PRT; 581 AA.  
 AC Q97GQ7;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE DNA modification methyltransferase.  
 GN CAC2309.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 OX NCBI\_TaxId=1488;  
 RX (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=1146286;  
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf J.T.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum";  
 RL J. Bacteriol. 183:4823-4838(2001).  
 DR EMBL: AE007731; AAK80265.1; -.  
 DR InterPro: IPR002296; NI2N6\_mtfase.  
 DR PRINTS: PR00507; NI2N6MTPRASE.  
 DR Trnasferase; Methyltransferase; Complete proteome.  
 SQ SEQUENCE 581 AA; 68752 MW; 91959B65F6B580 CRC64;

Query Match 63.2%; Score 36; DB 16; Length 581;  
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RASENTSYSTP 11  
 DB 530 KLGENTYEYYP 540

## RESULT 27

Q9KVI9 PRELIMINARY; PRT; 611 AA.  
 AC Q9KVI9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Vitamin B12 receptor.  
 GN VC0156.  
 OS Vibrrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.  
 OX NCBI\_TaxId=666;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EL TOR N16961 / SERTOTYPE O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwim M.L.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tectelin H., Richardson D.,  
 RA Esmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Ueberback T., Fleischmann R.D., Nielsen W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 RT cholerae";  
 RL Nature 406:477-483(2000).  
 DR EMBL: AE004105; AAF93332.1; -.  
 DR TIGR: VC0156; -.  
 DR InterPro: IPR000531; TonB\_boxC.  
 DR Pfam: PF00593; TonB\_boxC\_1.  
 DR PROSITE: PS00450; TONB\_DEPENDENT\_REC\_1; UNKNOWN\_1.  
 DR PROSITE: PS01156; TONB\_DEPENDENT\_REC\_2; UNKNOWN\_1.  
 KW Receptor; Complete proteome.  
 SQ SEQUENCE 611 AA; 68609 MW; 0C6D9A9A6A2063BE CRC64;

Query Match 63.2%; Score 36; DB 16; Length 611;  
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENTSYSTP 9  
 DB 242 RAVENITQY 250

## RESULT 28

Q97SRL PRELIMINARY; PRT; 617 AA.  
 AC Q97SRL;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Prollyl-tRNA synthetase.  
 GN SP0264.  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Streptococcus.  
 OX NCBI\_TaxId=1313;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TIGR4;  
 RX MEDLINE=21357209; PubMed=11463916;  
 RA Tectelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,  
 RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,  
 RA Durkin A.S., Gwim M., Kolonay J.F., Nelson W.C., Peterson J.D.,  
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,  
 RA Holtapple E., Khouri H., Wolf A.M., Ueberback T.R., Hansen C.L.,  
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,  
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,  
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;  
 RT "Complete genome sequence of a virulent isolate of Streptococcus  
 RT pneumoniae";  
 RL Science 293:498-506(2001).  
 DR EMBL: AE007339; AAK74442.1; -.  
 DR TIGR: SP0264; -.  
 DR InterPro: IPR002106; AACRNA\_ligaseII.  
 DR InterPro: IPR004154; HGP\_anticonodon.  
 DR InterPro: IPR004500; Profs\_fam\_II.  
 DR InterPro: IPR002314; tRNA-synt\_2b.  
 DR InterPro: IPR002316; tRNA-synt\_pro.  
 DR Pfam: PF03129; HGP\_anticonodon; 1.

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DR Pfam; PF00587; tRNA-Sync 2b; 1.
DR PRINTS; PRO1046; TRNASYNTPRO.
DR TIGRFAMs; TIGR00409; ProS_fam_11; 1.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
DR Anticodon-anticodon synthetase; Complete proteome.
SQ SEQUENCE 617 AA; 68652 MW; 367855B7EA9E1A38 CRC64;

Query Match
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RASENTSYSLP 11
Db 34 QVASGVSYSLP 44

RESULT 29
Q97276 PRELIMINARY; PRT; 637 AA.
ID Q97276;
AC Q97276;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein SSO1053.
GN SSO1053.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
NC NCBITaxID=2287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RA MEDLINE=11332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aways M.J., Chan-Weiner C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasus G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006724; AAK41317.1; -.
DR InterPro; IPR003880; Putative attach.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 637 AA; 74021 MW; 17EF943BBSAB13BF CRC64;

Query Match
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NIVSYSLP 11
Db 591 NVYSYSLP 597

RESULT 30
Q92F03 PRELIMINARY; PRT; 1067 AA.
ID Q92F03;
AC Q92F03;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein J10050.
GN J10050.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
NC NCBITaxID=1642;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;

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RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Bangeul P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duseurget O.,
RA Eutian K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Negtari H.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591973; CAC98272.1; -.
DR Listeriae; LMO00057; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 1068 AA; 119645 MW; 4341B4CD38F522DF CRC64;

Query Match
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASENTSYSLP 10
Db 845 RQENNTSYSLP 854

RESULT 32
Q8YA09 PRELIMINARY; PRT; 1068 AA.
ID Q8YA09;
AC Q8YA09;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Lmo0057.
GN LMO0057.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
NC NCBITaxID=1639;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-E / SEROVAR 1/2A;
RA MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duseurget O.,
RA Eutian K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Negtari H.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591973; CAC98272.1; -.
DR Listeriae; LMO00057; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 1068 AA; 119645 MW; 4341B4CD38F522DF CRC64;

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Q05352  
ID Q05352 PRELIMINARY; PRT; 1114 AA.  
AC Q05352;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Immuno-dominant variable surface antigen.  
OS Entamoeba histolytica.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=5759;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90354789; PubMed=1696956;  
RA Eelman U., Meraz M.A., Raueser S., Agabian N., Meza I.;  
RT "Characterization of an immuno-dominant variable surface antigen from  
RT pathogenic and nonpathogenic Entamoeba histolytica.";  
RL J. Exp. Med. 172:879-888(1990).  
DR EMBL; X55028; CAA38647.1, -.  
DR InterPro; IPR00130; 2n\_MTPeptide.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
SQ SEQUENCE 1114 AA; 125570 MW; 0445F9609311E1D CRC64;  
Query Match 63.2%; Score 36; DB 5; Length 1114;  
Best Local Similarity 45.5%; Pred. NO. 3.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 RASENIYSYLP 11  
Db 605 RVEDNYDYTP 615

RESULT 33  
Q020E6 PRELIMINARY; PRT; 109 AA.  
ID Q020E6  
AC Q020E6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Perin-mimicking anti-idiotope kappa chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Perin-Mimicking Antibodies Expressed  
RT in Mammalian Cells.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307938; AAL09422.1; -.  
DR InterPro; IPR003066; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
FT NON\_TER 1 1  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;  
Query Match 61.4%; Score 35; DB 11; Length 109;  
Best Local Similarity 70.0%; Pred. NO. 41;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RASENIYSYLP 10  
Db 24 RASGNHNYL 33

RESULT 34  
Q09HGI PRELIMINARY; PRT; 120 AA.  
ID Q09HGI  
AC Q09HGI;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Hypothetical protein Ta0267.  
GN TA0267.  
OS Thermoplasma acidophilum.  
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
OC Thermoplasmataceae; Thermoplasma.  
OX NCBI\_TaxID=2303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1728;  
RX MEDLINE=20479972; PubMed=11029001;  
RA Ruep A., Grail W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
RT "The genome sequence of the thermophilic scavenger Thermoplasma  
RT acidophilum.";  
RL Nature 407:508-513(2000).  
DR EMBL; AL445063; CAC11412.1; -.  
DR InterPro; IPR005182; DUF304.  
DR Pfam; PF03703; DUF304; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 120 AA; 13907 MW; F630AB0CB5772CED CRC64;  
Query Match 61.4%; Score 35; DB 17; Length 120;  
Best Local Similarity 66.7%; Pred. NO. 46;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ASENISYLP 10  
Db 14 SSKNIYNYL 22

RESULT 35  
Q09AST6 PRELIMINARY; PRT; 140 AA.  
ID Q09AST6  
AC Q09AST6;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE A11932410/F5D14.6.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,  
RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,  
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.W.,  
RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,  
RA Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,  
RA Theologis A., Ecker J.R.;  
RT "Arabidopsis cDNA clones.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Banh J., Bowser L.,  
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.W., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Arabidopsis ORF clones.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF361848; AAK32860.1; -.  
DR EMBL; AY066053; AAL47420.1; -.  
SQ SEQUENCE 140 AA; 15024 MW; A9B6C5B65EA2506 CRC64;

Query Match 61.4%; Score 35; DB 10; Length 140;  
Best Local Similarity 66.7%; Pred. NO. 54;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASENITYSL 10  
 Db 132 ASDNYASYI 140

RESULT 36  
 P95293 PRELIMINARY; PRT; 180 AA.

AC P95293;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 DE Molybdenum-containing formylmethanofuran dehydrogenase isoenzyme I  
 subunit B (EC 1.2.99.5).  
 GN FMDE CR MTH917.  
 OS Methanobacterium thermoautotrophicum, and  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter.  
 OX NCBI\_TaxID=187420, 145261;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.thermoautotrophicum; STRAIN=MARBURG / DSM 2133;  
 RA MEDLINE=97112485; PubMed=8954165;  
 RA Hochheimer A., Linder D., Thauer R.K., Hedderich R.;  
 RT "The molybdenum formylmethanofuran dehydrogenase operon and the  
 tungsten formylmethanofuran dehydrogenase operon from Methanobacterium  
 thermoautotrophicum. Structures and transcriptional regulation.";  
 RL Eur. J. Biochem. 242:156-162(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.thermoautotrophicum; STRAIN=DELTA H;  
 RA MEDLINE=98037514; PubMed=9371463;  
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pochler B., Qiu D.,  
 RA Spadotora R., Viscare R., Wang Y., Wierzbowski J., Gibson R.,  
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
 deltaH: functional analysis and comparative genomics.";  
 RL J. Bacteriol. 179:7135-7155(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.woffei;  
 RA Hochheimer A., Hedderich R., Thauer R.K.;  
 RT "The formylmethanofuran dehydrogenase isoenzymes in Methanobacterium  
 woffei and Methanobacterium thermoautotrophicum: Induction of the  
 molybdenum isoenzyme by molybdate and constitutive synthesis of the  
 tungsten isoenzyme.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CATALYZES THE REVERSIBLE OXIDATION OF CO2 AND  
 METHANOFURAN (MFR) TO N-FORMYLMETHANOFURAN (CHO-MFR). CAN ONLY  
 OXIDISE FORMYLMETHANOFURAN. THIS ENZYME IS OXYGEN-LABILE.  
 CC -1- CATALYTIC ACTIVITY: FORMYLMETHANOFURAN + H(2)O + ACCEPTOR = CO(2)  
 + METHANOFURAN + REDUCED ACCEPTOR.  
 CC -1- COFACTOR: MOLYBDENUM.  
 CC -1- ENZYME REGULATION: INACTIVATED BY CYANIDE.  
 CC -1- PATHWAY: FIRST STEP IN METHANOGENESIS.  
 CC -1- SUBUNIT: CONSISTS OF FIVE SUBUNITS; FMDB, FMDB, FMDC, FMDD, AND  
 FMDE.  
 CC -1- INDUCTION: BY GROWTH ON MOLYBDENUM, UNDER ANAEROBIC CONDITIONS.  
 DR EMBL: X97820; CAAG6400.1; -;  
 DR EMBL: AE000867; AAB85415.1; -;  
 DR EMBL: AF009689; CAA08786.1; -;  
 DR InterPro: IPR03814; FwDE.  
 DR Pfam: PF02663; FwDE; 1.  
 KM Oxidoreductase; Molybdenum; Methanogenesis; Complete proteome.  
 SQ SEQUENCE 180 AA; 20454 MW; D09C57F5FCABED2 CRC64;

Query Match 61.4%; Score 35; DB 17; Length 180;  
 Best Local Similarity 66.7%; Pred. No. 71;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 RASENITYSL 9  
 Db 132 RASENITYSL 140

RESULT 37  
 096003 PRELIMINARY; PRT; 200 AA.

AC 096003;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Roseophage SIO1.  
 GN Gp23.  
 OS Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
 OC T7-like viruses.  
 OX NCBI\_TaxID=136084;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rohwer F.L., Segall A.M., Steward G., Seguritan V., Breitbart M.,  
 RA Wolven F., Azam F.;  
 RT "The complete genomic sequence of the marine phage Roseophage SIO1  
 shares homology with nonmarine phages.";  
 RL Limnol. Oceanogr. 45:408-418(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rohwer F.L., Segall A.M., Steward G., Seguritan V., Breitbart M.,  
 RA Wolven F., Azam F.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF189021; AAG02605.1; -;  
 SQ SEQUENCE 200 AA; 20825 MW; 8D0FDAA312594E0C CRC64;

Query Match 61.4%; Score 35; DB 9; Length 200;  
 Best Local Similarity 55.6%; Pred. No. 80;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 SENITYSLP 11  
 Db 49 AEDVDYLP 57

RESULT 38  
 0962N2 PRELIMINARY; PRT; 270 AA.

AC 0962N2;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE PVLH14010 P.  
 GN PVLH14010W.  
 OS Plasmidium vivax.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.  
 OX NCBI\_TaxID=5855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tsvartchitch M., Fischer K., Huestis R., Saul A.;  
 RT "The sequence of 200 kb portion of a Plasmidium vivax chromosome  
 RT reveals a high degree of conservation with P. falciparum chromosome  
 RT 3.";  
 RL Mol. Biochem. Parasitol. 0:0-0(2001).  
 DR EMBL: AY003872; AAF99448.1; -;  
 SQ SEQUENCE 270 AA; 31249 MW; 670AF34217239D71 CRC64;

Query Match 61.4%; Score 35; DB 5; Length 270;  
 Best Local Similarity 50.0%; Pred. No. 1,1e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 RASENITYSL 10  
 Db 180 RSSNITYSL 189

```

RESULT 39
Q9CYFO PRELIMINARY; PRT; 298 AA.
AC Q9CYFO;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEN.
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA8633.1; -.
DR HSSP; P01607; IRE1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV_2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 61.4%; Score 35; DB 11; Length 298;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASENTSYL 10
DB 196 RASGNTHNYL 205

RESULT 40
O83275 PRELIMINARY; PRT; 357 AA.
AC O83275;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE N-acetylmutamoyl-L-alanine amidase (AMIA).
GN TP0247.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uitterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venier J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete";
RL Science 281:375-388(1998).
DR EMBL; AE001206; AAC65234.1; -.
DR TIGR; TP0247; -.
DR InterPro; IPR002508; Amidase_3.
DR Pfam; PF01520; Amidase_3; 1.
KM Complete proteome.
SQ SEQUENCE 357 AA; 39810 MW; C46BD7EDB3AEFB71 CRC64;

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Query Match 61.4%; Score 35; DB 16; Length 357;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASENTSYL 10
DB 162 RASQNYDDL 171

```

Search completed: July 18, 2003, 15:09:47  
Job time : 30.38 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:01:44 ; Search time 23.66 Seconds  
(without alignments)  
39.423 Million cell updates/sec

Title: US-10-007-790-9  
Perfect score: 34  
Sequence: 1 NAKLTLE 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	34	100.0	7	21	AAV87661		Murine PIP3 recogn
2	34	100.0	7	23	AAE22198		Murine MC-1 antido
3	34	100.0	92	23	AAE22190		Murine MC-1 antido
4	34	100.0	107	21	AAV87656		Murine PIP3 recogn
5	34	100.0	107	23	AAE22189		Murine MC-1 antido
6	34	100.0	495	23	AAE22193		Murine CCR5CD3 bi
7	31	91.2	149	23	ABR48303		Listeria monocytog
8	31	91.2	714	23	ABR97340		Novel human protei
9	29	85.3	99	18	AAW04596		Anti-DNA antibody
10	29	85.3	99	18	AAW04597		Anti-DNA antibody

11	29	85.3	99	18	AAW04598	Anti-DNA antibody
12	29	85.3	107	16	AAV878971	Light chain variab
13	29	85.3	107	17	AAW05822	Humanised 1D10 ant
14	29	85.3	107	18	AAW07439	Anti-DNA antibody
15	29	85.3	109	19	AAW46483	8019 VK antibody
16	29	85.3	123	22	AAE84742	Variable region of
17	29	85.3	126	12	AAE12235	Mouse Mab 2G12 L c
18	29	85.3	127	12	AAE12357	Light (kappa) cha
19	29	85.3	128	17	AAW03721	Anti-human gp39 MA
20	29	85.3	165	23	ABP00079	Human ORFX protein
21	29	85.3	171	17	AAW03725	Humanised Mab 39-1
22	29	85.3	214	17	AAW05828	Humanised 1D10 ant
23	29	85.3	243	15	AAE53148	VH and VL of Mab P
24	29	85.3	256	23	AAU72864	P4-15 single chain
25	29	85.3	258	23	ABW05962	Monoclonal antibod
26	29	85.3	258	23	ABW05963	Monoclonal antibod
27	29	85.3	258	23	ABW05990	Mouse monoclonal a
28	29	85.3	258	23	ABW05991	Mouse and human ch
29	29	85.3	258	23	ABW05992	Mouse and human ch
30	29	85.3	258	23	ABW05993	Mouse and human ch
31	29	85.3	258	23	ABW05994	Mouse and human ch
32	29	85.3	258	23	ABW05995	Human monoclonal a
33	29	85.3	258	23	ABW05996	Human monoclonal a
34	29	85.3	258	23	ABW05997	Human monoclonal a
35	29	85.3	287	23	ABW05982	Human monoclonal a
36	29	85.3	320	21	AAV37571	Chlamydia trachoma
37	29	85.3	350	20	AAV37571	Chlamydia trachoma
38	29	85.3	356	22	AAW80119	Corynebacterium gl
39	29	85.3	356	22	AAW80159	Corynebacterium gl
40	29	85.3	407	12	AAE12870	Substance P recept
41	29	85.3	407	14	AAE32800	Rat Substance P re
42	29	85.3	472	22	AAE89856	C glutaminc prote
43	29	85.3	477	22	AAE80118	Corynebacterium gl
44	29	85.3	477	22	AAE80158	Corynebacterium gl
45	29	85.3	502	23	AAO15140	Tomato GAD protein

## ALIGNMENTS

RESULT 1  
AAV87661  
ID AAV87661 standard; Protein; 7 AA.  
XX  
AC AAV87661;  
XX  
DT 11-AUG-2000 (first entry)  
XX  
DE Murine PIP3 recognizing Mab variable region light chain CDR2 region.  
XX  
XX PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR2;  
KW immunogen; antibody; light chain; complementarity determining region.  
XX  
OS Mus sp.  
XX  
PN JP2000083664-A.  
XX  
PD 28-MAR-2000.  
XX  
PF 07-SEP-1998; 98UP-0252921.  
XX  
PR 07-SEP-1998; 98UP-0252921.  
XX  
PA (FUKU/) FUKUI Y.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
XX  
DR WPI; 2000-353334/31.  
XX  
PT A monoclonal antibody recognizing  
PT phosphatidylinositol-3,4,5-triphosphate -  
XX  
XX Claim 11; Page 13; 15pp; Japanese.  
XX

CC This invention describes a novel antibody specifically recognizing  
CC inositol-3,4,5-triphosphate (PIP3). The antibody of the  
CC invention is used in immunogenic compositions in which a dead  
CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
CC antibody can be used in an immunoassay containing a step in which the  
CC above antibody or its variable region is reacted with PIP3 present in a  
CC sample and the bond based on their immunological reaction. The method  
CC can determine PIP3 easily in a high sensitivity. This sequence represents  
CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
CC chain complementarity determining region, CDR2 described in the method of  
CC the invention.

XX  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
1 NAKLTTE 7

Db 1 NAKLTTE 7

RESULT 2  
AAE22198  
ID AAE22198 standard; peptide; 7 AA.  
XX  
AC AAE22198;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Murine MC-1 antibody light chain variable domain (VL) CDR2 peptide.  
XX  
KM Chemokine construct; human immunodeficiency virus 1; allergic disease;  
KM skin disease; immunological disorder; autoimmune disease; psoriasis;  
KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
KM inflammatory renal disease; HIV-1; transplant rejection; murine; CDR2;  
KM light chain variable domain; VL; complementarity determining region 2;  
KM MC-1; antibody.

XX  
XX  
OS Mus sp.  
XX  
PN WO200220615-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-EP10433.  
XX  
PR 08-SEP-2000; 2000EP-0119694.  
PR 05-SEP-2001; 2001US-0948004.  
XX  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Mack M, Schloendorff D, Spring M;  
PI WPI; 2002-362240/39.  
DR  
XX  
PT Use of an antibody and/or chemokine construct that binds to a chemokine  
PT receptor, for eliminating cells latently infected with primate  
PT immunodeficiency virus, or treating, preventing and alleviating immune  
PT disorders -  
XX  
XX  
PS Disclosure; Page 116; 117pp; English.

CC The invention relates to the use of an antibody and/or chemokine  
CC construct that binds a chemokine receptor for preparing a pharmaceutical  
CC composition for eliminating cells latently infected with a primate  
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They  
CC are used in gene therapy and as vaccines. The antibody and/or chemokine  
CC construct is also used for preparing a pharmaceutical composition for  
CC treating, preventing and/or alleviating immunological disorders  
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes  
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes

CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin  
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
CC renal diseases and inflammatory bowel diseases and graft versus host  
CC and transplant rejections. The present sequence is murine MC-1 antibody  
CC light chain variable domain (VL) complementarity determining region 2  
CC (CDR2) peptide.

XX  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
1 NAKLTTE 7

Db 1 NAKLTTE 7

RESULT 3  
AAE22190  
ID AAE22190 standard; Protein; 92 AA.  
XX  
AC AAE22190;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Murine MC-1 antibody light chain variable domain (VL) (1) #2.  
XX  
XX  
KM Chemokine construct; human immunodeficiency virus 1; allergic disease;  
KM skin disease; immunological disorder; autoimmune disease; psoriasis;  
KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
KM inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;  
KM MC-1 antibody; VL; light chain variable domain; chemokine receptor 5.

XX  
XX  
OS Mus sp.  
XX  
PN WO200220615-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-EP10433.  
XX  
PR 08-SEP-2000; 2000EP-0119694.  
PR 05-SEP-2001; 2001US-0948004.  
XX  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Mack M, Schloendorff D, Spring M;  
PI WPI; 2002-362240/39.  
DR N-PSDB; AAD35249.  
XX  
XX  
PT Use of an antibody and/or chemokine construct that binds to a chemokine  
PT receptor, for eliminating cells latently infected with primate  
PT immunodeficiency virus, or treating, preventing and alleviating immune  
PT disorders -  
XX  
XX  
PS Claim 12; Page 49-50; 117pp; English.

CC The invention relates to the use of an antibody and/or chemokine  
CC construct that binds a chemokine receptor for preparing a pharmaceutical  
CC composition for eliminating cells latently infected with a primate  
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They  
CC are used in gene therapy and as vaccines. The antibody and/or chemokine  
CC construct is also used for preparing a pharmaceutical composition for  
CC treating, preventing and/or alleviating immunological disorders  
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes  
CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin  
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
CC renal diseases and inflammatory bowel diseases and graft versus host

CC and transplant rejections. The present sequence is murine MC-1 antibody  
CC light chain variable domain (VL)(1). This antibody is specific for  
CC human chemokine receptor 5 (CCR5).  
XX  
SQ Sequence 92 AA;

Query Match 100.0%; Score 34; DB 23; Length 92;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 NAKTLTE 7  
DB 42 NAKTLTE 48

RESULT 4  
AAE87656  
ID AAE87656 standard; Protein; 107 AA.  
XX  
XX AAE87656;  
XX

DT 11-AUG-2000 (first entry)  
XX

DE Murine PIP3 recognizing Mab variable region light chain protein.

XX PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;  
KW immunogen; antibody; light chain.  
XX

OS Mus sp.  
XX

PN JP2000083664-A.  
XX

PD 28-MAR-2000.  
XX

PT 07-SEP-1998; 98JP-0252921.  
XX

PR 07-SEP-1998; 98JP-0252921.  
XX

PA (FUKU/) FUKUI Y.  
XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

DR WPI; 2000-35334/31.  
XX

DR N-PSDB; AAE87656.  
XX

XX A monoclonal antibody recognizing  
PT phosphatidylinositol-3,4,5-triphosphate -

PS Claim 6; Page 12; 15pp; Japanese.  
XX

CC This invention describes a novel antibody specifically recognizing  
CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
CC invention is used in immunogenic compositions in which a dead  
CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
CC antibody can be used in an immunoassay containing a step in which the  
CC above antibody or its variable region is reacted with PIP3 present in a  
CC sample and the bond based on their immunological reaction. The method  
CC can determine PIP3 easily in a high sensitivity. This sequence represents  
CC the murine PIP3 recognizing monoclonal antibody variable region light  
CC chain described in the method of the invention.  
XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 34; DB 21; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NAKTLTE 7  
DB 50 NAKTLTE 56

RESULT 5  
AAE22189

ID AAE22189 standard; Protein; 107 AA.  
XX

AC AAE22189;  
XX

DT 25-JUL-2002 (first entry)  
XX

DE Murine MC-1 antibody light chain variable domain (VL)(1) #1.

XX Chemokine construct; human immunodeficiency virus 1; allergic disease;  
XX skin disease; immunological disorder; autoimmune disease; psoriasis;  
KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
KW inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;  
XX MC-1 antibody; VL; light chain variable domain; chemokine receptor 5.  
XX

OS Mus sp.  
XX

PN WO200220615-A2.  
XX

PD 14-MAR-2002.  
XX

PT 10-SEP-2001; 2001WO-EP10433.  
XX

PR 08-SEP-2000; 2000EP-0119694.  
XX

PR 05-SEP-2001; 2001US-0948004.  
XX

PA (MICR-) MICROMET AG.  
XX

PI Mack M, Schloendorff D, Spring M;  
XX

DR WPI; 2002-362240/39.  
XX

DR N-PSDB; AAD35248.  
XX

PT Use of an antibody and/or chemokine construct that binds to a chemokine  
PT receptor, for eliminating cells latently infected with primate  
PT immunodeficiency virus, or treating, preventing and alleviating immune  
PT disorders -  
XX  
XX Example 2; Page 49; 117pp; English.

CC The invention relates to the use of an antibody and/or chemokine  
CC construct that binds a chemokine receptor for preparing a pharmaceutical  
CC composition for eliminating cells latently infected with a primate  
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They  
CC are used in gene therapy and as vaccines. The antibody and/or chemokine  
CC construct is also used for preparing a pharmaceutical composition for  
CC treating, preventing and/or alleviating immunological disorders  
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes  
CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin  
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
CC renal diseases and inflammatory bowel diseases and graft versus host  
CC and transplant rejections. The present sequence is murine MC-1 antibody  
CC light chain variable domain (VL)(1). This antibody is specific for  
CC human chemokine receptor 5 (CCR5).  
XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 34; DB 23; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NAKTLTE 7  
DB 50 NAKTLTE 56

RESULT 6  
AAE22193  
ID AAE22193 standard; Protein; 495 AA.  
XX  
XX AAE22193;  
XX

DT	25-JUL-2002	(first entry)
XX		
DE	Murine CCR5xCD3 bispecific single chain antibody construct.	
XX		
KW	Chemokine construct; human immunodeficiency virus 1; allergic disease;	
KW	skin disease; immunological disorder; autoimmune disease; psoriasis;	
KW	multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;	
KW	diabetes; skin inflammation; atopic dermatitis; inflammatory disease;	
KW	inflammatory renal disease; HIV-1; transplant rejection; CCR5xCD3;	
KW	antibody; chemokine receptor 5; CD3 antigen; chimeric; murine.	
XX		
OS	Chimeric - Mus sp.	
OS	Chimeric - Unidentified.	
XX		
PN	WO200220615-A2.	
XX		
PD	14-MAR-2002.	
XX		
PF	10-SEP-2001; 2001WO-EP10433.	
XX		
PR	08-SEP-2000; 2000EP-0119694.	
PR	05-SEP-2001; 2001US-0948004.	
XX		
PA	(MICR-) MICROMET AG.	
XX		
PI	Mack M, Schloendorff D, Spring M;	
DR	WPI; 2002-362240/39.	
DR	N-PSDB; AAD35252.	
PT	Use of an antibody and/or chemokine construct that binds to a chemokine	
PT	receptor, for eliminating cells latently infected with primate	
PT	immunodeficiency virus, or treating, preventing and alleviating immune	
PT	disorders	
XX		
PS	Claim 29; Page 52; 117pp; English.	
XX		
CC	The invention relates to the use of an antibody and/or chemokine	
CC	construct that binds a chemokine receptor for preparing a pharmaceutical	
CC	composition for eliminating cells latently infected with a primate	
CC	immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They	
CC	are used in gene therapy and as vaccines. The antibody and/or chemokine	
CC	construct is also used for preparing a pharmaceutical composition for	
CC	treating, preventing and/or alleviating immunological disorders	
CC	including autoimmune diseases (e.g. multiple sclerosis, type I diabetes	
CC	and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin	
CC	inflammation, atopic dermatitis and psoriasis), inflammatory diseases	
CC	such as inflammatory joint diseases (chronic arthritis), inflammatory	
CC	renal diseases and inflammatory bowel diseases and graft versus host	
CC	and transplant rejections. The present sequence is CCR5xCD3 bispecific	
CC	single chain antibody construct. This antibody construct comprises	
CC	light chain variable domain (VL) and heavy chain variable (VH) domains	
CC	of murine MC-1 antibody specific for human chemokine receptor 5 (CCR5)	
CC	and VH and VL domains of an antibody specific for a CD3 antigen joined	
CC	by a peptide linker.	
XX		
SQ	Sequence 495 AA;	
XX		
QY	Query Match 100.0%; Score 34; DB 23; Length 495;	
DB	Best Local Similarity 100.0%; Pred. No. 31;	
DB	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
XX		
QY	1 NAKTLTTE 7	
DB		
DB	50 NAKTLTTE 56	
XX		
RESULT 7		
ABB48303		
ID	ABB48303 standard; Protein; 149 AA.	
XX		
AC	ABB48303;	
XX		

DT	05-FEB-2002	(first entry)
DE	Listeria monocytogenes protein #1007.	
KW	Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;	
KW	vitamin B12; bacterial infection; disease.	
XX		
OS	Listeria monocytogenes.	
PN	WO200177335-A2.	
PD	18-OCT-2001.	
XX		
PE	11-APR-2001; 2001WO-FR01118.	
XX		
PR	11-APR-2000; 2000FR-0004629.	
XX		
PA	(INSP ) INST PASTEUR.	
PI	Buchrieser C, Frangoul L, Couve E, Rusniok C, Fehli H, Dehoux P,	
PI	Dussuyget O, Cotelouan F, Nedjari M, Glaser P, Kunst F, Cossart P,	
PI	Daniels J, Goebel W, Krefit J, Kunh M, Ng E, Vazquez-Boland JA,	
PI	Domínguez-Bernal G, Garrido-García P, Tíerrez-Martínez A, Amend A,	
PI	Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,	
PI	Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N;	
PI	Madueno E, De Pablos B, Wehlund J, Kaerst U, Entian K, Hauf J;	
PI	Rose M, Voss H;	
DR	WPI; 2002-010914/01.	
XX		
PT	Genomic sequence for Listeria monocytogenes, useful e.g. for treatment	
PT	and prevention of Listeria and related bacterial infections, and	
PT	related polypeptides -	
XX		
PS	Claim 6; SEQ ID No 1008; 192pb; French.	
XX		
CC	The present invention relates to the genome sequence of Listeria	
CC	monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of	
CC	it are useful for selecting probes and primers for detecting genes in L.	
CC	monocytogenes and related organisms, and for studying genetic	
CC	polymorphisms and other genomes. The present sequence is a protein	
CC	encoded by the genome sequence of the present invention. Proteins	
CC	expressed from the genome sequence are useful for raising specific	
CC	antibodies, identification of L. monocytogenes and related organisms, and	
CC	for biosynthesis and biodegradation, especially biosynthesis of Vitamin	
CC	B12. The genome sequence and proteins encoded by it are also useful for	
CC	selecting compounds that regulate gene expression and cell replication	
CC	and modulate L. monocytogenes-related diseases. In addition, the genome	
CC	sequence and proteins encoded by it are useful in pharmaceutical and	
CC	vaccines compositions for the treatment or prevention of infections by L.	
CC	monocytogenes and related organisms.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SO	Sequence 149 AA;	
QY	Query Match 91.2%; Score 31; DB 23; Length 149;	
DB	Best Local Similarity 85.7%; Pred. No. 37;	
DB	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
XX		
QY	1 NAKTLTE 7	
DB	137 NAKTLTD 143	
XX		
AC	ABB97340	
XX	ABB97340;	
XX		
DT	27-JUN-2002 (first entry)	

XX Novel human protein SEQ ID NO: 608.  
DE  
XX Human; antihaemic; vulnerary; antiinflammatory; immunomodulator;  
KW antiinfectivity; cerebroprotective; cyrostatic; rheumatic; gene therapy;  
KW neuroprotective; antiparkinsonian; protein therapy; EST;  
KW expressed sequence tag.  
XX  
XX Homo sapiens.  
XX  
XX MO20022660-A2.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US26015.  
XX  
XX 11-SEP-2000; 2000US-0659671.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Zhou P, Aeundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX  
XX WPI; 2002-292408/33.  
DR N-PSDB; ABN32526.  
DR  
XX An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis -  
PT  
XX Example 2; SEQ ID NO 608; 509pp; English.  
XX  
XX The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention.  
XX  
XX Sequence 714 AA;  
SQ  
Query Match 91.2%; Score 31; DB 23; Length 714;  
Best Local Similarity 85.7%; Pred. No. 2.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NAKTTE 7  
|:|||||  
Db 106 NSKTLE 112  
RESULT 9  
ID AAM04596 standard; Protein; 99 AA.  
XX  
XX AAM04596;  
AC  
XX  
XX 12-AUG-1997 (first entry)  
DT  
XX  
XX Anti-DNA antibody 9f11 light chain variable region.  
DE  
XX  
XX light chain; variable region; anti-DNA; monoclonal; antibody;  
KW MAb 9f11; hairpin; diagnosis; inflammatory glomerulonephritis;  
KW systemic lupus erythematosus; screening; treatment; prevention;  
KW SLE; disease.  
XX  
XX Mus spp.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..22  
FT /label= framework\_1

FT Region 23..27  
FT /label= CDR\_I  
FT Region 28..41  
FT /label= framework\_II  
FT Region 42..58  
FT /label= CDR\_II  
FT Region 59..90  
FT /label= framework\_III  
FT Region 91..102  
FT /label= CDR\_III  
FT Region 103..115  
FT /label= J\_region  
XX  
XX WO9636361-A1.  
XX  
XX 21-NOV-1996.  
XX  
XX 16-MAY-1996; 96WO-US07113.  
XX  
XX 18-MAY-1995; 95US-0443540.  
XX  
XX (UNMI ) UNIV MICHIGAN.  
XX  
XX Glick GD, Swanson PC;  
PI  
XX  
XX WPI; 1997-011854/01.  
DR N-PSDB; AAT43741.  
DR  
XX  
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to  
PT develop prods. for diagnosis and treatment of disorders, e.g.  
PT glomerulonephritis or systemic lupus erythematosus  
XX  
XX Example; Fig 8; 102pp; English.  
XX  
XX The present sequence is the light chain variable region of the  
CC anti-DNA monoclonal antibody (MAb) 9f11, which has a high affinity  
CC for single stranded DNA, low or no affinity for double stranded DNA  
CC and specifically binds a DNA hairpin. The MAb can be used to diagnose  
CC disorders associated with the pathological complexation of DNA,  
CC e.g. inflammatory glomerulonephritis and systemic lupus  
CC erythematosus. It can also be used to generate reagents to screen  
CC for pharmaceutical agents, and treat and/or prevent an above  
CC disorder.  
CC Calf thymus DNA was used to immunise a MRJ-1pr mouse, spleen cells  
CC from which were then fused with Sp2/0 myeloma cells to give  
CC hybridomas producing the anti-DNA MAb. 9f11 was found to react  
CC strongly with single stranded DNA and poly(dI), and weakly with  
CC poly(dG).  
XX  
XX Sequence 99 AA;  
SQ  
Query Match 85.3%; Score 29; DB 18; Length 99;  
Best Local Similarity 85.7%; Pred. No. 65;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTTE 7  
|:|||||  
Db 42 NAKTLAE 48  
RESULT 10  
ID AAM04597 standard; Protein; 99 AA.  
XX  
XX AAM04597;  
AC  
XX  
XX 12-AUG-1997 (first entry)  
DT  
XX  
XX Anti-DNA antibody 15b10 light chain variable region.  
DE  
XX  
XX light chain; variable region; anti-DNA; monoclonal; antibody;  
KW MAb 15b10; hairpin; diagnosis; inflammatory glomerulonephritis;  
KW systemic lupus erythematosus; screening; treatment; prevention;

```

KW SLE; disease.
XX OS Mus spp.
XX Key Location/Qualifiers
XX FH Region 1..22
XX FT Region /label= framework_I
XX FT Region 23..27
XX FT Region /label= CDR_I
XX FT Region 28..41
XX FT Region /label= framework_II
XX FT Region 42..58
XX FT Region /label= CDR_II
XX FT Region 59..90
XX FT Region /label= framework_III
XX FT Region 91..102
XX FT Region /label= CDR_III
XX FT Region 103..115
XX FT Region /label= J_region
XX WM9636361-A1.
XX PD 21-NOV-1996.
XX PE 16-MAY-1996; 96WO-US07113.
XX PR 18-MAY-1995; 95US-0443540.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Glick GD, Swanson PC;
XX DR WI; 1997-011854/01.
XX DR N-PSDB; AAT43742.
XX PT Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX PT develop probe for diagnosis and treatment of disorders, e.g.
XX PT glomerulonephritis or systemic lupus erythematosus
XX PS Example; Fig 8; 102pp; English.
XX PS
XX CC The present sequence is the light chain variable region of the
XX CC anti-DNA monoclonal antibody (MAb) 15b10, which has a high affinity
XX CC for single stranded DNA, low or no affinity for double stranded DNA
XX CC and specifically binds a DNA hairpin. The MAb can be used to diagnose
XX CC disorders associated with the pathological complexation of DNA,
XX CC e.g. inflammatory glomerulonephritis and systemic lupus
XX CC erythematosus. It can also be used to generate reagents to screen
XX CC for pharmaceutical agents, and treat and/or prevent an above
XX CC disorder.
XX CC Calf thymus DNA was used to immunise a MRL-1pr mouse, spleen cells
XX CC from which were then fused with Sp2/0 myeloma cells to give
XX CC hybridomas producing the anti-DNA MAb. 15b10 was found to react
XX CC strongly with single stranded DNA and poly(dT), and weakly with
XX CC poly(dG).
XX SQ Sequence 99 AA;
XX
XX Query Match 85.3%; Score 29; DB 18; Length 99;
XX Best Local Similarity 85.7%; Pred. No. 65;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 NAKTLTE 7
XX Db |||||
XX 42 NAKTLAE 48
XX
XX RESULT 11
XX ID AAM04598
XX AC AAM04598 standard; Protein; 99 AA.
XX
XX AAM04598;
XX

```

DT		12-AUG-1997	(first entry)
XX			
DE	XX	Anti-DNA antibody 5f3 light chain variable region.	
KW	XX	Light chain; variable region; anti-DNA; monoclonal; antibody;	
KW	XX	MAB 5f3; hairpin; diagnosis; inflammatory glomerulonephritis;	
KW	XX	systemic lupus erythematosus; screening; treatment; prevention;	
KW	XX	SLE; disease.	
OS	XX		
MS	spp.		
FH	Key	Location/Qualifiers	
FT	Region	1..22	
FT	Region	/label= framework_I	
FT	Region	23..27	
FT	Region	/label= CDR_I	
FT	Region	28..41	
FT	Region	/label= framework_II	
FT	Region	42..58	
FT	Region	/label= CDR_II	
FT	Region	59..90	
FT	Region	/label= framework_III	
FT	Region	91..102	
FT	Region	/label= CDR_III	
FT	Region	103..115	
FT	Region	/label= J_region	
XX			
PN	WO9636361-A1.		
XX			
PD	21-NOV-1996.		
XX			
PF	16-MAY-1996;	96WO-US07113.	
XX			
PR	18-MAY-1995;	95US-0443540.	
XX			
PA	(UNMI ) UNIV MICHIGAN.		
XI	Glick GD, Swanson PC;		
PL	WPI; 1997-011854/O1.		
DR	N-PSDB; AAT43743.		
XX			
PT	Anti-DNA antibody which specifically binds DNA hairpin - useful to		
PT	develop prods. for diagnosis and treatment of disorders, e.g.		
PT	glomerulonephritis or systemic lupus erythematosus		
XX			
PS	Example; Fig 8; 102pp; English.		
XX			
CC	The present sequence is the light chain variable region of the		
CC	anti-DNA monoclonal antibody (MAB) 5f3, which has a high affinity		
CC	for single stranded DNA, low or no affinity for double stranded DNA		
CC	and specifically binds a DNA hairpin. The Mab can be used diagnose		
CC	disorders associated with the pathological complexation of DNA,		
CC	e.g. inflammatory glomerulonephritis and systemic lupus		
CC	erythematosus. It can also be used to generate reagents to screen		
CC	for pharmaceutical agents, and treat and/or prevent an above		
CC	disorder.		
CC	Calf thymus DNA was used to immunise a MRI-Lpr mouse, spleen cells		
CC	from which were then fused with Sp2/0 myeloma cells to give		
CC	hybridomas producing the anti-DNA Mab.		
XX			
Sequence	99 AA;		
OY	Query Match	85.3%;	Score 29; DB 18; Length 99;
Matches	Best Local Similarity	85.7%;	Pred. No. 65;
Db	6; Conservative	0;	Mismatches 1; Indels 0; Gaps 0.
	1 NAKTLTE 7		
	42 NAKTLAE 48		
RESULT	12		

AAR78971  
 ID AAR78971 standard; Protein: 107 AA.  
 AC AAR78971;  
 XX  
 DT 21-DEC-1995 (first entry)  
 XX  
 DE light chain variable region for monoclonal antibody 2D5.  
 XX  
 KM Monoclonal antibody; heavy metal; mercury; variable region;  
 XX light chain.  
 OS Synthetic.  
 XX  
 PN MO9520607-A.  
 XX  
 PD 03-AUG-1995.  
 XX  
 PF 27-JAN-1995; 95WO-US01199.  
 XX  
 PR 27-JAN-1994; 94US-0187407.  
 XX  
 PA (BION-) BIONEERASKA INC.  
 XX  
 PI Lopez O, Wagner FW, Wylie DE;  
 XX  
 DR WPI; 1995-275415/36.  
 XX  
 DR N-PSDB; AAQ97509.  
 XX  
 PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals  
 PS  
 XX  
 PS Claim 23; Page 69; 106pp; English.  
 XX  
 CC Hybridoma antibodies have been produced with the spleen cells of  
 CC BALB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing MAb's that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by MLV reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CH1 domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' end of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &  
 CC AAR79970-R79971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.  
 CC  
 XX  
 PS Sequence 107 AA;  
 XX  
 SQ  
 Query Match 85.3%; Score 29; DB 16; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 71;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NAKTLE 7  
 |||||  
 50 NAKTLAE 56  
 RESULT 13  
 AAW05822

ID AAW05822 standard; Protein: 107 AA.  
 XX  
 AC AAW05822;  
 XX  
 DT 27-JAN-1997 (first entry)  
 XX  
 DE Humanised ID10 antibody light chain variable region.  
 XX  
 KM B-cell lymphoma; humanised antibody; bispecific antibody;  
 XX myeloma; leukaemia; hybridoma; monoclonal antibody.  
 OS Chimeric Homo sapiens;  
 XX  
 OS Chimeric Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT 24..34  
 FT /label= CDR1  
 FT Region 50..56  
 FT /label= CDR2  
 FT Region 89..97  
 FT /label= CDR3  
 FT Misc-difference 43  
 FT /note= "human framework residue 43 is substd. by a  
 FT consensus amino acid of the equivalent  
 FT murine residue"  
 FT  
 FT Misc-difference 48  
 FT /note= "human framework residue 48 is substd. by  
 FT equivalent murine framework residue"  
 FT  
 FT Misc-difference 49  
 FT /note= "human framework residue 49 is substd. by  
 FT equivalent murine framework residue"  
 FT  
 FT Misc-difference 69  
 FT /note= "human framework residue 69 is substd. by  
 FT equivalent murine framework residue"  
 FT  
 FT Misc-difference 70  
 FT /note= "human framework residue 70 is substd. by  
 FT equivalent murine framework residue"  
 FT  
 PN MO9626964-A1.  
 XX  
 PD 06-SEP-1996.  
 XX  
 PF 29-FEB-1996; 96WO-US02754.  
 XX  
 PR 01-MAR-1995; 95US-0397411.  
 XX  
 PA (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Gingrich R, Link BK, Tao JY, Weiner G;  
 XX  
 DR WPI; 1996-412742/41.  
 XX  
 XX New bispecific antibody reactive with both T or NK cells and  
 PT malignant B cells - also their humanised forms and hybridomas  
 PT producing them, useful for treating or preventing leukaemia,  
 PT lymphoma and myeloma  
 PS  
 PS Claim 14; Fig 4a; 85pp; English.  
 XX  
 XX The variable region (AAW05822) of the humanised ID10 antibody light  
 CC chain (AAW05828) consists of human R3.5H5G kappa light chain variable  
 CC region framework (substd. at 5 positions with mouse or consensus  
 CC human amino acids) and complementarity determining regions from the  
 CC murine ID10 antibody specific for a 28/32 kDa heterodimeric antigen  
 CC present on the surface of malignant B-cells. It can be coexpressed  
 CC with humanised ID10 heavy chain (see also AAW05829) in e.g. mouse  
 CC myeloma NSO cells. Humanised antibody fragments can be incorporated  
 CC into novel bispecific antibodies reactive with both effector cell  
 CC antigens (see also AAW05824-25, AAW05826 and AAW05830) and malignant  
 CC B-cells.  
 CC  
 XX  
 PS Sequence 107 AA;  
 XX  
 SQ

Query Match 85.3%; Score 29; DB 17; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 71;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTITE 7  
 |||||  
 50 NAKTLAE 56

RESULT 14  
 AAW07439

ID AAW07439 standard; Protein; 107 AA.

XX AAW07439;

DT 12-AUG-1997 (first entry)

DE Anti-DNA antibody 9f11 group light chain variable region.

XX Light chain; variable region; anti-DNA; monoclonal; antibody;

KM 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis;

KM systemic lupus erythematosus; screening; treatment; prevention;

KM SLE; disease; consensus; putative.

XX Synthetic.

OS Key Location/Qualifiers

FT Region 1..23 /label= framework\_I

FT Region 24..34 /label= CDR\_I

FT Region 35..49 /label= framework\_II

FT Region 50..56 /label= CDR\_II

FT Region 57..88 /label= framework\_III

FT Region 89..97 /label= CDR\_III

FT Region 98..107 /label= J\_region

XX MO636361-A1.

XX 21-NOV-1996.

XX 16-MAY-1996; 96MO-US07113.

XX 18-MAY-1995; 95US-0443540.

XX (UNMI ) UNIV MICHIGAN.

XX Glick GD, Swanson PC;

XX WPI; 1997-011854/01.

XX N-PSE; AAT43808.

XX Anti-DNA antibody which specifically binds DNA hairpin - useful to

XX develop prods. for diagnosis and treatment of disorders, e.g.

XX glomerulonephritis or systemic lupus erythematosus

XX Example; Fig 9; 102pp; English.

XX The present sequence is the light chain variable region of the

XX group 9f11 putative consensus anti-DNA monoclonal antibody (Mab),

XX which has a high affinity for single stranded DNA, low or no

XX affinity for double stranded DNA and specifically binds a DNA

XX hairpin. The Mab can be used to diagnose disorders associated with the

XX pathological complexation of DNA, e.g. inflammatory

XX glomerulonephritis and systemic lupus erythematosus. It can also be

XX used to generate reagents to screen for pharmaceutical agents, and

XX treat and/or prevent an above disorder.

CC The sequence was derived by aligning homologous anti-DNA Mab,  
 CC whose sequences have been published, as well as several Mab of  
 CC other specificities obtained from a database search.

XX Sequence 107 AA;

QY 1 NAKTITE 7  
 |||||  
 50 NAKTLAE 56

Db 50 NAKTLAE 56

RESULT 15

ID AAW46483 standard; protein; 109 AA.

XX AAW46483;

DT 24-JUN-1998 (first entry)

DE 8019 VK antibody.

XX Diagnosis; photoaffinity compound; therapeutic; antibody; SIC5; 8019;

KM antigen; immuno-conjugate.

XX Homo sapiens.

XX MO9803870-A1.

XX 29-JAN-1998.

XX 22-JUL-1997; 97MO-US12223.

XX 23-JUL-1996; 96US-0681432.

XX (KENT ) UNIV KENTUCKY RES FOUND.

XX Haley BE, Kohler H, Pavlinkova G, Rajogopalan K;

XX WPI; 1998-120935/11.

XX Conjugates formed by site-specific attachment of nucleic

XX photo-affinity agents to antibodies - useful as immunoassay reagents

XX for detecting antigen, also immuno-therapeutic complex also

XX containing cytotoxin for treating cancer, infection or genetic

XX disease

XX Disclosure; Figure 12c; 75pp; English.

XX This is the amino acid sequence of 8019 VK antibody. The invention

XX relates to the site-specific photo-attachment of a nucleic

XX photoaffinity compound to an antibody which comprises reacting them

XX under conditions that promote attachment of the photoaffinity

XX compound to at least 1 nucleotide binding site in the antibody. Also

XX claimed are: photoaffinity compound-antibody conjugates produced this

XX way, and immuno-conjugates comprising cytotoxic or therapeutic agent

XX site-specifically attached to the photoaffinity compound in the

XX conjugate. When the conjugate is labelled it is used for detection or

XX quantitation of an antigen (Ag) by any standard immunoassay format,

XX while immuno-conjugates are used therapeutically, e.g. in cases of

XX tumours, infections or genetic diseases, or as imaging agents. The

XX photoaffinity compounds are attached under mild, physiological

XX conditions, particularly a single 2-5 minute photoactivation results in

XX almost 100% attachment (contrast conditions usually required to attach

XX molecules to antibodies.

XX Sequence 109 AA;

XX Query Match 85.3%; Score 29; DB 19; Length 109;

XX Best Local Similarity 85.7%; Pred. No. 72;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NAKTLTE 7  
 |||||  
 XX 50 NAKTLAE 56

RESULT 16  
 AAB84742  
 ID AAB84742 standard; protein; 123 AA.

XX AAB84742;

XX 17-SEP-2001 (first entry)

DE Variable region of the light chain of murine antibody 4H7H7.

XX Light chain; antibody 4H7H7; polyglutamine expansion;

KW neurodegenerative disorder; Huntington's disease.

XX Mus musculus.

XX WO200151522-A1.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00361.

XX 07-JAN-2000; 2000US-0478960.

XX (REGC ) UNIV CALIFORNIA.

XX Finkbeiner S;

XX WPI; 2001-451842/48.

PT Novel antibody useful for detecting the presence of polyglutamine  
 expansion comprising protein in a sample, binds to the protein in a  
 manner that differs from the 1C2 monoclonal antibody -

XX Disclosure; Page 18; 35pp; English.

XX The present chain represents the variable region of the heavy chain  
 CC of murine antibody 4H7H7. This antibody recognizes a protein having a  
 CC polyglutamine expansion, where the number percentage of non-glutamine  
 CC residues in the polyglutamine expansion does not exceed 10. The  
 CC antibody binds to the protein in a manner that differs from the 1C2  
 CC monoclonal antibody. The antibodies are used to modulate intracellular  
 CC binding activity of polyglutamine expansion. The antibodies are useful  
 CC for detecting an agent capable of modulating the binding interaction  
 CC between polyglutamine expansion comprising protein in a cell and a  
 CC target of the protein. They are also useful in immunoassays that are  
 CC capable of providing the detection of disease associated polyglutamine  
 CC expansion containing proteins. The antibodies are useful for treating  
 CC a host suffering from a disease condition associated with the presence  
 CC of polyglutamine expansion containing protein, such as neurodegenerative  
 CC disorders, e.g. Huntington's disease.

XX Sequence 123 AA;

Query Match 85.3%; Score 29; DB 22; Length 123;

Best Local Similarity 85.7%; Pred. No. 83;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 |||||  
 XX 48 NAKTLAE 54

RESULT 17  
 AAR12235

ID AAR12235 standard; Protein; 126 AA.

XX

AC AAR12235;

XX 19-AUG-1991 (first entry)

DE Mouse Mab 2G12 L chain V region.

XX HIV-1; chimera.

XX Mus sp.

XX WO9107494-A.

XX 30-MAY-1991.

XX 13-NOV-1990; 90WO-US06627.

XX 13-NOV-1989; 89US-0433703.

XX (XOMA-) XOMA CORP.

XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;

XX WPI; 1991-178106/24.

XX N-PSDB; AAQ12015.

XX New chimeric mouse human antibodies - used in treatment, diagnosis

XX and prophylaxis of HIV infections.

XX Disclosure; Fig 8; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse-  
 CC human Abs against HIV-1 comprising human Ig constant regions and  
 CC murine variable regions. These novel sequence are useful in  
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be  
 CC produced by a bacterial, yeast or mammalian expression system.

XX Sequence 126 AA;

Query Match 85.3%; Score 29; DB 12; Length 126;

Best Local Similarity 85.7%; Pred. No. 85;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 |||||  
 XX 70 NAKTLAE 76

RESULT 18

ID AAR12357 standard; Protein; 127 AA.

XX AAR12357;

XX 15-AUG-1991 (first entry)

XX Light (kappa) chain variable region of murine 2G12 immuno-

XX globulin.

XX Chimeric antibodies; immunoconjugates; HIV; AIDS.

XX Mus musculus.

XX WO9107493-A.

XX 30-MAY-1991.

XX 13-NOV-1990; 90WO-US06615.

XX 13-NOV-1989; 89US-0433730.

XX (XOMA-) XOMA CORP.

XX (GREC ) GREEN CROSS CORP.

PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 XX WPI: 1991-178044/24.  
 DR N-PSDB; AAQ12059.  
 XX  
 PT New chimeric mouse-human antibodies - used to detect, kill and  
 PT remove HIV-1 antigen from sample  
 XX  
 PS Discloure; fig 8; 107pp; English.  
 XX  
 CC This is the light(kappa)-chain variable (V) region of a mouse  
 CC monoclonal antibody (Mab), 2G12, and is specific for an HIV-1  
 CC viral antigen. It is used in the construction of a chimeric  
 CC Mab comprising heavy and light chains having murine V regions  
 CC and human C regions. The chimeric Mabs are more effective than  
 CC murine Mab 2G12 since they have an increased compatibility in  
 CC humans. The heavy and light chain V-regions are joined by  
 CC manipulating their respective joining (J) regions, to generate  
 CC restriction enzyme recognition sites. The chimeric Mabs can be  
 CC used as immunocongulates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV.  
 CC See also AAQ12056-58 and AAQ12060-63.  
 SQ Sequence 127 AA;  
 Query Match 85.3%; Score 29; DB 12; Length 127;  
 Best Local Similarity 85.7%; Pred. No. 86;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NAKLTLE 7  
 DB 70 NAKTLAE 76  
 RESULT 19  
 ID AAM03721 standard; Protein; 128 AA.  
 XX  
 AC AAM03721;  
 DT 02-APR-1997 (first entry)  
 XX  
 DE Anti-human gp39 Mab 39-1.106 light chain variable region.  
 XX  
 KW Light chain; variable region; murine; mouse; anti-human; disease;  
 KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
 KW diagnosis; inhibition; B-cell; activation; treatment; disorder;  
 KW immune; autoimmune; allergic response; organ rejection; drug;  
 KW graft versus host; cell imaging; tumour; targeted; delivery;  
 KW targeted.  
 KW  
 XX Mus musculus.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= sig\_peptide  
 FT Peptide 21..128  
 FT /label= mat\_peptide  
 FT Region 44..54  
 FT /note= "complementarity determining region 1"  
 FT Region 70..76  
 FT /note= "complementarity determining region 2"  
 FT Region 109..117  
 FT /note= "complementarity determining region 3"  
 FT  
 PN WO9623071-A2.  
 XX  
 XX 01-AUG-1996.  
 XX  
 XX 26-JAN-1996; 96WO-US01119.  
 XX  
 XX 26-JAN-1995; 95US-0379057.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX  
 PI Aruffo AA, Bajorath J, Gilliland LK, Gordon MD;  
 PI Harrie LJ, Hollenbaugh D, Siadek AW;  
 XX  
 DR WPI: 1996-362694/36.  
 DR N-PSDB; AAT35973.  
 XX  
 PT Monoclonal antibodies specific for different epitope(s) on human  
 PT gp39 - used for inhibiting B cell activation and for the diagnosis  
 PT of various disorders, e.g. cancer, psoriasis etc..  
 XX  
 PS Claim 89; Fig 6A; 167pp; English.  
 XX  
 CC The present sequence is the light chain variable region of the  
 CC murine anti-human glycoprotein (gp) 39 monoclonal antibody (Mab)  
 CC 39-1.106 (a member of the murine kappa V subfamily). The Mab was  
 CC prep'd. by immunising a 6-8 week old BALB/c mouse with a gp39-CD8  
 CC fusion protein, and 3 days later harvesting and fusing spleen and  
 CC lymph cells to mouse melanoma cells, to produce an anti-human gp39  
 CC Mab producing hybridoma. The Mab may be useful for diagnosing  
 CC disease states, inhibiting B-cell activation and for treating  
 CC immunological disorders, e.g. autoimmune disorders, allergic  
 CC responses, organ rejection and graft versus host disease. It may  
 CC also be used for imaging cells which express gp39 on their surface,  
 CC e.g. tumour cells, and to target therapeutic agents to such cells.  
 CC The Mab inhibits the CD40/gp39 interaction, therefore limiting both  
 CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.  
 CC specific to these antigens. A typical compsn. for intramuscular  
 CC injection pref. contains 50 mg of Mab in 1 ml of sterile buffered  
 CC water.  
 CC  
 XX  
 SQ Sequence 128 AA;  
 Query Match 85.3%; Score 29; DB 17; Length 128;  
 Best Local Similarity 85.7%; Pred. No. 87;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NAKLTLE 7  
 DB 70 NAKTLAE 76  
 RESULT 20  
 ID ABP00079 standard; Protein; 165 AA.  
 XX  
 AC ABP00079;  
 DT 25-JUN-2002 (first entry)  
 XX  
 DE Human ORFX protein sequence SEQ ID NO:140.  
 XX  
 KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200192523-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 29-MAY-2001; 2001WO-US10836.  
 XX  
 XX 30-MAY-2000; 2000US-206132P.  
 XX 29-AUG-2000; 2000US-228716P.  
 XX  
 PA (CURA-) CURAGEN CORP.

PI	XX	Shimkets RA, Leach MD;
DR	XX	WPI; 2002-106308/14.
XX	XX	N-PSDB; ABN15831.
PT	XX	Novel human polypeptides and polynucleotides useful for diagnosing,
PT	XX	preventing and treating cardiovascular disease, neurodegenerative,
PT	XX	hyperproliferative disorders and autoimmune disorders -
PS	XX	Disclosure; SEQ ID 140; 1037pp; English.
CC	XX	The present invention describes substantially purified human proteins
CC	XX	(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC	XX	in the specification). ABN15762 to ABR27252 encode the human ORFX
CC	XX	proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC	XX	treating or preventing a pathology associated with an ORFX-associated
CC	XX	disorder in humans, and in the manufacture of a medicament for treating a
CC	XX	syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC	XX	sequences can be used in gene therapy. ORFX sequences can be used in the
CC	XX	treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC	XX	psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC	XX	osteoarthritis, neurodegenerative disorders, disorders related to organ
CC	XX	transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC	XX	lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC	XX	storage disease, various immune deficiencies and disorders, infectious
CC	XX	diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC	XX	arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC	XX	disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC	XX	useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC	XX	bone degenerative disorders, or periodontal disease, and for gut
CC	XX	protection or regeneration and treatment of lung or liver fibrosis,
CC	XX	reperfusion injury in various tissues and conditions resulting from
CC	XX	systemic cytokine damage.
CC	XX	N.B. The sequence data for this patent did not form part of the printed
CC	XX	specification, but was obtained in electronic format directly from WIPO
CC	XX	at ftp.wipo.int/pub/published_pct_sequences.
SQ	XX	Sequence 165 AA:
Query Match		85.3% Score 29; DB 23; Length 165;
Best Local Similarity		71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative		2; Mismatches 0; Indels 0; Gaps 0
QY		1 NAKTLTE 7      :    :::
Dd		126 NAKTTTD 132
RESULT 21		
AAM03725	ID	AAM03725 standard; Protein; 171 AA.
AC	XX	AAM03725;
XX	XX	02-APR-1997 (first entry)
DE	XX	Humanised Mab 39-1.106 light chain variable region.
XX	XX	Light chain; variable region; murine; mouse; anti-human; disease;
KM	XX	glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;
KM	XX	diagnosis; inhibition; B-cell; activation; treatment; disorder;
KM	XX	immune; autoimmunity; allergic response; organ rejection; drug;
KM	XX	graft versus host; cell imaging; tumour; targeted; delivery;
KM	XX	targeted; humanised.
OS	XX	Mus musculus.
XX	XX	Key Location/Qualifiers
FH	FT	Misc-difference 2 /note= "corresponding codon TAG"
FT	FT	Misc-difference 11 /note= "corresponding codon TAA"
FT	FT	

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FT      Misc-difference 157      /note= "corresponding codon TAA"
FT      Misc-difference 165      /note= "corresponding codon TAA"
XX      MO9623071-A2.
XX      PD      01-AUG-1996.
XX      PF      26-JAN-1996;      96WO-US01119.
XX      PR      26-JAN-1995;      95US-0379057.
XX      PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      PI      Aruffo AA, Bajorath J, Gilliland LK,      Gordon ML;
XX      PI      Harris LJ, Hollenbaugh D, Sladak AW;
XX      DR      WPI; 1996-362694/36.
XX      DR      N-PSDB; AAT36018.
XX      PT      Monoclonal antibodies specific for different epitope(s) on human
XX      PS      gp39 - used for inhibiting B cell activation and for the diagnosis
XX      PS      of various disorders, e.g. cancer, psoriasis etc..
XX      PS      Example 13; Fig 16; 167pp; English.
XX      CC      The present sequence is the light chain variable region of the
XX      CC      humanised murine anti-human glycoprotein (gp) 39 monoclonal
XX      CC      antibody (MAB) 39-1.106. The Mab may be useful for diagnosing
XX      CC      disease states, inhibiting B-cell activation and for treating
XX      CC      immunological disorders, e.g. autoimmune disorders, allergic
XX      CC      responses, organ rejection and graft versus host disease. It may
XX      CC      also be used for imaging cells which express gp39 on their surface,
XX      CC      e.g. tumor cells, and to target therapeutic agents to such cells.
XX      CC      The Mab inhibits the CD40/gp39 interaction, therefore limiting both
XX      CC      prim. and sec. responses to T-cell dependent antigens and Ab prodn.
XX      CC      specific to these antigens. A typical compn. for intramuscular
XX      CC      injection pref. contains 50 mg of Mab in 1 ml of sterile buffered
XX      CC      water.
XX      SQ      Sequence      171 AA;

OY      Query Match      85.3%;      Score 29;      DB 17;      Length 171;
OY      Best Local Similarity      85.7%;      Pred. No. 1.2e+02;
OY      Matches      6;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;
OY      DB      92 NAKTLAE 98
OY      1 NAKTLTE 7
OY      |||||
OY      |||||

RESULT 22
ID      AAM05828      standard; Protein; 214 AA.
XX      AAM05828;
XX      DT      27-JAN-1997      (first entry)
XX      DE      Humanised 1D10 antibody light chain.
XX      KW      B-cell lymphoma; humanised antibody; bispecific antibody;
XX      KW      myeloma; leukaemia; hybridoma; monoclonal antibody.
XX      OS      Chimeric Homo sapiens;
XX      OS      Chimeric Mus sp.
XX      FH      Key      Location/Qualifiers
XX      FT      Domain      1..107
XX      FT      /label= Variable_domain
XX      FT      24..33
XX      FT      /label= CDR1

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FT Region 49..55
FT /label= CDR2
FT Region 89..97
FT /label= CDR3
FT Domain 108..214
FT /label= Human_C-kappa_domain
XX
XX WO9626964-A1.
XX
XX 06-SEP-1996.
XX
XX 29-FEB-1996; 96WO-US02754.
XX
XX 01-MAR-1995; 95US-0397411.
XX
XX (TOMA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Gingrich R, Link BK, Tso JY, Weiner G;
XX
XX WPI; 1996-412742/41.
XX
XX New bispecific antibody reactive with both T or NK cells and
XX malignant B cells - also their humanised forms and hybridomas
XX producing them, useful for treating or preventing leukaemia,
XX lymphoma and myeloma
XX
XX Example 4; Fig 4c; 85pp; English.
XX
XX The humanised ID10 antibody light chain (AAW05828) includes a
XX variable region (see also AAW05822) consisting of human R3.5HG light
XX chain variable region framework and complementarity determining
XX regions from the murine ID10 antibody specific for a 28/32 kDa
XX antigen found on the surface of malignant B-cells. It can be
XX coexpressed with humanised ID10 heavy chain (see also AAW05829) in
XX mammalian host cells. Bispecific antibodies can be constructed that
XX include a first binding fragment comprising humanised M291 heavy and
XX light chain variable regions (see also AAW05826, AAW05830), and a second
XX binding fragment comprising humanised ID10 heavy and light chain
XX variable regions. Such antibodies are reactive with both T or NK
XX cells and malignant B cells, and have therapeutic and diagnostic
XX applns.
XX
XX Sequence 214 AA;
SQ
Query Match 85.3%; Score 29; DB 17; Length 214;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NAKLTTE 7
Db 50 NAKTLAE 56
RESULT 23
AAW53148
ID AAR53148 standard; Protein: 243 AA.
XX
XX AAR53148;
XX
XX 07-DEC-1994 (first entry)
XX
XX VH and VL of MAb PRL.
XX
XX PE38KDEL, plasmid; pUL140; heavy; chain; light; variable region; VH;
XX VL; monoclonal antibody; MAb; PRL; PCR; amplity; PRL-hybridoma RNA;
XX primer; complementarity determining regions; CDR; drug; cytotoxin;
XX prostate cell associated antigen; radioisotope; PCAA; prostate;
XX cells; cancer; diagnosis; benign prostate hyperplasia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX
XX FH

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FT Protein 1..118
FT /label= PRL VH
FT Peptide 119..133
FT /label= Linker
FT Protein 134..243
FT /label= PRL VL
XX
XX WO9409150-A.
XX
XX 28-APR-1994.
XX
XX 22-SEP-1993; 93WO-US09166.
XX
XX 08-OCT-1992; 92US-0958140.
XX
XX (USSH ) US SEC DEPT HEALTH.
XX
XX Pastan IH;
XX
XX WPI; 1994-151334/18.
XX
XX N-PSDB; AAQ64476.
XX
XX Monoclonal antibody specific for prostate cells - used in the
XX diagnosis and treatment of conditions involving abnormal growth
XX of prostate cells, esp prostate cancer.
XX
XX Example 3; Fig 1; 64pp; English.
XX
XX This sequence is encoded by the PE38KDEL fragment of the plasmid
XX pUL140 and represents the heavy chain and light chain variable regions
XX (VH and VL) of the monoclonal antibody (MAb) PRL. The cDNA encoding
XX this sequence was derived by PCR amplification of reverse transcribed
XX PRL-hybridoma RNA using the primer sequences given in AAQ64477-81. The
XX VH and VL complementarity determining regions (CDRs) are used in the
XX construction of the MAb of the invention which competes with PRL
XX for binding to a prostate cell associated antigen. The MAb of the
XX invention can be used for targeting a drug, cytotoxin or radioisotope
XX to prostate cells of a patient suffering from prostate cancer. It can
XX also be used for diagnosing the presence of prostate cancer in an
XX individual and for the diagnosis and treatment of other conditions
XX involving abnormal growth of prostate cells, eg. benign prostate
XX hyperplasia. The MAb reacts strongly with prostate cancer cells but
XX only weakly with a few other normal human tissues. The effect of
XX therapy on normal prostate cells does not threaten the overall health
XX of the patient.
XX
XX Sequence 243 AA;
SQ
Query Match 85.3%; Score 29; DB 15; Length 243;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NAKLTTE 7
Db 183 NAKTLAE 189
RESULT 24
AAU72864
ID AAU72864 standard; Protein: 256 AA.
XX
XX AAU72864;
XX
XX 26-FEB-2002 (first entry)
XX
XX P4-15 single chain Fv.
XX
XX Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
XX autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
XX intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
XX prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
XX sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI10;
XX helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;

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KM 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;  
KM P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;  
KM p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.  
XX  
OS Homo sapiens.  
XX  
PN W0200171005-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 26-MAR-2001; 2001WO-EP03414.  
XX  
PR 24-MAR-2000; 2000EP-0106467.  
PA (KUFE/) KUFER P.  
XX  
PI Kufer P, Rietmuller G, Lutterbuese R, Borschert K, Kischel R;  
PI Mayer M, Hofmeister R;  
XX  
DR WPI; 2002-055119/07.  
XX  
DR N-PSDB; AAS97138.  
XX  
PT Multifunctional polypeptides comprising binding sites that specifically  
PT recognise extracellular groups of the NKG2D receptor complex and  
PT domains which function as receptors or ligands, useful for treating  
PT cancers and infectious diseases -  
XX  
PS Example 7; Fig 16; 114pp; English.  
XX  
CC The invention relates to a multifunctional polypeptide comprising a  
CC domain with a binding site that specifically recognises an extracellular  
CC group of the NKG2D receptor complex and a second domain which functions  
CC as a receptor or ligand. The polypeptide and its associated  
CC polynucleotide are used for the preparation of a pharmaceutical  
CC composition for the treatment of cancer, infections and/or autoimmune  
CC conditions. The cancer may be a tumour of the head and neck, stomach,  
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,  
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,  
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.  
CC The infectious diseases can be caused by viruses, bacteria, fungi,  
CC protozoa or helminths. The autoimmune diseases include multiple  
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior  
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent  
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and  
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D  
CC receptor and the polypeptides of the invention.  
XX  
SQ Sequence 256 AA;  
QY  
Db 1 NAKTLTE 7  
187 NAKTLAE 193  
Query Match 85.3%; Score 29; DB 23; Length 256;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PN JP2001333780-A.  
XX  
XX 04-DEC-2001.  
PD  
XX 29-MAY-2000; 2000JP-0158575.  
XX  
PF 29-MAY-2000; 2000JP-0158575.  
XX  
PR 29-MAY-2000; 2000JP-0158575.  
PA (KEIO-) GH KEIO GIJUKU.  
XX  
DR WPI; 2002-135945/18.  
XX  
XX A protein fused with a monoclonal antibody against an antigen present  
PT on cell surfaces -  
PT  
PS Claim 14; Page 9; 24pp; Japanese.  
XX  
CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a specifically claimed amino  
CC acid sequence from the present invention.  
XX  
SQ Sequence 258 AA;  
QY  
Db 1 NAKTLTE 7  
191 NAKTLAE 197  
Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 25  
ABB05962  
ID ABB05962 standard; protein; 258 AA.  
XX  
AC ABB05962;  
XX  
DT 09-MAY-2002 (first entry)  
XX  
DE Monoclonal antibody related amino acid sequence SEQ ID NO:1.  
XX  
KM Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX  
OS Mus sp.  
OS Synthetic.  
XX

RESULT 26  
ABB05963  
ID ABB05963 standard; protein; 258 AA.  
XX  
AC ABB05963;  
XX  
DT 09-MAY-2002 (first entry)  
XX  
DE Monoclonal antibody related amino acid sequence SEQ ID NO:2.  
XX  
KM Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN JP2001333780-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 29-MAY-2000; 2000JP-0158575.

XX 29-MAY-2000; 2000JP-0158575.  
PR (KEIO-) GH KEIO GIUKU.  
XX WPI; 2002-135945/18.  
XX A protein fused with a monoclonal antibody against an antigen present  
PT on cell surfaces -  
XX  
PS Claim 15; Page 9; 24pp; Japanese.  
XX  
CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a specifically claimed amino  
CC acid sequence from the present invention.  
XX  
SQ Sequence 258 AA;  
CC  
Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLTE 7  
Db 191 NAKTLAE 197  
XX  
RESULT 27  
ABB05990  
ID ABB05990 standard; Protein; 258 AA.  
XX  
AC ABB05990;  
XX  
DT 09-MAY-2002 (first entry)  
XX  
DE Mouse monoclonal antibody related protein sequence BB.  
XX  
KM Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX  
OS Mus sp.  
XX  
OS Synthetic.  
XX  
PN JP2001333780-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 29-MAY-2000; 2000JP-0158575.  
XX  
PR 29-MAY-2000; 2000JP-0158575.  
XX  
PA (KEIO-) GH KEIO GIUKU.  
XX

DR WPI; 2002-135945/18.  
DR N-PSDB; ABA94200.  
XX  
PT A protein fused with a monoclonal antibody against an antigen present  
PT on cell surfaces -  
XX  
PS Example; Fig 9; 24pp; Japanese.  
XX  
CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.  
XX  
SQ Sequence 258 AA;  
CC  
Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLTE 7  
Db 191 NAKTLAE 197  
XX  
RESULT 28  
ABB05991  
ID ABB05991 standard; Protein; 258 AA.  
XX  
AC ABB05991;  
XX  
DT 09-MAY-2002 (first entry)  
XX  
DE Mouse and human chimeric monoclonal antibody related protein CVB.  
XX  
KM Monoclonal antibody; fusion protein; antigen; cell surface; receptor;  
XX  
KM chimeric.  
XX  
OS Chimeric - Mus sp.  
XX  
OS Chimeric - Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN JP2001333780-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 29-MAY-2000; 2000JP-0158575.  
XX  
PR 29-MAY-2000; 2000JP-0158575.  
XX  
PA (KEIO-) GH KEIO GIUKU.  
XX  
DR WPI; 2002-135945/18.  
DR N-PSDB; ABA94201.  
XX

XX A protein fused with a monoclonal antibody against an antigen present  
PT on cell surfaces -  
XX  
XX Example; Fig 10; 24pp; Japanese.  
XX  
CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.  
XX  
SQ Sequence 258 AA;  
XX  
Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLTE 7  
Db 191 NAKTLAE 197  
XX  
RESULT 29  
ABB05992  
ID ABB05992 standard; Protein; 258 AA.  
XX  
AC ABB05992;  
XX  
DT 09-MAY-2002 (first entry)  
XX  
DE Mouse and human chimeric monoclonal antibody related protein Cab.  
XX  
KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;  
XX chimeric.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN JP2001333780-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 29-MAY-2000; 2000JP-0158575.  
XX  
PR 29-MAY-2000; 2000JP-0158575.  
XX  
PA (KEIO-) GH KEIO GIJUKU.  
XX  
XX WPI; 2002-135945/18.  
DR N-PSDB; ABA94202.  
XX  
PT A protein fused with a monoclonal antibody against an antigen present

PT on cell surfaces -  
XX  
XX Example; Fig 11; 24pp; Japanese.  
XX  
CC The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.  
XX  
SQ Sequence 258 AA;  
XX  
Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLTE 7  
Db 191 NAKTLAE 197  
XX  
RESULT 30  
ABB05993  
ID ABB05993 standard; Protein; 258 AA.  
XX  
AC ABB05993;  
XX  
DT 09-MAY-2002 (first entry)  
XX  
DE Mouse and human chimeric monoclonal antibody related protein DB.  
XX  
KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;  
XX chimeric.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN JP2001333780-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 29-MAY-2000; 2000JP-0158575.  
XX  
PR 29-MAY-2000; 2000JP-0158575.  
XX  
PA (KEIO-) GH KEIO GIJUKU.  
XX  
XX WPI; 2002-135945/18.  
DR N-PSDB; ABA94203.  
XX  
PT A protein fused with a monoclonal antibody against an antigen present  
XX on cell surfaces -

PS Example; Fig 12; 24pp; Japanese.  
 CC The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal  
 CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a  
 CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC mouse type monoclonal antibody is converted to prepare a single-stranded  
 CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the  
 CC human type monoclonal antibody to prepare a human type single-stranded  
 CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
 CC gene is expressed in a microbe to prepare a recombinant protein of the  
 CC human type single-stranded immunoprotein. Also described is a method for  
 CC introducing the above complex of monoclonal antibody-fused protein  
 CC through a cell surface receptor. The method is used for the preparation  
 CC of a monoclonal antibody-fused protein against a receptor present on cell  
 CC surface. The present sequence represents a protein sequence which is  
 CC given in an example from the present invention.

SO Sequence 258 AA;  
 Query Match 85.3%; Score 29; DB 23; Length 258;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAKTLE 7  
 Db 191 NAKTLE 197

RESULT 31  
 ABB05994  
 ID ABB05994 standard; Protein; 258 AA.  
 AC ABB05994;  
 DT 09-MAY-2002 (first entry)  
 DE Mouse and human chimeric monoclonal antibody related protein BC.  
 KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor;  
 KW chimeric.  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 OS Synthetic.  
 PN JP2001333780-A.  
 PD 04-DEC-2001.  
 PF 29-MAY-2000; 2000JP-0158575.  
 PR 29-MAY-2000; 2000JP-0158575.  
 PA (KEIO-) GH KEIO GIJUKU.  
 DR WPI; 2002-135945/18.  
 DR N-PSDB; ABA94204.  
 XX A protein fused with a monoclonal antibody against an antigen present  
 PT on cell surfaces -  
 PS Example; Fig 13; 24pp; Japanese.

CC The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the  
 CC combining site for the gene. Also described is a complex of a monoclonal  
 CC antibody-fused protein which is a complex of monoclonal antibody-fused  
 CC protein and a DNA, and a method for the preparation of a monoclonal  
 CC antibody-fused protein against a receptor present on cell surface in  
 CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
 CC said monoclonal antibody against a receptor present on cell surface is  
 CC used as the template to amplify a single-stranded antibody gene of a  
 CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
 CC mouse type monoclonal antibody is converted to prepare a single-stranded  
 CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
 CC the amino acid tail is added to the single-stranded antibody gene of the  
 CC human type monoclonal antibody to prepare a human type single-stranded  
 CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
 CC gene is expressed in a microbe to prepare a recombinant protein of the  
 CC human type single-stranded immunoprotein. Also described is a method for  
 CC introducing the above complex of monoclonal antibody-fused protein  
 CC through a cell surface receptor. The method is used for the preparation  
 CC of a monoclonal antibody-fused protein against a receptor present on cell  
 CC surface. The present sequence represents a protein sequence which is  
 CC given in an example from the present invention.

SO Sequence 258 AA;  
 Query Match 85.3%; Score 29; DB 23; Length 258;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAKTLE 7  
 Db 191 NAKTLE 197

RESULT 32  
 ABB05995  
 ID ABB05995 standard; Protein; 258 AA.  
 AC ABB05995;  
 DT 09-MAY-2002 (first entry)  
 DE Human monoclonal antibody related protein sequence CVC.  
 KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
 KW Homo sapiens.  
 OS Synthetic.  
 PN JP2001333780-A.  
 PD 04-DEC-2001.  
 PF 29-MAY-2000; 2000JP-0158575.  
 PR 29-MAY-2000; 2000JP-0158575.  
 PA (KEIO-) GH KEIO GIJUKU.  
 DR WPI; 2002-135945/18.  
 DR N-PSDB; ABA94205.  
 XX A protein fused with a monoclonal antibody against an antigen present  
 PT on cell surfaces -  
 PS Example; Fig 14; 24pp; Japanese.  
 CC The present invention describes a protein which is fused with a  
 CC monoclonal antibody against an antigen present on cell surface and which  
 CC can transfer a gene by combining with the gene and containing a human  
 CC type single-stranded monoclonal antibody and a peptide which is the

CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

SQ Sequence 258 AA;

Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NAKTLTE 7  
Db 191 NAKTLAE 197

RESULT 33

ABB05996 standard; Protein; 258 AA.

AC ABB05996;

DT 09-MAY-2002 (first entry)

DE Human monoclonal antibody related protein sequence CAC.

KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.

OS Homo sapiens.

OS Synthetic.

XX JP2001333780-A.

XX 04-DEC-2001.

XX 29-MAY-2000; 2000JP-0158575.

XX 29-MAY-2000; 2000JP-0158575.

XX (KEIO-) GH KEIO GIJUKU.

XX WPI: 2002-135945/18.

XX N-PSDB; ABA94206.

XX A protein fused with a monoclonal antibody against an antigen present

XX on cell surfaces -

XX Example; Fig 15; 24pp; Japanese.

XX The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in

CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the  
CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

SQ Sequence 258 AA;

Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NAKTLTE 7  
Db 191 NAKTLAE 197

RESULT 34

ABB05997 standard; Protein; 258 AA.

AC ABB05997;

DT 09-MAY-2002 (first entry)

DE Human monoclonal antibody related protein sequence DC.

KW Monoclonal antibody; fusion protein; antigen; cell surface; receptor.

OS Homo sapiens.

OS Synthetic.

XX JP2001333780-A.

XX 04-DEC-2001.

XX 29-MAY-2000; 2000JP-0158575.

XX 29-MAY-2000; 2000JP-0158575.

XX (KEIO-) GH KEIO GIJUKU.

XX WPI: 2002-135945/18.

XX N-PSDB; ABA94207.

XX A protein fused with a monoclonal antibody against an antigen present

XX on cell surfaces -

XX Example; Fig 16; 24pp; Japanese.

XX The present invention describes a protein which is fused with a  
CC monoclonal antibody against an antigen present on cell surface and which  
CC can transfer a gene by combining with the gene and containing a human  
CC type single-stranded monoclonal antibody and a peptide which is the  
CC combining site for the gene. Also described is a complex of a monoclonal  
CC antibody-fused protein which is a complex of monoclonal antibody-fused  
CC protein and a DNA, and a method for the preparation of a monoclonal  
CC antibody-fused protein against a receptor present on cell surface in  
CC which: (1) an mRNA extracted from a hybridoma cell having productivity of  
CC said monoclonal antibody against a receptor present on cell surface is  
CC used as the template to amplify a single-stranded antibody gene of a  
CC mouse type monoclonal antibody by PCR; (2) the framework portion of the

CC mouse type monoclonal antibody is converted to prepare a single-stranded  
CC antibody gene of a human type monoclonal antibody; (3) a gene encoding  
CC the amino acid tail is added to the single-stranded antibody gene of the  
CC human type monoclonal antibody to prepare a human type single-stranded  
CC immunoprotein gene; and (4) the human type single-stranded immunoprotein  
CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

CC  
XX  
SQ Sequence 258 AA;

QY 1 NAKTLE 7  
Db 191 NAKTLE 197

Query Match 85.3%; Score 29; DB 23; Length 258;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 35  
ABB05982 ID ABB05982 standard; Protein; 287 AA.  
XX  
XX ABB05982;  
XX  
XX 09-MAY-2002 (first entry)  
XX  
XX Monoclonal antibody related protein sequence PBH.  
XX  
XX Monoclonal antibody; fusion protein; antigen; cell surface; receptor.  
XX  
XX Unidentified.  
XX  
XX JF2001333780-A.  
XX  
XX 04-DEC-2001.  
XX  
XX 29-MAY-2000; 2000UP-0158575.  
XX  
XX 29-MAY-2000; 2000UP-0158575.  
XX  
XX (KEIO-) GH KEIO GIUKU.  
XX  
XX WPI; 2002-135945/18.  
XX  
XX N-PSDB; ABA94192.  
XX  
XX A protein fused with a monoclonal antibody against an antigen present  
XX on cell surfaces -  
XX  
XX Example; Fig 1; 24pp; Japanese.  
XX  
XX The present invention describes a protein which is fused with a  
XX monoclonal antibody against an antigen present on cell surface and which  
XX can transfer a gene by combining with the gene and containing a human  
XX type single-stranded monoclonal antibody and a peptide which is the  
XX combining site for the gene. Also described is a complex of a monoclonal  
XX antibody-fused protein which is a complex of monoclonal antibody-fused  
XX protein and a DNA, and a method for the preparation of a monoclonal  
XX antibody-fused protein against a receptor present on cell surface in  
XX which: (1) an mRNA extracted from a hybridoma cell having productivity of  
XX said monoclonal antibody against a receptor present on cell surface is  
XX used as the template to amplify a single-stranded antibody gene of a  
XX mouse type monoclonal antibody by PCR; (2) the framework portion of the  
XX mouse type monoclonal antibody is converted to prepare a single-stranded  
XX antibody gene of a human type monoclonal antibody; (3) a gene encoding  
XX the amino acid tail is added to the single-stranded antibody gene of the  
XX human type monoclonal antibody to prepare a human type single-stranded  
XX immunoprotein gene; and (4) the human type single-stranded immunoprotein

CC gene is expressed in a microbe to prepare a recombinant protein of the  
CC human type single-stranded immunoprotein. Also described is a method for  
CC introducing the above complex of monoclonal antibody-fused protein  
CC through a cell surface receptor. The method is used for the preparation  
CC of a monoclonal antibody-fused protein against a receptor present on cell  
CC surface. The present sequence represents a protein sequence which is  
CC given in an example from the present invention.

CC  
XX  
SQ Sequence 287 AA;

QY 1 NAKTLE 7  
Db 205 NAKTLE 211

Query Match 85.3%; Score 29; DB 23; Length 287;  
Best Local Similarity 85.7%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 36  
AAG48704 ID AAG48704 standard; Protein; 320 AA.  
XX  
XX AAG48704;  
XX  
XX 18-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 61533.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX  
XX EPI033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
XX  
XX 05-MAR-1999; 99US-0123180.  
XX  
XX 09-MAR-1999; 99US-0123548.  
XX  
XX 23-MAR-1999; 99US-0125788.  
XX  
XX 25-MAR-1999; 99US-0126264.  
XX  
XX 29-MAR-1999; 99US-0126785.  
XX  
XX 01-APR-1999; 99US-0127462.  
XX  
XX 06-APR-1999; 99US-0128234.  
XX  
XX 08-APR-1999; 99US-0128714.  
XX  
XX 16-APR-1999; 99US-0129845.  
XX  
XX 19-APR-1999; 99US-0130077.  
XX  
XX 21-APR-1999; 99US-0130449.  
XX  
XX 23-APR-1999; 99US-0130510.  
XX  
XX 28-APR-1999; 99US-0130891.  
XX  
XX 30-APR-1999; 99US-0131449.  
XX  
XX 30-APR-1999; 99US-0132048.  
XX  
XX 04-MAY-1999; 99US-0132407.  
XX  
XX 05-MAY-1999; 99US-0132484.  
XX  
XX 06-MAY-1999; 99US-0132485.  
XX  
XX 07-MAY-1999; 99US-0132486.  
XX  
XX 11-MAY-1999; 99US-0132487.  
XX  
XX 14-MAY-1999; 99US-0132488.  
XX  
XX 14-MAY-1999; 99US-0134218.  
XX  
XX 14-MAY-1999; 99US-0134219.  
XX  
XX 14-MAY-1999; 99US-0134221.  
XX  
XX 18-MAY-1999; 99US-0134370.  
XX  
XX 19-MAY-1999; 99US-0134768.  
XX  
XX 20-MAY-1999; 99US-0134941.  
XX  
XX 21-MAY-1999; 99US-0135124.  
XX  
XX 24-MAY-1999; 99US-0135353.  
XX  
XX 99US-0135629.

PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151338.  
PR 01-SEP-1999; 99US-0151930.  
PR 01-SEP-1999; 99US-0152363.  
PR 07-SEP-1999; 99US-0153070.  
PR 10-SEP-1999; 99US-0153758.  
PR 13-SEP-1999; 99US-0154018.  
PR 15-SEP-1999; 99US-0154939.  
PR 16-SEP-1999; 99US-0154779.  
PR 20-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157865.  
PR 06-OCT-1999; 99US-0157753.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159637.  
PR 18-OCT-1999; 99US-0159584.  
PR 18-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 22-OCT-1999; 99US-0161044.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.

PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 85.3%; Score 29; DB 21; Length 320;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAKLTLE 7  
:|||||  
Db 4 HAKLTLE 10

RESULT 37  
AAV37571  
ID AAV37571 standard; Protein; 350 AA.

XX AAV37571;

XX 07-OCT-1999 (first entry)

DE Chlamydia trachomatis surface exposed protein.

XX Vaccine; eye disease; conventional trachoma; nongonococcal urethritis; epididymitis; genital disease; perinephritis;  
XX paratrachoma; inclusion conjunctivitis; genital disease; perinephritis;  
XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis;  
XX Bartholinitis; pneumopathy; venereal lymphogranulomatosis.

OS Chlamydia trachomatis.

PN WO928475-A2.

PD 10-JUN-1999.

XX 27-NOV-1998; 98MO-IB01939.

XX 04-NOV-1998; 98US-0107077.

PR 28-NOV-1997; 97FR-0015041.

PR 17-DEC-1997; 97FR-0016034.

XX (GEST ) GENSET.

XX Griffais R;

XX MPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis

XX Disclosure; Page 1226-1227; 1755BP; English.

XX AAV36754-Y37949 are encoded by open reading frames (ORFs) of the genome  
XX of Chlamydia trachomatis (see AA201425). The polypeptides can be used as  
XX vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences  
XX can also be used to control growth of the microorganism. Chlamydia  
XX trachomatis is responsible for a large number of diseases, e.g. eye  
XX diseases such as conventional trachoma, nongonococcal urethritis,  
XX paratrachoma, and inclusion conjunctivitis; genital diseases such as  
XX nongonococcal urethritis, epididymitis, cervicitis, salpingitis,  
XX perinephritis, Bartholinitis, pneumopathy in breast feeding infants;  
XX and venereal lymphogranulomatosis. The polypeptides of the invention  
XX may be of use in treating these diseases.

CC Sequence 350 AA;

Query Match 85.3%; Score 29; DB 20; Length 350;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAKLTLE 7  
:|||||  
Db 121 NAKLTLE 127

RESULT 38

AAB80119  
ID AAB80119 standard; Protein; 356 AA.

XX AAB80119;

XX 30-APR-2001 (first entry)

DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:972.

XX Corynebacterium glutamicum; metabolic pathway protein; MP protein;  
XX fine chemical production; microorganism; organic acid; nucleoside;  
XX nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;  
XX lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;  
XX carbohydrate; aromatic compound; cofactor; polypeptide; enzyme.

OS Corynebacterium glutamicum.

PN WO200100843-A2.

PD 04-JAN-2001.

XX 23-JUN-2000; 2000MO-IB00923.

XX 25-JUN-1999; 99US-0141031.

PR 01-JUL-1999; 99DE-1030476.

PR 02-JUL-1999; 99US-0142101.

PR 08-JUL-1999; 99DE-1031415.

PR 08-JUL-1999; 99DE-1031418.

PR 08-JUL-1999; 99DE-1031419.

PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.

PR 08-JUL-1999; 99DE-1031434.

PR 08-JUL-1999; 99DE-1031435.

PR 08-JUL-1999; 99DE-1031443.

PR 08-JUL-1999; 99DE-1031453.

PR 08-JUL-1999; 99DE-1031457.

PR 08-JUL-1999; 99DE-1031465.

PR 08-JUL-1999; 99DE-1031478.

PR 08-JUL-1999; 99DE-1031510.

PR 08-JUL-1999; 99DE-1031541.

PR 08-JUL-1999; 99DE-1031573.

PR 08-JUL-1999; 99DE-1031592.

PR 08-JUL-1999; 99DE-1031632.

PR 08-JUL-1999; 99DE-1031634.

PR 08-JUL-1999; 99DE-1031636.

PR 09-JUL-1999; 99DE-1032125.

PR 09-JUL-1999; 99DE-1032126.

PR 09-JUL-1999; 99DE-1032130.

PR 09-JUL-1999; 99DE-1032186.

PR 09-JUL-1999; 99DE-1032206.

PR 09-JUL-1999; 99DE-1032227.

PR 09-JUL-1999; 99DE-1032228.

PR 09-JUL-1999; 99DE-1032229.

PR 09-JUL-1999; 99DE-1032230.

PR 14-JUL-1999; 99DE-1032232.

PR 14-JUL-1999; 99DE-1032826.

PR 14-JUL-1999; 99DE-1032828.

PR 14-JUL-1999; 99DE-1033004.

PR 14-JUL-1999; 99DE-1033006.

PR 14-JUL-1999; 99DE-1033005.

PR 12-AUG-1999; 99US-0148613.

PR 27-AUG-1999; 99DE-1040764.

PR 27-AUG-1999; 99DE-1040765.

PR 27-AUG-1999; 99DE-1040766.

PR 27-AUG-1999; 99DE-1040832.

PR 31-AUG-1999; 99DE-1041378.

PR 31-AUG-1999; 99DE-1041379.

PR 31-AUG-1999; 99DE-1041380.

PR 31-AUG-1999; 99DE-1041394.

PR 31-AUG-1999; 99DE-1041396.

PR 03-SEP-1999; 99DE-1042076.

PR 03-SEP-1999; 99DE-1042077.

PR 03-SEP-1999; 99DE-1042079.  
 PR 03-SEP-1999; 99DE-1042086.  
 PR 03-SEP-1999; 99DE-1042087.  
 PR 03-SEP-1999; 99DE-1042088.  
 PR 03-SEP-1999; 99DE-1042095.  
 PR 03-SEP-1999; 99DE-1042124.  
 PR 03-SEP-1999; 99DE-1042129.  
 PR 09-MAR-2000; 2000US-0187970.  
 XX  
 XX (BADI ) BASF AG.  
 PA  
 PI Pompeius M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;  
 DR WPI; 2001-137957/14.  
 DR N-PSDB; AAF72238.  
 XX  
 XX Nucleic acids from Corynebacterium glutamicum encoding metabolic  
 PT pathway proteins, useful for producing fine chemicals in  
 PT microorganisms, including organic acids, nonproteinogenic amino acids,  
 and purine and pyrimidine bases -  
 XX  
 PS Claim 20; Page 1490-1491; 1737pp; English.  
 XX  
 CC AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic  
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum  
 CC MP nucleic acids are useful for the production of fine chemicals.  
 CC in microorganisms, including organic acids, nonproteinogenic amino  
 CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,  
 CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic  
 CC compounds, vitamins, cofactors, polyketides and enzymes.  
 XX  
 SQ Sequence 356 AA;  
 OY 1 NAKTLE 7  
 Db 279 NAKTIRD 285  
 Query Match 85.3%; Score 29; DB 22; Length 356;  
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 39  
 ID AAB80159  
 XX AAB80159 standard; Protein; 356 AA.  
 AC AAB80159;  
 XX  
 XX 30-APR-2001 (first entry)  
 DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:1052.  
 XX  
 KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;  
 KW fine chemical production; microorganism; organic acid; nucleoside;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;  
 KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;  
 KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN WO200100843-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000MO-IB00923.  
 XX  
 XX 25-JUN-1999; 99US-0141031.  
 PR 01-JUL-1999; 99DE-1030476.  
 PR 02-JUL-1999; 99US-0142101.  
 PR 08-JUL-1999; 99DE-1031415.  
 PR 08-JUL-1999; 99DE-1031418.  
 PR 08-JUL-1999; 99DE-1031419.  
 PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.  
 PR 08-JUL-1999; 99DE-1031428.  
 PR 08-JUL-1999; 99DE-1031434.  
 PR 08-JUL-1999; 99DE-1031435.  
 PR 08-JUL-1999; 99DE-1031443.  
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 PR 08-JUL-1999; 99DE-1031457.  
 PR 08-JUL-1999; 99DE-1031465.  
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 PR 08-JUL-1999; 99DE-1031510.  
 PR 08-JUL-1999; 99DE-1031541.  
 PR 08-JUL-1999; 99DE-1031573.  
 PR 08-JUL-1999; 99DE-1031592.  
 PR 08-JUL-1999; 99DE-1031632.  
 PR 08-JUL-1999; 99DE-1031634.  
 PR 08-JUL-1999; 99DE-1031636.  
 PR 08-JUL-1999; 99DE-1031625.  
 PR 09-JUL-1999; 99DE-1032126.  
 PR 09-JUL-1999; 99DE-1032130.  
 PR 09-JUL-1999; 99DE-1032186.  
 PR 09-JUL-1999; 99DE-1032206.  
 PR 09-JUL-1999; 99DE-1032227.  
 PR 09-JUL-1999; 99DE-1032229.  
 PR 09-JUL-1999; 99DE-1032230.  
 PR 14-JUL-1999; 99DE-1032922.  
 PR 14-JUL-1999; 99DE-1032926.  
 PR 14-JUL-1999; 99DE-1032928.  
 PR 14-JUL-1999; 99DE-1033004.  
 PR 14-JUL-1999; 99DE-1033005.  
 PR 14-JUL-1999; 99DE-1033006.  
 PR 12-AUG-1999; 99US-0148613.  
 PR 27-AUG-1999; 99DE-1040764.  
 PR 27-AUG-1999; 99DE-1040765.  
 PR 27-AUG-1999; 99DE-1040766.  
 PR 27-AUG-1999; 99DE-1040832.  
 PR 31-AUG-1999; 99DE-1041378.  
 PR 31-AUG-1999; 99DE-1041379.  
 PR 31-AUG-1999; 99DE-1041380.  
 PR 31-AUG-1999; 99DE-1041394.  
 PR 31-AUG-1999; 99DE-1041396.  
 PR 03-SEP-1999; 99DE-1042076.  
 PR 03-SEP-1999; 99DE-1042077.  
 PR 03-SEP-1999; 99DE-1042079.  
 PR 03-SEP-1999; 99DE-1042086.  
 PR 03-SEP-1999; 99DE-1042087.  
 PR 03-SEP-1999; 99DE-1042088.  
 PR 03-SEP-1999; 99DE-1042095.  
 PR 03-SEP-1999; 99DE-1042124.  
 PR 03-SEP-1999; 99DE-1042129.  
 PR 09-MAR-2000; 2000US-0187970.  
 XX  
 PA (BADI ) BASF AG.  
 PI Pompeius M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;  
 DR WPI; 2001-137957/14.  
 DR N-PSDB; AAF72238.  
 XX  
 XX Nucleic acids from Corynebacterium glutamicum encoding metabolic  
 PT pathway proteins, useful for producing fine chemicals in  
 PT microorganisms, including organic acids, nonproteinogenic amino acids,  
 and purine and pyrimidine bases -  
 XX  
 PS Claim 20; Page 1595-1596; 1737pp; English.  
 XX  
 CC AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic  
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum  
 CC MP nucleic acids are useful for the production of fine chemicals  
 CC in microorganisms, including organic acids, nonproteinogenic amino  
 CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,  
 CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic  
 CC compounds, vitamins, cofactors, polyketides and enzymes.

XX  
SQ Sequence 356 AA;

Query Match 85.3%; Score 29; DB 22; Length 356;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
|||:|:  
Db 279 NAKLTID 285

## RESULT 40

AAR12970  
ID AAR12970 standard; Protein; 407 AA.

XX  
AC AAR12970;

XX  
DT 26-SEP-1991 (first entry)

XX  
DE Substance P receptor.

XX  
KM Analgesic; antiinflammatory; anticonvulsant.

XX  
PN JP03133998-A.

XX  
PD 07-JUN-1991.

XX  
PF 17-OCT-1989; 89JP-0270039.

XX  
PR 17-OCT-1989; 89JP-0270039.

XX  
PA (MITU ) MITSUBISHI KASEI CORP.

XX  
DR WPI; 1991-211763/29.

XX  
DR N-PSDB; AAQ12560.

XX  
PT New substance P receptor protein and gene - for production of  
PT diagnostics and as analgesics, antiinflammatories and  
PT anticonvulsants.

XX  
PS Claim 1; Fig 1; 13pp; Japanese.

XX  
CC Substance P is a pain transmitter and the receptor is an effective  
CC masking protein of substance P. It may be used as an analgesic, an  
CC antiinflammatory drug or an anticonvulsant. It can also be used in  
CC diagnosis.

XX  
SQ Sequence 407 AA;

Query Match 85.3%; Score 29; DB 12; Length 407;

Best Local Similarity 71.4%; Pred. No. 3.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
|||:|:  
Db 391 NSKLTTE 397

Search completed: July 18, 2003, 15:06:44  
Job time : 24.66 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:46 ; Search time 8.12 Seconds  
(without alignments)  
25.365 Million cell updates/sec

Title: US-10-007-790-9

Perfect score: 34

Sequence: 1 NAKTLTE 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	7	4	US-09-257-069-9	Sequence 9, Appl1
2	34	100.0	107	4	US-09-257-069-4	Sequence 4, Appl1
3	29	85.3	94	3	US-08-881-037-68	Sequence 68, Appl1
4	29	85.3	99	3	US-08-881-037-33	Sequence 33, Appl1
5	29	85.3	99	3	US-08-881-037-34	Sequence 34, Appl1
6	29	85.3	99	3	US-08-881-037-35	Sequence 35, Appl1
7	29	85.3	107	3	US-08-888-366-24	Sequence 24, Appl1
8	29	85.3	107	3	US-08-881-037-69	Sequence 69, Appl1
9	29	85.3	107	3	US-08-881-037-70	Sequence 70, Appl1
10	29	85.3	107	3	US-08-881-037-72	Sequence 72, Appl1
11	29	85.3	107	3	US-08-397-411-1	Sequence 1, Appl1
12	29	85.3	107	3	US-08-397-411-2	Sequence 2, Appl1
13	29	85.3	108	2	US-08-379-057-27	Sequence 27, Appl1
14	29	85.3	108	2	US-08-379-057-28	Sequence 28, Appl1
15	29	85.3	128	2	US-08-379-057-12	Sequence 12, Appl1
16	29	85.3	214	3	US-08-397-411-5	Sequence 5, Appl1
17	29	85.3	227	1	US-08-681-432-2	Sequence 2, Appl1
18	29	85.3	243	1	US-07-958-140-2	Sequence 2, Appl1
19	29	85.3	243	5	PCT-US93-09166-2	Sequence 2, Appl1
20	29	85.3	407	5	PCT-US92-06532-7	Sequence 6, Appl1
21	29	85.3	407	5	PCT-US92-06532-7	Sequence 7, Appl1
22	28	82.4	213	4	US-09-134-001C-4587	Sequence 4587, Ap
23	28	82.4	484	4	US-09-134-001C-5063	Sequence 5063, Ap
24	27	79.4	100	1	US-08-681-812-6	Sequence 6, Appl1
25	27	79.4	133	2	US-08-861-549-4	Sequence 4, Appl1
26	27	79.4	205	2	US-08-861-549-1	Sequence 1, Appl1
27	27	79.4	205	2	US-08-861-549-3	Sequence 3, Appl1

28	27	79.4	958	1	US-08-426-236-4	Sequence 4, Appl1
29	26	76.5	7	2	US-08-765-783A-82	Sequence 82, Appl1
30	26	76.5	7	4	US-09-416-557-82	Sequence 82, Appl1
31	26	76.5	24	2	US-08-146-028-90	Sequence 90, Appl1
32	26	76.5	24	4	US-08-723-425A-90	Sequence 90, Appl1
33	26	76.5	24	4	US-09-112-206-90	Sequence 90, Appl1
34	26	76.5	26	2	US-08-146-028-91	Sequence 91, Appl1
35	26	76.5	26	4	US-08-723-425A-91	Sequence 91, Appl1
36	26	76.5	26	4	US-09-112-206-91	Sequence 91, Appl1
37	26	76.5	31	2	US-08-845-926-7	Sequence 7, Appl1
38	26	76.5	31	4	US-09-351-296-7	Sequence 7, Appl1
39	26	76.5	36	2	US-08-146-028-89	Sequence 89, Appl1
40	26	76.5	36	4	US-08-723-425A-89	Sequence 89, Appl1
41	26	76.5	36	4	US-09-112-206-89	Sequence 89, Appl1
42	26	76.5	107	3	US-08-933-983-76	Sequence 76, Appl1
43	26	76.5	107	5	PCT-US94-07659-8	Sequence 8, Appl1
44	26	76.5	126	2	US-08-765-783A-73	Sequence 73, Appl1
45	26	76.5	126	2	US-08-765-783A-77	Sequence 77, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-257-069-9  
; Sequence 9, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-9  
  
Query Match 100.0%; Score 34; DB 4; Length 7;  
Best local Similarity 100.0%; Pred No. 1.9e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
|||||  
Db 1 NAKTLTE 7  
  
RESULT 2  
US-09-257-069-4  
; Sequence 4, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-4

Query Match 100.0%; Score 34; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
|||||  
50 NAKLTTE 56

## RESULT 3

US-08-881-037-68  
; Sequence 68, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIORITY INFORMATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Koniski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-68

Query Match 85.3%; Score 29; DB 3; Length 94;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
|||||  
50 NAKLTTE 56

## RESULT 4

US-08-881-037-33  
; Sequence 33, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIORITY INFORMATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Koniski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-33

Query Match 85.3%; Score 29; DB 3; Length 99;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKLTTE 7  
|||||  
42 NAKLTTE 48

## RESULT 5

US-08-881-037-34  
; Sequence 34, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIORITY INFORMATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-34

Query Match 85.3%; Score 29; DB 3; Length 99;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
DB 42 NAKTLAE 48

RESULT 6  
US-08-881-037-35  
Sequence 35, Application US/08881037  
Patent No. 6080588  
GENERAL INFORMATION:  
APPLICANT: Glick, Gary D.  
APPLICANT: Swanson, Patrick C.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
City: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-35

Query Match 85.3%; Score 29; DB 3; Length 99;  
Best Local Similarity 85.7%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
DB 42 NAKTLAE 48

RESULT 7  
US-08-888-366-24  
Sequence 24, Application US/08888366  
Patent No. 5972656  
GENERAL INFORMATION:  
APPLICANT: Lopez, Osvaldo  
APPLICANT: Wylie, Dwane E.  
APPLICANT: Wagner, Fred W.  
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 90 South 7th street, 3100 No. 5972656west Ctr.  
City: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,366  
FILING DATE: 03-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,407  
FILING DATE: 27-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,542  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/493,299  
FILING DATE: 14-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/324,392  
FILING DATE: 14-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.39USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-24

Query Match 85.3%; Score 29; DB 2; Length 107;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
DB 50 NAKTLAE 56

RESULT 8  
US-08-881-037-69  
Sequence 69, Application US/08881037  
Patent No. 6080588

GENERAL INFORMATION:  
APPLICANT: Glick, Gary D.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Konski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-69

Query Match 85.3%; Score 29; DB 3; Length 107;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAKTLE 7  
Db 50 NAKTLAE 56

RESULT 9  
US-08-881-037-70  
Sequence 70, Application US/08881037  
Patent No. 6080588  
GENERAL INFORMATION:  
APPLICANT: Glick, Gary D.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037

FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Konski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-70

Query Match 85.3%; Score 29; DB 3; Length 107;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAKTLE 7  
Db 50 NAKTLAE 56

RESULT 10  
US-08-881-037-72  
Sequence 72, Application US/08881037  
Patent No. 6080588  
GENERAL INFORMATION:  
APPLICANT: Glick, Gary D.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Konski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
US-08-881-037-72  
Query Match 85.3%; Score 29; DB 3; Length 107;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLE 7  
Db 50 NAKTLAE 56  
RESULT 11  
US-08-397-411-1  
Sequence 1, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: B-cell Lymphoma and Cell Line  
TITLE OF INVENTION: B-cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-1  
Query Match 85.3%; Score 29; DB 3; Length 107;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLE 7  
Db 50 NAKTLAE 56  
RESULT 12  
US-08-397-411-2  
Sequence 2, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:

APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: B-cell Lymphoma and Cell Line  
TITLE OF INVENTION: B-cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ. ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-2  
Query Match 85.3%; Score 29; DB 3; Length 107;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLE 7  
Db 50 NAKTLAE 56  
RESULT 13  
US-08-379-057-27  
Sequence 27, Application US/08379057  
Patent No. 5876950  
GENERAL INFORMATION:  
APPLICANT: Siadak, Anthony W.  
APPLICANT: Hollenbaugh, Diane L.  
APPLICANT: Gilliland, Lisa K.  
APPLICANT: Gordon, Marcia L.  
APPLICANT: Bajorath, Jürgen  
APPLICANT: Aruffo, Alejandro A.  
TITLE OF INVENTION: Monoclonal Antibodies Specific For  
TITLE OF INVENTION: Different Epitopes of Human gp93 and Methods For Their Use  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,057  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0133-  
TELEPHONE: (206) 727-3670  
TELEFAX: (206) 727-3601  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-379-057-27

Query Match 85.3%; Score 29; DB 2; Length 108;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 50 NAKTLAE 56

RESULT 14  
US-08-379-057-28  
Sequence 28, Application US/08379057  
Patent No. 5876950  
GENERAL INFORMATION:  
APPLICANT: Siadak, Anthony W.  
APPLICANT: Hollenbaugh, Diane L.  
APPLICANT: Gilliland, Lisa K.  
APPLICANT: Gordon, Marcia L.  
APPLICANT: Bajorath, Jurgen  
APPLICANT: Aruffo, Alejandro A.  
TITLE OF INVENTION: Monoclonal Antibodies Specific For  
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,057  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0133-  
TELEPHONE: (206) 727-3670  
TELEFAX: (206) 727-3601  
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-379-057-28

Query Match 85.3%; Score 29; DB 2; Length 108;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 50 NAKTLAE 56

RESULT 15  
US-08-379-057-12  
Sequence 12, Application US/08379057  
Patent No. 5876950  
GENERAL INFORMATION:  
APPLICANT: Siadak, Anthony W.  
APPLICANT: Hollenbaugh, Diane L.  
APPLICANT: Gilliland, Lisa K.  
APPLICANT: Gordon, Marcia L.  
APPLICANT: Bajorath, Jurgen  
APPLICANT: Aruffo, Alejandro A.  
TITLE OF INVENTION: Monoclonal Antibodies Specific For  
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,057  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0133-  
TELEPHONE: (206) 727-3670  
TELEFAX: (206) 727-3601  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-379-057-12

Query Match 85.3%; Score 29; DB 2; Length 128;  
Best Local Similarity 85.7%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 70 NAKTLAE 76

RESULT 16  
US-08-397-411-5  
Sequence 5, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-5

Query Match 85.3%; Score 29; DB 3; Length 214;  
Best Local Similarity 85.7%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 50 NAKTLAE 56

RESULT 17  
US-08-681-432-2  
Sequence 2, Application US/08681432  
Patent No. 5800991  
GENERAL INFORMATION:  
APPLICANT: HALEY, Boyd E.  
APPLICANT: KOHLER, Heinz  
APPLICANT: RAJAGOPALAN, Krishnan  
APPLICANT: PAVINKOVA, Gabriela  
TITLE OF INVENTION: NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY  
TITLE OF INVENTION: COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR  
TITLE OF INVENTION: MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND  
TITLE OF INVENTION: THERAPEUTICS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BURN, DOANE, SWECKER & MATTHIS  
STREET: P.O. Box 1404

CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/681,432  
FILING DATE: 23-JUL-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/208,822  
FILING DATE: 11-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Teekin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 028750-132  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-681-432-2

Query Match 85.3%; Score 29; DB 1; Length 227;  
Best Local Similarity 85.7%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 50 NAKTLAE 56

RESULT 18  
US-07-958-140-2  
Sequence 2, Application US/07958140  
Patent No. 5489525  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira H.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/958,140  
FILING DATE: 19921008  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 15280-77  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-958-140-2

Query Match 85.3%; Score 29; DB 1; Length 243;  
Best Local Similarity 85.7%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 183 NAKTLAE 189

RESULT 19  
PCT-US93-09166-2  
Sequence 2, Application PC/TUS9309166  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira H.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09166  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 15280-77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 243 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-09166-2

Query Match 85.3%; Score 29; DB 5; Length 243;  
Best Local Similarity 85.7%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 183 NAKTLAE 189

RESULT 20  
US-08-390-000A-6  
Sequence 6, Application US/08390000A  
Patent No. 5985583  
GENERAL INFORMATION:  
APPLICANT: Sealfon, Stuart C.  
TITLE OF INVENTION: Cloning and Expression of  
Gonadotropin-Releasing Hormone Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Penile & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,000A  
FILING DATE: 17-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6923-052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 407 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-390-000A-6

Query Match 85.3%; Score 29; DB 2; Length 407;  
Best Local Similarity 71.4%; Pred. No. 62;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLE 7  
Db 391 NSKTMTE 397

RESULT 21  
PCT-US92-06532-7  
Sequence 7, Application PC/TUS9206532  
GENERAL INFORMATION:  
APPLICANT: Krause, James B.  
TITLE OF INVENTION: Human Substance P Receptor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD  
STREET: 800 N. Lindbergh Blvd.  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 63167  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06532  
FILING DATE: 19920805  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyer, Scott J.  
REGISTRATION NUMBER: 25,275  
REFERENCE/DOCKET NUMBER: 07-24(776)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)694-3117  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 407 amino acids  
TYPE: AMINO ACID

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-06532-7

Query Match 85.3%; Score 29; DB 5; Length 407;  
Best Local Similarity 71.4%; Pred. No. 62;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 391 NAKTLTE 397

RESULT 22  
US-09-134-001C-4587  
Sequence 4587, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4587  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4587

Query Match 82.4%; Score 28; DB 4; Length 213;  
Best Local Similarity 85.7%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 46 NAKTLTE 52

RESULT 23  
US-09-134-001C-5063  
Sequence 5063, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 5063  
LENGTH: 484  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5063

Query Match 82.4%; Score 28; DB 4; Length 484;  
Best Local Similarity 85.7%; Pred. No. 1,3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 1 NAKTLTE 7

Db 323 NAKTLTE 329

RESULT 24  
US-08-681-812-6  
Sequence 6, Application US/08681812  
Patent No. 5763593  
GENERAL INFORMATION:  
APPLICANT: Young, Richard A.  
APPLICANT: Gadois, Ellen L.  
APPLICANT: Chao, David M.  
TITLE OF INVENTION: TBP-Associated Global Negative Regulator  
TITLE OF INVENTION: and Methods of Use Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/681,812  
FILING DATE: 29-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH196-07  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-9540  
TELEFAX: 617-861-6240  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-681-812-6

Query Match 79.4%; Score 27; DB 1; Length 100;  
Best Local Similarity 83.3%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
Db 61 NAKTLMT 66

RESULT 25  
US-08-681-549-4  
Sequence 4, Application US/08681549  
Patent No. 5874246  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: NEW TRANSCRIPTION REPRESSOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,549  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0306 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1244714  
US-08-861-549-4

Query Match 79.4%; Score 27; DB 2; Length 193;  
Best Local Similarity 83.3%; Pred. No. 77;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAKTLT 6  
|||||  
Db 49 NAKTMT 54

RESULT 26  
US-08-861-549-1  
Sequence 1, Application US/08861549  
Patent No. 5874246  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NEW TRANSCRIPTION REPRESSOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,549  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0306 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SYNORAB01  
CLONE: 1620089  
US-08-861-549-1

Query Match 79.4%; Score 27; DB 2; Length 205;  
Best Local Similarity 83.3%; Pred. No. 82;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAKTLT 6  
|||||  
Db 61 NAKTMT 66

RESULT 27  
US-08-861-549-3  
Sequence 3, Application US/08861549  
Patent No. 5874246  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NEW TRANSCRIPTION REPRESSOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,549  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0306 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1491710  
US-08-861-549-3

Query Match 79.4%; Score 27; DB 2; Length 205;  
Best Local Similarity 83.3%; Pred. No. 82;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAKTLT 6  
|||||  
Db 61 NAKTMT 66

```

RESULT 28
US-08-426-236-4
; Sequence 4, Application US/08426236
; Patent No. 5629188
; GENERAL INFORMATION:
; APPLICANT: Shida, Kiyotaka
; APPLICANT: Schimmel, Paul R.
; APPLICANT: Rimpaster, Tracy L.
; TITLE OF INVENTION: Human Alanyl-tRNA Synthetase Proteins,
; TITLE OF INVENTION: Nucleic Acids and Tester Strains Comprising Same
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,236
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI94-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 958 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-426-236-4

Query Match          79.4%; Score 27; DB 1; Length 958;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKLTTE 7
Db      858 NAKAITE 864

RESULT 29
US-08-765-783A-82
; Sequence 82, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsumoto, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-82

Query Match          76.5%; Score 26; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKLTTE 7
Db      1 NAKTLAD 7

RESULT 30
US-09-416-557-82
; Sequence 82, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsumoto, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,557
; FILING DATE: 12-October-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,783
; FILING DATE: 7-March-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959

```

REFERENCE/DOCKET NUMBER: 35029-20001.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-416-557-82

Query Match 76.5%; Score 26; DB 4; Length 7;  
Best Local Similarity 71.4%; Pred. No. 1.9e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLT 7  
Db 1 NAKTLAD 7

RESULT 31  
US-08-146-028-90  
Sequence 90, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1

NAME/KEY: Modified-site  
LOCATION: 24  
US-08-146-028-90

Query Match 76.5%; Score 26; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
Db 14 NAKTLT 19

RESULT 32  
US-08-723-425A-90  
Sequence 90, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHUYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
NAME/KEY: Modified-site  
LOCATION: 24  
US-08-723-425A-90

Query Match 76.5%; Score 26; DB 4; Length 24;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
Db 14 NAKTLT 19

RESULT 33  
US-09-112-206-90  
Sequence 90, Application US/09112206  
Patent No. 6210903  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206

```

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV type 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 24
; US-09-112-206-90

```

```

Query Match          76.5%; Score 26; DB 4; Length 24;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 NAKTLT 6
        ||:||||
Db      14 NAKTLT 19

```

```

RESULT 34
US-08-146-028-91
; Sequence 91, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV type 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 26
; US-08-146-028-91

```

```

Query Match          76.5%; Score 26; DB 2; Length 26;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 NAKTLT 6
        ||:||||
Db      4 NAKTLT 9

```

```

RESULT 35
US-08-723-425A-91
; Sequence 91, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHAYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV type 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 26
; US-08-723-425A-91

```

```

Query Match          76.5%; Score 26; DB 4; Length 26;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 NAKTLT 6
        ||:||||
Db      4 NAKTLT 9

```

```

RESULT 36
US-09-112-206-91
; Sequence 91, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

```

NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,028  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 26  
US-09-112-206-91

Query Match 76.5%; Score 26; DB 4; Length 26;  
Best Local Similarity 83.3%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTIT 6  
DB 4 NAKTIT 9

RESULT 37  
US-08-845-926-7  
Sequence 7, Application US/08845926  
Patent No. 5935778  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,926  
FILING DATE: 04-28-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/598,993  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2

FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis C Virus  
US-08-845-926-7

Query Match 76.5%; Score 26; DB 2; Length 31;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTIT 6  
DB 12 NAKTIT 17

RESULT 38  
US-09-351-296-7  
Sequence 7, Application US/09351296  
Patent No. 6447992  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, Christoph  
APPLICANT: WEINHUES-THELEN, Ursula-Henrike  
APPLICANT: SCHMITT, Urban  
APPLICANT: JUNG, G nther-Gerhard  
APPLICANT: IHLENFELDT, HANS-Georg  
APPLICANT: KRAAS, Wolfgang  
TITLE OF INVENTION: Method for serological typing using  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street N.W. Suite 330  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/351,296  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/845,926  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 04 302.2  
FILING DATE: 09-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis C Virus  
US-09-351-296-7

Query Match 76.5%; Score 26; DB 4; Length 31;  
Best Local Similarity 83.3%; Pred. No. 17;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
DB 12 NAKTLT 17

RESULT 39  
US-08-146-028-89  
Sequence 89, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (PPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 36  
US-08-146-028-89

Query Match 76.5%; Score 26; DB 2; Length 36;  
Best Local Similarity 83.3%; Pred. No. 20;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
DB 14 NAKTLT 19

RESULT 40  
US-08-723-425A-89  
Sequence 89, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHIE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV type 2  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 36  
US-08-723-425A-89

Query Match 76.5%; Score 26; DB 4; Length 36;  
Best Local Similarity 83.3%; Pred. No. 20;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
DB 14 NAKTLT 19

Search completed: July 18, 2003, 15:11:51  
Job time : 9.12 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:09:56 ; Search time 18.06 Seconds  
(without alignments)  
46.031 Million cell updates/sec

Title: US-10-007-790-9  
Perfect score: 34  
Sequence: 1 NAKTLITE 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	85.3	101	15	US-10-096-246-18
2	29	85.3	106	15	US-10-096-246-15
3	29	85.3	108	15	US-10-096-246-19
4	29	85.3	302	15	US-10-156-761-8682
5	29	85.3	472	11	US-09-738-626-3610
6	29	85.3	502	15	US-10-006-852-18
7	29	85.3	660	15	US-10-007-693-139
8	27	79.4	100	11	US-09-881-752A-112
9	27	79.4	205	11	US-09-789-054A-42
10	27	79.4	500	11	US-09-731-872-466
11	27	79.4	572	10	US-09-815-242-10049
12	27	79.4	572	10	US-09-815-242-11086
13	27	79.4	582	10	US-09-815-242-113898
14	26	76.5	7	10	US-09-730-857-82
15	26	76.5	24	14	US-10-318-200-22
16	26	76.5	31	15	US-10-196-174-7

17	26	76.5	107	12	US-09-977-283A-76	Sequence 76, Appl
18	26	76.5	108	15	US-10-096-246-17	Sequence 17, Appl
19	26	76.5	126	10	US-09-730-857-73	Sequence 73, Appl
20	26	76.5	126	10	US-09-730-857-77	Sequence 77, Appl
21	26	76.5	127	10	US-09-730-857-27	Sequence 27, Appl
22	26	76.5	127	12	US-09-977-283A-5	Sequence 5, Appl
23	26	76.5	127	12	US-09-977-283A-9	Sequence 9, Appl
24	26	76.5	128	10	US-09-799-848-2	Sequence 2, Appl
25	26	76.5	218	15	US-10-142-201B-8	Sequence 8, Appl
26	26	76.5	251	10	US-09-935-390A-30	Sequence 30, Appl
27	26	76.5	268	10	US-09-875-456A-14	Sequence 14, Appl
28	26	76.5	277	10	US-09-922-217-693	Sequence 693, App
29	26	76.5	277	11	US-09-833-263-693	Sequence 693, App
30	26	76.5	277	15	US-10-025-380-693	Sequence 693, App
31	26	76.5	299	15	US-10-213-990-39	Sequence 39, Appl
32	26	76.5	303	11	US-09-738-626-6409	Sequence 6409, Ap
33	26	76.5	320	10	US-09-745-763-150	Sequence 150, App
34	26	76.5	325	10	US-09-925-301-969	Sequence 969, App
35	26	76.5	362	11	US-09-738-626-6967	Sequence 6967, Ap
36	26	76.5	416	10	US-09-815-242-10139	Sequence 10139, A
37	26	76.5	429	15	US-10-156-761-11065	Sequence 11065, A
38	26	76.5	447	11	US-09-738-626-6982	Sequence 6982, Ap
39	26	76.5	457	10	US-09-815-242-12670	Sequence 12670, A
40	26	76.5	512	10	US-09-922-217-1093	Sequence 1093, Ap
41	26	76.5	512	11	US-09-833-263-1093	Sequence 1093, Ap
42	26	76.5	512	15	US-10-025-380-1093	Sequence 1093, Ap
43	26	76.5	512	15	US-10-245-103-110	Sequence 110, App
44	26	76.5	512	15	US-10-245-107-110	Sequence 110, App
45	26	76.5	512	15	US-10-245-143-110	Sequence 110, App

#### ALIGNMENTS

#### RESULT 1

US-10-096-246-18  
; Sequence 18, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor  
; FILE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)  
; FILE REFERENCE: NEU-0007  
; CURRENT APPLICATION NUMBER: US/10/096, 246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-18

Query Match 85.3%; Score 29; DB 15; Length 101;  
Best Local Similarity 85.7%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLITE 7  
Db 43 NAKTLAE 49

#### RESULT 2

US-10-096-246-15  
; Sequence 15, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc  
; FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-15

Query Match 85.3%; Score 29; DB 15; Length 106;  
Best Local Similarity 85.7%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 50 NAKTLAE 56

RESULT 3  
US-10-096-246-19  
; Sequence 19, Application US/10096246  
; Publication No. US2003010060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc  
; FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-19

Query Match 85.3%; Score 29; DB 15; Length 108;  
Best Local Similarity 85.7%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 50 NAKTLAE 56

RESULT 4  
US-10-156-761-8682  
; Sequence 8682, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADATOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 8682  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-8682

Query Match 85.3%; Score 29; DB 15; Length 302;  
Best Local Similarity 85.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 163 DAKTLTE 169

RESULT 5  
US-09-738-626-3610  
; Sequence 3610, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 3610  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-3610

Query Match 85.3%; Score 29; DB 11; Length 472;  
Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 274 NAKTLTD 280

RESULT 6  
US-10-006-852-18  
; Sequence 18, Application US/10006852  
; Publication No. US20030046732A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinnerseely, Alan M.  
; APPLICANT: Turano, Frank J.  
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production  
; FILE REFERENCE: 7224-65  
; CURRENT APPLICATION NUMBER: US/10/006,852  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: US 60/246,367  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 502

; TYPE: PRT

; ORGANISM: Lycopersicon esculentum

US-10-006-852-18

Query Match 85.3%; Score 29; DB 15; Length 502;

Best Local Similarity 85.7%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

Db 351 NAKVLTE 357

RESULT 7

US-10-007-693-139

; Sequence 139, Application US/10007693

; Publication No. US20020146776A1

; GENERAL INFORMATION:

; APPLICANT: Bhatia, Ajay

; APPLICANT: Probst, Peter

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT

; FILE REFERENCE: 210121.515C2

; CURRENT APPLICATION NUMBER: US/10/007,693

; CURRENT FILING DATE: 2001-12-05

; NUMBER OF SEQ ID NOS: 157

; SEQ ID NO 139

; LENGTH: 660

; TYPE: PRT

; ORGANISM: Chlamydia trachomatis

US-10-007-693-139

Query Match 85.3%; Score 29; DB 15; Length 660;

Best Local Similarity 85.7%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

Db 120 NAKTLAE 126

RESULT 8

US-09-881-752A-112

; Sequence 112, Application US/09881752A

; Patent No. US20020115078A1

; GENERAL INFORMATION:

; APPLICANT: Kleanthous, Harold

; APPLICANT: Al-Garawi, Amal

; APPLICANT: Miller, Charles

; APPLICANT: Tomb, Jean-Francois

; APPLICANT: Oomen, Raymond P.

; TITLE OF INVENTION: Identification of Polynucleotides

; FILE REFERENCE: Encoding No. US20020115078A1el Helicobacter Polypeptides in the

; CURRENT APPLICATION NUMBER: US/09/881,752A

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 08/833,457

; PRIOR FILING DATE: 1997-04-01

; NUMBER OF SEQ ID NOS: 370

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 112

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-09-881-752A-112

Query Match 79.4%; Score 27; DB 11; Length 100;

Best Local Similarity 71.4%; Pred. No. 80;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

Db 91 NAKTLAQ 97

RESULT 9

US-09-789-054A-42

; Sequence 42, Application US/09789054A

; Publication No. US20020184659A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Zhu, Qun

; TITLE OF INVENTION: PLANT GENES ENCODING DR1 AND DRAP1, A GLOBAL REPRESSOR COMPLEX OF

; FILE REFERENCE: BB1107 US CIP

; CURRENT APPLICATION NUMBER: US/09/789,054A

; CURRENT FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 09/485558

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: PCT/US98/16688

; PRIOR FILING DATE: 1998-08-12

; PRIOR APPLICATION NUMBER: 60/055,865

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 42

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-789-054A-42

Query Match 79.4%; Score 27; DB 11; Length 205;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6

Db 61 NAKTMT 66

RESULT 10

US-09-731-872-466

; Sequence 466, Application US/09731872

; Patent No. US20020102604A1

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Bougueleret, Lydie

; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

; FILE REFERENCE: 78.US3.REG

; CURRENT APPLICATION NUMBER: US/09/731,872

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,629

; PRIOR FILING DATE: 1999-12-08

; PRIOR APPLICATION NUMBER: US 60/187,470

; PRIOR FILING DATE: 2000-03-06

; NUMBER OF SEQ ID NOS: 482

; SOFTWARE: Patent.pm

; SEQ ID NO 466

; LENGTH: 500

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-731-872-466

Query Match 79.4%; Score 27; DB 11; Length 500;

Best Local Similarity 83.3%; Pred. No. 4.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6

Db 458 NAKTMT 463

```
RESULT 11
US-09-815-242-10049
; Sequence 10049, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10049
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10049

Query Match 79.4%; Score 27; DB 10; Length 572;
Best Local Similarity 71.4%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 259 NAKTIAE 265

RESULT 12
US-09-815-242-11086
; Sequence 11086, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11086
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-11086

Query Match 79.4%; Score 27; DB 10; Length 582;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 258 NAKTIAE 264

RESULT 13
US-09-815-242-13898
; Sequence 13898, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13898
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13898

Query Match 79.4%; Score 27; DB 10; Length 582;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 259 NAKTIAE 265
```

QY 1 NAKTLTE 7  
Db 269 NAKTIAE 275

RESULT 14  
US-09-730-857-82  
; Sequence 82, Application US/09730857  
; Patent No. US20020082396A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; Matsumoto, Yoshinori  
; Yamada, Yoshiaki  
; Sato, Koh  
; Tsuchiya, Masayuki  
; Yamazaki, Tatsumi  
; TITLE OF INVENTION: Reshaped Human Antibody to  
; Interleukin-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/730,857  
; FILING DATE: 07-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/416,557  
; FILING DATE: 1999-10-12  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 35029-20001.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-730-857-82

Query Match 76.5%; Score 26; DB 10; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 1 NAKTLAD 7

RESULT 15  
US-10-318-200-22  
; Sequence 22, Application US/10318200  
; Publication No. US20030129746A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: DELPA, ERIK  
; APPLICANT: BUYSSE, MARIE-ANGE

; TITLE OF INVENTION: EPITOPES IN VIRAL ENVELOPE PROTEINS AND SPECIFIC  
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST THESE EPITOPES: USE FOR  
; FILE REFERENCE: 2551-47  
; CURRENT APPLICATION NUMBER: US/10/318,200  
; CURRENT FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: US/09/645,470  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: PCT/EP99/02154  
; PRIOR FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: EP 98870060.5  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
US-10-318-200-22

Query Match 76.5%; Score 26; DB 14; Length 24;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
Db 3 NAKTLT 8

RESULT 16  
US-10-196-174-7  
; Sequence 7, Application US/10196174  
; Publication No. US20030108974A1  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, Christoph  
; WEINHUES-THELEN, Ursula-Henrike  
; SCHMITT, Urban  
; JUNG, G nther-Gerhard  
; IHLENFELDT, HANS-Georg  
; KRAAS, Wolfgang  
; TITLE OF INVENTION: Method for serological typing using  
; type-specific antigens  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/196,174  
; FILING DATE: 17-Jul-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/351,296  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/845,926  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: DE 195 04 302.2  
; FILING DATE: 09-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murray, Robert B.  
; REGISTRATION NUMBER: 22,980  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-5000  
; TELEFAX: (202)638-4810  
; INFORMATION FOR SEQ ID NO: 7:

```
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 31 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: <Unknown>
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
/ ; ORIGINAL SOURCE:
/ ; ORGANISM: Hepatitis C Virus
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-196-174-7

Query Match          76.5%; Score 26; DB 15; Length 31;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAKTLT 6
DB      12 NAKTLT 17

RESULT 17
US-09-977-283A-76
/ ; Sequence 76, Application US/09977283A
/ ; Publication No. US20030031664A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: Reed, Guy L.
/ ; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
/ ; FILE REFERENCE: 0609.4320003
/ ; CURRENT APPLICATION NUMBER: US/09/977,283A
/ ; CURRENT FILING DATE: 2001-10-16
/ ; PRIOR APPLICATION NUMBER: 08/934,000
/ ; PRIOR FILING DATE: 1997-09-19
/ ; PRIOR APPLICATION NUMBER: 60/026,356
/ ; PRIOR FILING DATE: 1996-09-20
/ ; NUMBER OF SEQ ID NOS: 81
/ ; SOFTWARE: Patentin version 3.1
/ ; SEQ ID NO 76
/ ; LENGTH: 107
/ ; TYPE: PRT
/ ; ORGANISM: Artificial Sequence
/ ; FEATURE:
/ ; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody
/ ; NAME/KEY: MISC FEATURE
/ ; LOCATION: (74)..(74)
/ ; OTHER INFORMATION: May be any Amino Acid
US-09-977-283A-76

Query Match          76.5%; Score 26; DB 12; Length 107;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKTLTE 7
DB      50 NAKTLAD 56

RESULT 18
US-10-096-246-17
/ ; Sequence 17, Application US/10096246
/ ; Publication No. US20030100060A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: The Minister of National Defence, Government of Canada
/ ; APPLICANT: Fulton, R E
/ ; APPLICANT: Alvi, Azhar E
/ ; APPLICANT: Nagata, Leslie
/ ; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
/ ; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
/ ; FILE REFERENCE: NEL-0007
/ ; CURRENT APPLICATION NUMBER: US/10/096,246
/ ; CURRENT FILING DATE: 2002-03-13
/ ; NUMBER OF SEQ ID NOS: 37
/ ; SOFTWARE: Patentin version 3.1
/ ; SEQ ID NO 17
```

```
/ ; LENGTH: 108
/ ; TYPE: PRT
/ ; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-17

Query Match          76.5%; Score 26; DB 15; Length 108;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKTLTE 7
DB      50 NAKTLAD 56

RESULT 19
US-09-730-857-73
/ ; Sequence 73, Application US/09730857
/ ; Patent No. US20020082396A1
/ ; GENERAL INFORMATION:
/ ; APPLICANT: Matsushima, Kouji
/ ; Matsushima, Kouji
/ ; Yamada, Yoshiki
/ ; Sato, Koh
/ ; Tsuchiya, Masayuki
/ ; Yamazaki, Tatsumi
/ ; TITLE OF INVENTION: Reshaped Human Antibody to
/ ; INTERLEUKIN-8
/ ; NUMBER OF SEQUENCES: 105
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: MORRISON & FOERSTER
/ ; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
/ ; CITY: Washington
/ ; STATE: DC
/ ; COUNTRY: USA
/ ; ZIP: 20006-1888
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: Diskette
/ ; COMPUTER: IBM Compatible
/ ; OPERATING SYSTEM: DOS
/ ; SOFTWARE: FastSeq for Windows Version 2.0
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/09/730,857
/ ; FILING DATE: 07-Dec-2000
/ ; CLASSIFICATION: <Unknown>
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: 09/416,557
/ ; FILING DATE: 1999-10-12
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: Murashige, Kate H
/ ; REGISTRATION NUMBER: 29,959
/ ; REFERENCE/DOCKET NUMBER: 35029-20001.10
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 202-887-1500
/ ; TELEFAX: 202-822-0168
/ ; TELEX: <Unknown>
/ ; INFORMATION FOR SEQ ID NO: 73:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 126 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
/ ; FRAGMENT TYPE: internal
/ ; FEATURE:
/ ; NAME/KEY: Signal Sequence
/ ; LOCATION: 1...19
/ ; OTHER INFORMATION:
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-730-857-73

Query Match          76.5%; Score 26; DB 10; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 NAKTLTE 7  
Db ||||| :  
69 NAKTLAD 75

## RESULT 20

US-09-730-857-77

; Sequence 77, Application US/09730857

; Patent No. US20020082396A1

; GENERAL INFORMATION:

; APPLICANT: Matsumoto, Kouji

; Matsumoto, Yoshihiro

; Yamada, Yoshiki

; Sato, Koh

; Tsuchiya, Masayuki

; Yamazaki, Tatsumi

; TITLE OF INVENTION: Reshaped Human Antibody to

; Interleukin-8

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON &amp; FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION NUMBER: US/09/730,857

; FILING DATE: 07-Dec-2000

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/416,557

; FILING DATE: 1999-10-12

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 35029-20001.10

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELEX: &lt;Unknown&gt;

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 126 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLESCULE TYPE: protein

; FRAGMENT TYPE: internal

; FEATURE:

; NAME/KEY: Signal Sequence

; LOCATION: 1...19

; OTHER INFORMATION:

; SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-09-730-857-77

## Query Match

Best Local Similarity 76.5%; Score 26; DB 10; Length 126;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db ||||| :  
69 NAKTLAD 75

## RESULT 21

US-09-730-857-27

; Sequence 27, Application US/09730857

; Patent No. US20020082396A1

; GENERAL INFORMATION:

; APPLICANT: Matsumoto, Kouji

; Matsumoto, Yoshihiro

; Yamada, Yoshiki

; Sato, Koh

; Tsuchiya, Masayuki

; Yamazaki, Tatsumi

; TITLE OF INVENTION: Reshaped Human Antibody to

; Interleukin-8

; NUMBER OF SEQUENCES: 105

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON &amp; FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION NUMBER: US/09/730,857

; FILING DATE: 07-Dec-2000

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/416,557

; FILING DATE: 1999-10-12

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 35029-20001.10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELEX: &lt;Unknown&gt;

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 127 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLESCULE TYPE: protein

; FRAGMENT TYPE: internal

; FEATURE:

; NAME/KEY: Signal Sequence

; LOCATION: 1...20

; OTHER INFORMATION:

; SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-730-857-27

## Query Match

Best Local Similarity 76.5%; Score 26; DB 10; Length 127;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db ||||| :  
70 NAKTLAD 76

## RESULT 22

US-09-977-283A-5

; Sequence 5, Application US/09977283A

; Publication No. US20030031664A1

; GENERAL INFORMATION:

; APPLICANT: Reed, Guy L.

; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis

; FILE REFERENCE: 0609.4320003

; CURRENT APPLICATION NUMBER: US/09/977,283A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 08/934,000  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/026,356  
; PRIOR FILING DATE: 1996-09-20  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 5  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
; NAME/KEY: MISC FEATURE  
; LOCATION: (-12)...(-12)  
; OTHER INFORMATION: May be either Gly or Ala  
US-09-977-283A-5

Query Match 76.5%; Score 26; DB 12; Length 127;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 70 NAKTLAD 76

RESULT 23  
US-09-977-283A-9  
; Sequence 9, Application US/09977283A  
; Publication No. US20030031664A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Guy L.  
; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis  
; FILE REFERENCE: 0609.4320003  
; CURRENT APPLICATION NUMBER: US/09/977,283A  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 08/934,000  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/026,356  
; PRIOR FILING DATE: 1996-09-20  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 9  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody  
US-09-977-283A-9

Query Match 76.5%; Score 26; DB 12; Length 127;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 70 NAKTLAD 76

RESULT 24  
US-09-799-848-2  
; Sequence 2, Application US/09799848  
; Patent No. US20010044145A1  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett  
; APPLICANT: Cook, Phillip  
; APPLICANT: Crooke, Stanley  
; APPLICANT: Wu, Hongliang  
; APPLICANT: Lima, Walter  
; TITLE OF INVENTION: METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF  
; FILE REFERENCE: ISFH-0521  
; CURRENT APPLICATION NUMBER: US/09/799,848  
; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 09/343,809  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 09/684,254  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/203,716  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: US 60/067,458  
; PRIOR FILING DATE: 1997-12-04  
; PRIOR APPLICATION NUMBER: US 09/453,514  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: US 09/144,611  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: US 08/861,306  
; PRIOR FILING DATE: 1997-04-21  
; PRIOR APPLICATION NUMBER: US 08/244,993  
; PRIOR FILING DATE: 1994-06-21  
; PRIOR APPLICATION NUMBER: US 07/814,961  
; PRIOR FILING DATE: 1991-12-24  
; PRIOR APPLICATION NUMBER: US 09/462,280  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: PCT/US98/13966  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: US 08/889,296  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 08/411,734  
; PRIOR FILING DATE: 1995-04-03  
; PRIOR APPLICATION NUMBER: US 08/007,996  
; PRIOR FILING DATE: 1993-10-21  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 2  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-799-848-2

Query Match 76.5%; Score 26; DB 10; Length 128;  
Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 67 DSKTLTE 73

RESULT 25  
US-10-142-201B-8  
; Sequence 8, Application US/10142201B  
; Publication No. US20030022205A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MPI2001-106PIRN(M)  
; CURRENT APPLICATION NUMBER: US/10/142,201B  
; CURRENT FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: US 60/289,893  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-142-201B-8

Query Match 76.5%; Score 26; DB 15; Length 218;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||:|

```
Db          50 NAKTTFTE 56

RESULT 26
US-09-935-390A-30
; Sequence 30, Application US/09935390A
; Patent No. US20020076761A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; Quianjin, Hu
; Garcia, Pablo
; Williams, Lewis T.
; Kothakota, Srinivas
; TITLE OF INVENTION: Secreted Human Proteins
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,390A
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/988,671
; FILING DATE: 1997-12-11
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. R. Potter
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 1369.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2718
; TELEFAX: (510) 655-3542
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020076761A1e
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-935-390A-30

Query Match          76.5%; Score 26; DB 10; Length 251;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          1 NAKTTLTE 7
Db          63 NIKTVTE 69

RESULT 27
US-09-875-456A-14
; Sequence 14, Application US/09875456A
; Patent No. US20020045229A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human betala sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/09/875,456A
; CURRENT FILING DATE: 2001-09-10

Db          50 NAKTTFTE 56

Query Match          76.5%; Score 26; DB 10; Length 251;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          1 NAKTTLTE 7
Db          63 NIKTVTE 69

RESULT 28
US-09-922-217-693
; Sequence 693, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSTICS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-693

Query Match          76.5%; Score 26; DB 10; Length 277;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          1 NAKTTLTE 7
Db          63 NEKTVTE 69

RESULT 29
US-09-833-263-693
; Sequence 693, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 693
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; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-263-693

Query Match          76.5%; Score 26; DB 11; Length 277;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 63 NEKTVTE 69

RESULT 30
US-10-025-380-693
; Sequence 693, Application US/10023380
; Publication No. US20020192191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-380-693

Query Match          76.5%; Score 26; DB 15; Length 277;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 63 NEKTVTE 69

RESULT 31
US-10-213-990-39
; Sequence 39, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 39
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-39

Query Match          76.5%; Score 26; DB 15; Length 299;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 76 NTKTLSE 82

RESULT 32
US-09-738-626-6409
; Sequence 6409, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6409
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6409

Query Match          76.5%; Score 26; DB 11; Length 303;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 87 NGETLTE 93

RESULT 33
US-09-745-763-150
; Sequence 150, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 219
```

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Genetics Institute, Inc.  
;/ STREET: 87 CambridgePark Drive.  
;/ CITY: Cambridge  
;/ STATE: MA  
;/ COUNTRY: U.S.A.  
;/ ZIP: 02140  
;/  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/745,763  
;/ FILING DATE: 18-Jun-2000  
;/ CLASSIFICATION: <Unknown>  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Spurger, Suzanne A.  
;/ REGISTRATION NUMBER: 41,323  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (617) 498-8284  
;/ TELEFAX: (617) 876-5851  
;/ INFORMATION FOR SEQ ID NO: 150:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 320 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: <Unknown>  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 150:  
;/ US-09-745-763-150

Query Match 76.5%; Score 26; DB 10; Length 320;  
Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 63 NIKTVTE 69

RESULT 34  
US-09-925-301-969  
;/ Sequence 969, Application US/09925301  
;/ Patent No. US20020052308A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Rosen et al.  
;/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
;/ FILE REFERENCE: PA106  
;/ CURRENT APPLICATION NUMBER: US/09/925,301  
;/ CURRENT FILING DATE: 2001-08-10  
;/ PRIOR APPLICATION NUMBER: PCT/US00/05882  
;/ PRIOR FILING DATE: 2000-03-08  
;/ PRIOR APPLICATION NUMBER: 60/124,270  
;/ PRIOR FILING DATE: 1999-03-12  
;/ NUMBER OF SEQ ID NOS: 1694  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 969  
;/ LENGTH: 325  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
;/ US-09-925-301-969

Query Match 76.5%; Score 26; DB 10; Length 325;  
Best Local Similarity 71.4%; Pred. No. 4.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 68 NIKTVTE 74

RESULT 35

US-09-738-626-6967  
;/ Sequence 6967, Application US/09738626  
;/ Publication No. US20020197605A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: NAKAGAWA, SATOSHI  
;/ APPLICANT: MIZOGUCHI, HIROSHI  
;/ APPLICANT: ANDO, SEIKO  
;/ APPLICANT: HAYASHI, MIKIRO  
;/ APPLICANT: OCHIAI, KEIKO  
;/ APPLICANT: YOKOI, HARUHIKO  
;/ APPLICANT: TATEISHI, NAKO  
;/ APPLICANT: SENOH, AKIHIRO  
;/ APPLICANT: IKEDA, MASATO  
;/ APPLICANT: OZAKI, AKIO  
;/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
;/ FILE REFERENCE: 249-125  
;/ CURRENT APPLICATION NUMBER: US/09/738,626  
;/ CURRENT FILING DATE: 2000-12-18  
;/ PRIOR APPLICATION NUMBER: JP 99/377484  
;/ PRIOR FILING DATE: 1999-12-16  
;/ PRIOR APPLICATION NUMBER: JP 00/159162  
;/ PRIOR FILING DATE: 2000-04-07  
;/ PRIOR APPLICATION NUMBER: JP 00/280988  
;/ PRIOR FILING DATE: 2000-08-03  
;/ NUMBER OF SEQ ID NOS: 7059  
;/ SOFTWARE: PatentIn ver. 3.0  
;/ SEQ ID NO 6967  
;/ LENGTH: 362  
;/ TYPE: PRT  
;/ ORGANISM: Corynebacterium glutamicum  
;/ US-09-738-626-6967

Query Match 76.5%; Score 26; DB 11; Length 362;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKTLTE 7  
Db 151 AKTITE 156

RESULT 36  
US-09-815-242-10139  
;/ Sequence 10139, Application US/09815242  
;/ Patent No. US20020061569A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Haselbeck, Robert  
;/ APPLICANT: Ohlsen, Kari L.  
;/ APPLICANT: Zyskind, Judith W.  
;/ APPLICANT: Wall, Daniel  
;/ APPLICANT: Trawick, John D.  
;/ APPLICANT: Carr, Grant J.  
;/ APPLICANT: Yamamoto, Robert T.  
;/ APPLICANT: Xu, H. Howard  
;/ TITLE OF INVENTION: Identification of Essential Genes in  
;/ FILE REFERENCE: ELITRA.011A  
;/ CURRENT APPLICATION NUMBER: US/09/815,242  
;/ CURRENT FILING DATE: 2001-03-21  
;/ PRIOR APPLICATION NUMBER: 60/191,078  
;/ PRIOR FILING DATE: 2000-03-21  
;/ PRIOR APPLICATION NUMBER: 60/206,848  
;/ PRIOR FILING DATE: 2000-05-23  
;/ PRIOR APPLICATION NUMBER: 60/207,727  
;/ PRIOR FILING DATE: 2000-05-26  
;/ PRIOR APPLICATION NUMBER: 60/242,578  
;/ PRIOR FILING DATE: 2000-10-23  
;/ PRIOR APPLICATION NUMBER: 60/253,625  
;/ PRIOR FILING DATE: 2000-11-27  
;/ PRIOR APPLICATION NUMBER: 60/257,931  
;/ PRIOR FILING DATE: 2000-12-22  
;/ PRIOR APPLICATION NUMBER: 60/269,308  
;/ PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10139  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-815-242-10139

Query Match 76.5%; Score 26; DB 10; Length 416;  
Best Local Similarity 83.3%; Pred. No. 6.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
|:|||||  
Db 385 NAKTVT 390

RESULT 37  
US-10-156-761-11065  
; Sequence 11065, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 11065  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-11065

Query Match 76.5%; Score 26; DB 15; Length 429;  
Best Local Similarity 71.4%; Pred. No. 6.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|:|||||  
Db 92 DARTLTE 98

RESULT 38  
US-09-738-626-6982  
; Sequence 6982, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 6982  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-6982

Query Match 76.5%; Score 26; DB 11; Length 447;  
Best Local Similarity 71.4%; Pred. No. 6.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|:|||||  
Db 330 NAKTLAD 336

RESULT 39  
US-09-815-242-12670  
; Sequence 12670, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12670  
; LENGTH: 457  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12670

Query Match 76.5%; Score 26; DB 10; Length 457;  
Best Local Similarity 71.4%; Pred. No. 7.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|:|||||  
Db 266 NSNTLTE 272

RESULT 40  
US-09-922-217-1093

; Sequence 1093, Application US/09922217  
; Patent No. US20020076414A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Smith, Carole Lynn  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.471C13  
; CURRENT APPLICATION NUMBER: US/09/922,217  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1093  
; LENGTH: 512  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-922-217-1093

Query Match 76.5%; Score 26; DB 10; Length 512;  
Best Local Similarity 71.4%; Pred. No. 8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
| | | | |  
Db 298 NEKTVTE 304

Search completed: July 18, 2003, 15:35:57  
Job time : 19.06 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:05 ; Search time 9.1 Seconds  
(without alignments)  
73.950 Million cell updates/sec

Title: US-10-007-790-9  
Perfect score: 34  
Sequence: 1 NAKLTLE 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	149	2	AC1608
2	31	91.2	149	2	AG1245
3	29	85.3	62	2	PL0266
4	29	85.3	97	2	PH1068
5	29	85.3	98	2	PH1069
6	29	85.3	101	2	S20810
7	29	85.3	106	2	B47329
8	29	85.3	107	2	PL0080
9	29	85.3	128	2	S31488
10	29	85.3	211	1	WMBEMA
11	29	85.3	211	1	WMBEMB
12	29	85.3	229	1	MVFCMH
13	29	85.3	229	2	H91089
14	29	85.3	229	2	C85935
15	29	85.3	261	2	S72639
16	29	85.3	320	1	S55244
17	29	85.3	351	2	MBEEMH
18	29	85.3	407	2	A34357
19	29	85.3	407	2	S20304
20	29	85.3	416	2	A99419
21	29	85.3	468	2	P97482
22	29	85.3	484	2	P88483
23	29	85.3	491	2	AH3416
24	29	85.3	493	2	D98209
25	29	85.3	493	2	AE3077
26	29	85.3	494	2	AE2700
27	29	85.3	502	2	S56177
28	29	85.3	601	2	T38736
29	29	85.3	715	2	C70174

30	29	85.3	763	2	S35908
31	29	85.3	1801	2	T26774
32	28	82.4	131	2	F97868
33	28	82.4	181	2	A71852
34	28	82.4	184	2	E64663
35	28	82.4	215	2	S18714
36	28	82.4	236	2	H70691
37	28	82.4	247	2	B97619
38	28	82.4	247	2	A12841
39	28	82.4	268	2	G70553
40	28	82.4	287	2	AG2414
41	28	82.4	296	2	A34543
42	28	82.4	304	2	T27593
43	28	82.4	304	2	T27594
44	28	82.4	317	2	E96792
45	28	82.4	328	2	E86880

ALIGNMENTS

RESULT 1

AC1608

arginine repressor homolog lin1404 [imported] - Listeria innocua (strain Clp11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001

C:Accession: AC1608

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; PMID:21537279; PMID:11679669

A:Accession: AC1608

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96635.1; PID:gl6413877; GSPDB:GN00178

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lin1404

C:Superfamily: Escherichia coli arginine repressor argR

Query Match 91.2%; Score 31; DB 2; Length 149;

Best Local Similarity 85.7%; Pred. No. 12;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTLE 7

Db 137 NAKLTLD 143

RESULT 2

AG1245

arginine repressor homolog lmo1367 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001

C:Accession: AG1245

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; PMID:21537279; PMID:11679669

A:Accession: AG1245

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <GLA>

A:Cross-references: GB:NC\_003210; PIDN:CAC99445.1; PID:gl6410783; GSPDB:GN00177

A:Experimental source: strain EGD-e  
 C:Genetics:  
 A:Gene: lmo1367  
 C:Superfamily: Escherichia coli arginine repressor argR

Query Match 91.2%; Score 31; DB 2; Length 149;  
 Best Local Similarity 85.7%; Pred. No. 12;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 DB 137 NAKTLTD 143

## RESULT 3

PL0266

Ig kappa chain V region (anti-DNA, 6PVK) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-May-1997  
 C:Accession: PL0266  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:9011618; PMID:2104919  
 A:Accession: PL0266  
 A:Molecule type: mRNA  
 A:Residues: 1-62 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-5/Region: framework 2  
 F:6-12/Region: complementarity-determining 2  
 F:13-44/Region: framework 3  
 F:45-53/Region: complementarity-determining 3  
 F:54-62/Region: framework 4

Query Match 85.3%; Score 29; DB 2; Length 62;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 DB 6 NAKTLAE 12

## RESULT 4

PH1068

Ig light chain V region (clone sl7.166) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C:Accession: PH1068  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
 A:Reference number: PH0971; MUID:92381444; PMID:1512540  
 A:Accession: PH1068  
 A:Molecule type: mRNA  
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
 A:Residues: 1-97 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 97;  
 Best Local Similarity 85.7%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 DB 49 NAKTLAE 55

## RESULT 5

PH1069

Ig light chain V region (clone 185-cl) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C:Accession: PH1069  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
 A:Reference number: PH0971; MUID:92381444; PMID:1512540  
 A:Accession: PH1069  
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
 A:Residues: 1-98 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 98;  
 Best Local Similarity 85.7%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 DB 50 NAKTLAE 56

## RESULT 6

S20810

Ig kappa chain V region (hybridoma C8) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S20810  
 R:Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.  
 submitted to the EMBL Data Library, September 1990  
 A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine antib  
 A:Reference number: S20809  
 A:Accession: S20810  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <HOO>  
 A:Cross-references: EMBL:X54693; NID:G50251; PIDN:CAA38509.1; PID:G50252  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 101;  
 Best Local Similarity 85.7%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 DB 43 NAKTLAE 49

## RESULT 7

B47329

Ig kappa chain V region (PRI) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Sep-1993 #sequence\_revision 17-Jul-1994 #text\_change 21-Jan-2000  
 C:Accession: B47329  
 R:Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993  
 A:Title: A recombinant immunotoxin that is active on prostate cancer cells and that is c  
 A:Reference number: B47329; MUID:93133825; PMID:8421689  
 A:Accession: B47329  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-106 <BRI>

A:Experimental source: Balb/c  
 A>Note: sequence modified after extraction from NCBI backbone  
 A>Note: sequence extracted from NCBI backbone (NCBIN:122874)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 106;  
Best Local Similarity 85.7%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|||||  
Db 50 NAKTLAE 56

## RESULT 8

PLO080  
Ig kappa chain V region (E4) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PLO080  
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1989  
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A:Reference number: PLO080; MUID:89094248; PMID:2492056  
A:Accession: PLO080  
A:Molecule type: mRNA  
A:Residues: 1-107 <MEE>  
A:Cross-references: GB:X59596; GB:Y00794; NID:G51574; PIDN:CAA41471.1; PID:G938255  
A:Experimental source: strain BALB/c  
A:Note: 106-Leu is translated from the codon CUN  
A:Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclonal  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 107;  
Best Local Similarity 85.7%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|||||  
Db 50 NAKTLAE 56

## RESULT 9

S31488  
Ig kappa chain precursor V region (F11) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S31488  
R:Bespalov, I.A.; Shiyanov, P.A.; Lukashevich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponov  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S31488  
A:Accession: S31488  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <BES>  
A:Cross-references: EMBL:X69859; NID:G50929; PIDN:CAA49493.1; PID:G50930  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 128;  
Best Local Similarity 85.7%; Pred. No. 29;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|||||  
Db 70 NAKTLAE 76

## RESULT 10

WMEEMA  
23.5K protein - Marek's disease virus (type 1, strain BC-1)  
C:Species: Marek's disease virus

A:Note: host Gallus gallus (chicken)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 08-Apr-1994  
C:Accession: J50389  
R:Ihara, T.; Kato, A.; Ueda, S.; Ishihama, A.; Hirai, K.  
Virus Genes 3, 127-140, 1989  
A:Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene between Mdi  
A:Reference number: A22818; MUID:90142542; PMID:2559540  
A:Accession: J50389  
A:Molecule type: DNA  
A:Residues: 1-211 <IHA>  
C:Superfamily: turkey herpesvirus 23.5K protein

Query Match 85.3%; Score 29; DB 1; Length 211;  
Best Local Similarity 85.7%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|||||  
Db 118 NAKTLVE 124

## RESULT 11

WMBEMB  
23.5K protein - Marek's disease virus (type 1, strains Mds and GA)  
N:Alternate names: UL45h protein  
C:Species: Marek's disease virus  
A:Note: host Gallus gallus (chicken)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999  
C:Accession: B22818; JQ2207  
R:Ihara, T.; Kato, A.; Ueda, S.; Ishihama, A.; Hirai, K.  
Virus Genes 3, 127-140, 1989  
A:Title: Comparison of the sequence of the secretory glycoprotein A (gA) gene between Mdi  
A:Reference number: A22818; MUID:90142542; PMID:2559540  
A:Accession: B22818  
A:Molecule type: DNA  
A:Residues: 1-211 <IHA>  
A:Experimental source: strain Mds  
R:Yanagida, N.; Yoshida, S.; Nazerian, K.; Lee, L.F.  
J. Gen. Virol. 74, 1837-1845, 1993  
A:Title: Nucleotide and predicted amino acid sequences of Marek's disease virus homologues  
A:Reference number: JQ2199; MUID:93389438; PMID:8397281  
A:Accession: JQ2207

Query Match 85.3%; Score 29; DB 1; Length 211;  
Best Local Similarity 85.7%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
|||||  
Db 118 NAKTLVE 124

## RESULT 12

WVECHM  
mutator muth - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 30-Sep-1988 #sequence\_revision 17-Oct-1997 #text\_change 01-Mar-2002  
C:Accession: H65065; A27506  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: H65065  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-229 <BLAT>  
A:Cross-references: GB:AE000367; GB:U00096; NID:G1789195; PIDN:AAC75870.1; PID:G1789196;

A:Experimental source: strain K-12, substrain MG1655  
R:Grafstrom, R.H.; Hoess, R.H.  
Nucleic Acids Res. 15, 3073-3084, 1987  
A:Title: Nucleotide sequence of the Escherichia coli mutH gene.  
A:Reference number: A27506; MUID:87174827; PMID:3031619  
A:Accession: A27506

A:Molecule type: DNA  
A:Residues: 1-82, 'L', '84-129, 'RL', '132-135, 'A', '137-229 <GRA>  
A:Cross-references: GB:Y00113; NID:942064; PIDN:CAA68292.1; PID:942065  
A:Note: the authors translated the codon CTG for residue 83 as Val  
C:Comment: Two temperature-sensitive mutants have also been isolated and sequenced.  
C:Genetics:

A:Gene: mutH

A:Map position: 61 min

C:Superfamily: mutator mutH

Query Match 85.3%; Score 29; DB 1; Length 229;  
Best Local Similarity 85.7%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||| |||  
Db 189 NAKALTE 195

#### RESULT 13

H91089 methyl-directed mismatch repair [imported] - Escherichia coli (strain O157:H7, substrain

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001

C:Accession: H91089

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: H91089

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-229 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA837111.1; PID:G13363160; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs3688

C:Superfamily: mutator mutH

Query Match 85.3%; Score 29; DB 2; Length 229;  
Best Local Similarity 85.7%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||| |||  
Db 189 NAKALTE 195

#### RESULT 14

C85935 methyl-directed mismatch repair [imported] - Escherichia coli (strain O157:H7, substrain

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: C85935

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C85935

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-229 <STO>

A:Cross-references: GB:AE005174; NID:912517320; PIDN:AA057943.1; GSPDB:GN00145; UNGP:241

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: mutH  
C:Superfamily: mutator mutH

Query Match 85.3%; Score 29; DB 2; Length 229;  
Best Local Similarity 85.7%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||| |||  
Db 189 NAKALTE 195

#### RESULT 15

S72639

hypothetical primary sigma factor - Thermoanaerobacterium thermosulfurigenes

C:Species: Thermoanaerobacterium thermosulfurigenes

C:Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 08-Oct-1999

C:Accession: S72639

R:Matuschek, M.; Sahm, K.; Bahl, H.

submitted to the EMBL Data Library, March 1996

A:Description: Characterization of genes from Thermoanaerobacterium thermosulfurigenes EN

A:Reference number: S72635

A:Accession: S72639

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-261 <MAT>

A:Cross-references: EMBL:U50951; NID:G1542972; PIDN:AAB08043.1; PID:G1542976

C:Genetics:

A:Gene: sigma

C:Superfamily: Lyme disease spirochete probable RNA polymerase sigma factor; transcripti

F:30-255/Domain: transcription initiation factor sigma katF homology <KTP>

Query Match 85.3%; Score 29; DB 2; Length 261;

Best Local Similarity 85.7%; Pred. No. 59;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||| |||  
Db 217 NLKTLTE 223

#### RESULT 16

S55244

polyubiquitin 4 - Arabidopsis thaliana

N:Alternate names: ubiquitin-like protein 9

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S55244; S61069

R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.

Genetics 139, 921-939, 1995

A:Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like prote

A:Reference number: S55242; MUID:95229071; PMID:7713442

A:Accession: S55244

A:Molecule type: DNA

A:Residues: 1-320 <CAL>

A:Cross-references: EMBL:L05365

A:Experimental source: ecotype Columbia

R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.

submitted to the EMBL Data Library, June 1995

A:Reference number: S61069

A:Accession: S61069

A:Molecule type: DNA

A:Residues: 1-76, 'I', '78-111, 'V', '113-212, 'M', '214-320 <CAF>

A:Cross-references: EMBL:L05365

C:Superfamily: polyubiquitin 4; ubiquitin homology

C:Keywords: nucleus; polyprotein; protein degradation

F:1-76/Product: ubiquitin #status predicted <UB1>

F:1-76/Domain: ubiquitin homology <UBH1>

F:77-152/Product: ubiquitin #status predicted <UB2>

F:77-152/Domain: ubiquitin homology <UBH2>

F:153-228/Product: ubiquitin #status predicted <UB3>

F:153-228/Domain: ubiquitin homology <UBH3>

F:229-305/Product: ubiquitin #status predicted <UB4>

F:229-305/Domain: ubiquitin homology <UBH4>

Query Match 85.3%; Score 29; DB 1; Length 320;  
Best Local Similarity 85.7%; Pred. No. 72;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
:|||||  
Db 4 HAKTLTE 10

## RESULT 17

E84096  
Hypothetical protein BH3573 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: E84096  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maqui, N.; Fuji, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: E84096  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-351 <STO>  
A:Cross-references: GB:AP001519; GB:BA000004; NID:gl0176109; PIDN:BA807292.1; GSPDB:GN00  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH3573

Query Match 85.3%; Score 29; DB 2; Length 351;  
Best Local Similarity 85.7%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
:|||||  
Db 110 NASTLTE 116

## RESULT 18

A34357  
neurokinin 1 receptor - rat  
N:Alternate names: NK-1 receptor; substance P receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 19-May-2000  
C:Accession: A38692; A34357; A40089  
J:Hershey, A.D.; Dykema, P.E.; Krause, J.E.  
R:Biol. Chem. 266, 4366-4374, 1991  
A>Title: Organization, structure, and expression of the gene encoding the rat substance  
A:Reference number: A38692; MUID:91154239; PMID:1705552  
A:Accession: A38692  
A:Molecule type: DNA  
A:Residues: 1-407 <HER>  
A:Cross-references: GB:M34751  
J:Fukota, Y.; Sasai, Y.; Tanaka, K.; Fujiwara, T.; Tsuchida, K.; Shigemoto, R.; Kakizuka  
J. Biol. Chem. 264, 17649-17652, 1989  
A>Title: Molecular characterization of a functional cDNA for rat substance P receptor.  
A:Reference number: A34357; MUID:90036822; PMID:2478537  
A:Accession: A34357  
A:Molecule type: mRNA  
A:Residues: 1-407 <YOK>  
A:Cross-references: GB:J05097; NID:g207051; PIDN:AAA42175.1; PID:g207052  
R:Hershey, A.D.; Krause, J.E.  
Science 247, 958-962, 1990  
A>Title: Molecular characterization of a functional cDNA encoding the rat substance P re  
A:Reference number: A40089; MUID:90161991; PMID:2154852  
A:Accession: A40089  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-74, 'R', '76-212', 'A', '214-407 <HE2>  
A:Cross-references: GB:M31477  
C:Superfamily: neurokinin 1 receptor  
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 85.3%; Score 29; DB 2; Length 407;  
Best Local Similarity 71.4%; Pred. No. 92;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
:|||||  
Db 391 NSKTWTE 397

## RESULT 19

S20304  
neurokinin 1 receptor - mouse  
N:Alternate names: NK-1 receptor; substance P receptor  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 02-Jun-2000  
C:Accession: S20304; I56216; I73044  
R:Sundelin, J.B.; Provvedini, D.M.; Wahlestedt, C.R.; Laurill, H.; Pohl, J.S.; Peterson,  
Eur. J. Biochem. 203, 625-631, 1992  
A>Title: Molecular cloning of the murine substance K and substance P receptor genes.  
A:Reference number: S20303; MUID:92137253; PMID:1370937  
A:Accession: S20304  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-407 <SUN>  
A:Cross-references: GB:X62934; NID:g54206; PIDN:CAA44707.1; PID:g54207  
R:Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstein, J.  
J. Immunol. 152, 1830-1835, 1994  
A>Title: Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansoni  
A:Reference number: I56216; MUID:94165478; PMID:8120392  
A:Accession: I56216  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 63-290 <COO1>  
A:Cross-references: GB:L27826; NID:g450286; PIDN:AAA17891.1; PID:g480776  
A:Experimental source: tissue brain  
A:Accession: I73044  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 63-290 <COO2>  
A:Cross-references: GB:L27828; NID:g450290; PIDN:AAA17892.1; PID:g480778  
A:Experimental source: tissue granuloma  
C:Superfamily: neurokinin 1 receptor  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 85.3%; Score 29; DB 2; Length 407;  
Best Local Similarity 71.4%; Pred. No. 92;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
:|||||  
Db 391 NSKTWTE 397

## RESULT 20

A99419  
Hypothetical protein leuc [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C:Accession: A99419  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A>Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: A99419  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-416 <KUP>  
A:Cross-references: GB:AE006641; NID:gl3815772; PIDN:AAK42608.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: leuc

C:Superfamily: aconitate hydratase

Query Match 85.3%; Score 29; DB 2; Length 416;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
:|||||  
Db 3 SAKTLTE 9  
  
RESULT 21  
F97482  
amp nucleosidase [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: F97482  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; PMID:11743194  
A:Accession: F97482  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-468 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK86815.1; PID:gl5156023; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_1849  
A:Map position: circular chromosome

Query Match 85.3%; Score 29; DB 2; Length 468;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
:|||||  
Db 266 NAKTITD 272

RESULT 22  
B88483  
protein mel-32 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C:Accession: B88483  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; PMID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: B88483  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-484 <STO>  
A:Cross-references: GB:chr\_III; PIDN:AAE53830.1; PID:g485099; GSPDB:GN00021; CESP:mel-32  
C:Genetics:  
A:Gene: mel-32  
A:Map position: 3  
C:Superfamily: glycine hydroxymethyltransferase

Query Match 85.3%; Score 29; DB 2; Length 484;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
:|||||  
Db 336 NAKTLAE 342

RESULT 23  
AH3416

AMP nucleosidase (EC 3.2.2.4) [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
C:Accession: AH3416  
R:Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, I.  
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AH3416  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-491 <KUR>  
A:Cross-references: GB:AE008917; PIDN:AAI52499.1; PID:gl7983308; GSPDB:GN00190  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BME11318  
A:Map position: 1  
C:Keywords: glycosidase; hydrolase

Query Match 85.3%; Score 29; DB 2; Length 491;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
:|||||  
Db 289 NAKTITD 295

RESULT 24  
D98209  
aldehyde dehydrogenase dhas [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 11-Jan-2002  
C:Accession: D98209  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; PMID:11743194  
A:Accession: D98209  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-493 <KUR>  
A:Cross-references: GB:AE007870; PIDN:AAK89198.1; PID:gl5159016; GSPDB:GN00170  
C:Genetics:  
A:Gene: AGR\_L\_1241  
A:Map position: linear chromosome  
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 85.3%; Score 29; DB 2; Length 493;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
:|||||  
Db 85 NAKTLAE 91

RESULT 25  
AE3077  
aldehyde dehydrogenase dhas [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002  
C:Accession: AE3077  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L.  
; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; PMID:11743193

A:Accession: AE3077  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-493 <KUR>  
 A:Cross-references: GB:AE008689; PIDN: AAL45035.1; PID: g17742698; GSPDB: GN00187  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: dhaS  
 A:Map position: linear chromosome  
 C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 85.3%; Score 29; DB 2; Length 493;  
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 |||||  
 Db 85 NAKTLAE 91

RESULT 26  
 AF2700  
 AMP nucleosidase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C:Accession: AF2700  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell  
 e; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID: 11743193  
 A:Accession: AF2700  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-494 <KUR>  
 A:Cross-references: GB:AE008688; PIDN: AAL42020.1; PID: g17739395; GSPDB: GN00186  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: amn  
 A:Map position: circular chromosome

Query Match 85.3%; Score 29; DB 2; Length 494;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 |||||  
 Db 292 NAKTIND 298

RESULT 27  
 S56177  
 probable glutamate decarboxylase - tomato  
 C:Species: Lycopersicon esculentum (tomato)  
 C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 28-May-1999  
 C:Accession: S56177  
 R:Gallego, P.P.; Whotton, L.; Piton, S.; Grierson, D.; Gray, J.E.  
 Plant Mol. Biol. 27, 1143-1151, 1995  
 A:Title: A role for glutamate decarboxylase during tomato ripening: the characterisation  
 A:Reference number: S56177; MUID: 95284363; PMID: 7766895  
 A:Accession: S56177  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-502 <GAL>  
 A:Cross-references: GB:X80840; NID: G993002; PIDN: CAA56812.1; PID: g995555  
 C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 85.3%; Score 29; DB 2; Length 502;  
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 |||||  
 Db 351 NAKVLTE 357

RESULT 28  
 T38736  
 hypothetical protein SPAC3H1.04c - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T38736  
 R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL Data Library, December 1995  
 A:Reference number: Z21808  
 A:Accession: T38736  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-601 <GEN>  
 A:Cross-references: EMBL: Z68144; PIDN: CAA92257.1; GSPDB: GN000066; SPDB: SPAC3H1.04c  
 A:Experimental source: strain 972h-; cosmid c3H1  
 C:Genetics:  
 A:Gene: SPDB: SPAC3H1.04c  
 A:Map position: 1  
 A:Introns: 549/3

Query Match 85.3%; Score 29; DB 2; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6  
 |||||  
 Db 366 NAKTLT 371

RESULT 29  
 C70174  
 methyl-accepting chemotaxis protein (mcp-2) homolog - Lyme disease spirochete  
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 08-Oct-1999  
 C:Accession: C70174  
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,  
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A:Authors: Smith, H.O.; Venter, J.C.  
 A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
 A:Reference number: A70100; MUID: 98065943; PMID: 9403685  
 A:Accession: C70174  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-715 <KLE>  
 A:Cross-references: GB:AE001161; GB:AE000783; NID: G2688515; PIDN: AAC66955.1; PID: G268852;  
 A:Experimental source: strain B31

Query Match 85.3%; Score 29; DB 2; Length 715;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
 |||||  
 Db 248 NPKTLTE 254

RESULT 30  
 S35908  
 ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - Lactococcus lactis subsp. lactis  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 19-Jan-2001  
 C:Accession: S35908  
 R:Huang, D.C.; Huang, X.F.; Novel, G.; Novel, M.  
 Mol. Microbiol. 7, 957-965, 1993  
 A:Title: Two genes present on a transposon-like structure in Lactococcus lactis are invol

A:Reference number: S35907; MUID:93247497; PMID:8387149  
A:Accession: S35908  
A:Molecule type: DNA  
A:Residues: 1-763 <HUA>  
A:Cross-references: EMBL:X62333; NID:g296463; PIDN:CAA44207.1; PID:g296464  
C:Genetics:  
A:Gene: clpL  
A:Genome: plasmid  
C:Superfamily: endopeptidase Clp ATP-binding chain  
C:Keywords: ATP; hydrolase; molecular chaperone; nucleotide binding; P-loop; serine protease  
F:181-188/Region: nucleotide-binding motif A (P-loop)  
F:248-253/Region: nucleotide-binding motif B  
F:511-518/Region: nucleotide-binding motif A (P-loop)  
F:580-585/Region: nucleotide-binding motif B  
F:187/Binding site: ATP (Lys) #status predicted  
F:517/Binding site: ATP (Lys) #status predicted

Query Match 85.3%; Score 29; DB 2; Length 763;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
| | | | |  
Db 565 NAKTLTE 571

RESULT 31  
T26774  
hypothetical protein Y39G8C.b - Caenorhabditis elegans.  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26774  
R:Smyle, R.  
submitted to the EMBL Data Library, October 1998

A:Reference number: Z20263  
A:Accession: T26774  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1801 <WIL>  
A:Cross-references: EMBL:AL032634; PIDN:CAB54418.1; GSPDB:GN00019; CBSP:Y39G8C.b  
A:Experimental source: clone Y39G8C  
C:Genetics:  
A:Gene: CBSP:Y39G8C.b  
A:Map position: 1  
A:Introns: 69/3; 117/2; 186/3; 226/3; 268/3; 371/3; 540/3; 857/1; 881/3; 1025/3; 1077/1;

Query Match 85.3%; Score 29; DB 2; Length 1801;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
| | | | |  
Db 1574 NAKTLAE 1580

RESULT 32  
F97868  
hypothetical protein RC1350 [imported] - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: F97868  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R  
Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: F97868  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-131 <KUR>  
A:Cross-references: GB:AE006914; PIDN:AAL03888.1; PID:g15620494; GSPDB:GN00173  
C:Genetics:  
A:Gene: RC1350

Query Match 82.4%; Score 28; DB 2; Length 131;  
Best Local Similarity 71.4%; Pred. No. 50;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
| | | | |  
Db 14 NGKTITE 20

RESULT 33  
A1852  
hypothetical protein jhp1076 - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
C:Accession: A1852  
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J  
Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho  
A:Reference number: A1800; MUID:99120557; PMID:9923682  
A:Accession: A1852  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-181 <ARN>  
A:Cross-references: GB:AE001535; GB:AE001439; NID:g4155664; PIDN:AAD06656.1; PID:g415567  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: jhp1076

Query Match 82.4%; Score 28; DB 2; Length 181;  
Best Local Similarity 85.7%; Pred. No. 69;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
| | | | |  
Db 173 NAKTLLE 179

RESULT 34  
E84663  
conserved hypothetical protein HP1149 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C:Accession: E84663  
R:Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKenney  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: E84663  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-184 <TOW>  
A:Cross-references: GB:AE000621; GB:AE000511; NID:g2314301; PIDN:AAD08193.1; PID:g2314304

Query Match 82.4%; Score 28; DB 2; Length 184;  
Best Local Similarity 85.7%; Pred. No. 70;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
| | | | |  
Db 176 NAKTLLE 182

RESULT 35  
S18714  
ribosomal protein S7 - Thermococcus celer  
C:Species: Thermococcus celer  
C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 13-Aug-1999  
C:Accession: S18714; S25569

R;Klenk, H.P.; Schwass, V.; Zillig, W.  
Nucleic Acids Res. 19, 6047, 1991  
A;Title: Nucleotide sequence of the genes encoding the L30, S12 and S7 equivalent ribosomal proteins of *Escherichia coli* strain 43868  
A;Reference number: S18710; MUID:92051399; PMID:1840672  
A;Accession: S18714  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-215 <KLE>  
A;Cross-references: EMBL:X60305; NID:G58408; PIDN:CAA42850.1; PID:G58413  
A;Experimental source: DSM 2476  
R;Klenk, H.P.; Schwass, V.; Lottspeich, F.; Zillig, W.  
Nucleic Acids Res. 20, 4659, 1992  
A;Title: Nucleotide sequence of the genes encoding the three largest subunits of the DNA polymerase III of *Escherichia coli* strain 43868  
A;Reference number: S25562; MUID:93027167; PMID:1408768  
A;Accession: S25569  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-197, S', 199-213, 'RA' <KLE>  
A;Cross-references: EMBL:X67313; NID:G48138; PIDN:CAA47728.1; PID:G48146  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
C;Genetics:  
A;Gene: rps7  
C;Superfamily: Escherichia coli ribosomal protein S7  
C;Keywords: protein biosynthesis; ribosome

Query Match 82.4%; Score 28; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLTLE 7  
|||||  
Db 2 AKLTLE 7

RESULT 36  
H70691  
Hypothetical protein RV2821c - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C;Accession: H70691  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: H70691  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <COL>  
A;Cross-references: GB:281331; GB:AL123456; NID:G3261650; PIDN:CAB03665.1; PID:G1648899  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: RV2821c  
C;Superfamily: hypothetical protein MJ1669

Query Match 82.4%; Score 28; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLTLE 7  
|||||  
Db 117 AKLTLE 122

RESULT 37  
B97619  
26K periplasmic immunogenic protein precursor (28K outer membrane protein) AGR\_C\_3922 [i  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C;Accession: B97619

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain C58  
A;Reference number: A97359; PMID:11743194  
A;Accession: B97619  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-247 <KUR>  
A;Cross-references: GB:AE007869; PIDN:AAK87907.1; PID:G15157303; GSPDB:GN00169  
C;Genetics:  
A;Gene: AGR\_C\_3922  
A;Map position: circular chromosome

Query Match 82.4%; Score 28; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLTLE 7  
|||||  
Db 183 AKLTLE 188

RESULT 38  
A12841  
periplasmic immunogenic protein [imported] - *Agrobacterium tumefaciens* (strain C58, Dupor  
C;Species: *Agrobacterium tumefaciens*  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
C;Accession: A12841  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; erage, G.; Gilliet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, K.; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.; ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A;Reference number: AB2577; PMID:11743193  
A;Accession: A12841  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-247 <KUR>  
A;Cross-references: GB:AE006588; PIDN:AAL43151.1; PID:G17740627; GSPDB:GN00186  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: pp26  
A;Map position: circular chromosome

Query Match 82.4%; Score 28; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLTLE 7  
|||||  
Db 183 AKLTLE 188

RESULT 39  
G70553  
probable echA10 protein - *Mycobacterium tuberculosis* (strain H37RV)  
C;Species: *Mycobacterium tuberculosis*  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C;Accession: G70553  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: G70553  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-268 <COL>

A;Cross-references: GB:Z95584; GB:AL123456; NID:G3261774; PIDN:CAB09030.1; PID:g2117180  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: echA10  
C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology  
F;35-187/Domain: enoyl-CoA hydratase homology <ECH>

Query Match 82.4%; Score 28; DB 2; Length 268;  
Best Local Similarity 85.7%; Pred. No. 1e+02; Mismatches 0; Gaps 0;  
Matches 6; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 NAKLTLE 7  
|||  
Db 223 NAKLTLE 229

RESULT 40  
AG2414  
hypothetical protein all4871 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp.  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C;Accession: AG2414  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AG2414  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-287 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BA076570.1; PID:g17134008; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all4871

Query Match 82.4%; Score 28; DB 2; Length 287;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02; Mismatches 0; Gaps 0;  
Matches 6; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 NAKLTLE 7  
|||  
Db 223 NAKLTLE 229

Search completed: July 18, 2003, 15:10:46  
Job time : 10.1 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:20 ; Search time 4.34 Seconds  
(without alignments)  
66.897 Million cell updates/sec

Title: US-10-007-790-9  
Perfect score: 34  
Sequence: 1 NAKTLTE 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	29	85.3	211	1 UL45_HSVMB	P22652 marek's dis
2	29	85.3	211	1 UL45_HSVMM	P22653 marek's dis
3	29	85.3	228	1 MUTH_ECOLI	P06722 escherichia
4	29	85.3	407	1 NKIR_MOUSE	P30548 mus musculus
5	29	85.3	407	1 NKIR_RAT	P14600 rattus norv
6	29	85.3	416	1 LEU2_SULSO	Q97vy2 sulfolobus
7	29	85.3	502	1 DCE_LYCES	P54767 lycopersico
8	29	85.3	507	1 GLYC_CABEL	P50432 caenorhabdi
9	29	85.3	601	1 YAN4_SCHPO	Q10070 schizosacch
10	29	85.3	763	1 CLPL_LACLA	Q06716 lactococcus
11	28	82.4	181	1 RIMM_HELPY	Q92k65 helicobacte
12	28	82.4	184	1 RIMM_HELPY	O25767 helicobacte
13	28	82.4	215	1 RS7_THRCE	P29159 thermococcu
14	28	82.4	296	1 SAPR_STRPU	P11761 strongyloce
15	28	82.4	407	1 NKIR_CAVPO	P30547 cavia porce
16	28	82.4	446	1 SR54_MYCGE	P47294 mycoplasma
17	28	82.4	503	1 DHAB_GADCA	P56533 gadus calla
18	28	82.4	604	1 Z300_HUMAN	Q96re9 homo sapien
19	28	82.4	839	1 Y422_MYCPN	P75175 mycoplasma
20	28	82.4	849	1 VNCS_ASEDE	P27454 aedes denso
21	28	82.4	1202	1 DPOM_ASCIM	P22374 ascobolus i
22	27	79.4	52	1 RL33_HELPY	P56055 helicobacte
23	27	79.4	187	1 LEPU_BACSU	P42959 bacillus su
24	27	79.4	229	1 S3AG_BACSU	P49784 bacillus su
25	27	79.4	266	1 HMUV_YERPE	Q56993 yersinia pe
26	27	79.4	322	1 ADT_SCHPO	Q09188 schizosacch
27	27	79.4	334	1 FMRA_CALPA	Q01133 calliactis
28	27	79.4	426	1 CLPX_VIBCH	Q9kgs7 vibrio chol
29	27	79.4	442	1 FLGE_BORBU	Q44767 borrelia bu
30	27	79.4	449	1 CAPX_STAAU	P39860 staphylococ
31	27	79.4	572	1 SYP_ECOLI	P16659 escherichia
32	27	79.4	572	1 SYP_HAEIN	P43830 haemophilus
33	27	79.4	582	1 KICH_YEAST	P20485 saccharomyc

RESULT 1  
UL45\_HSVMB  
ID UL45\_HSVMB STANDARD; PRT; 211 AA.  
AC P22652;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE UL45 homolog protein.  
UL45H.  
OS Marek's disease herpesvirus (strain bc-1) (MDHV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Marek's disease-like viruses.  
OX NCBI\_TaxID=10387;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90142542; PubMed=2559540;  
RA Ihara T., Kato A., Ueda S., Ishihama A., Hirai K.;  
RT "Comparison of the sequence of the secretory glycoprotein A (gA) gene  
in Md5 and BC-1 strains of Marek's disease virus type 1.";  
RL Virus Genes 3:127-140(1989).  
CC -!- SIMILARITY: BELONGS TO THE UL45 FAMILY.

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or send an email to license@isb-sib.ch).  
CC  
CC EMBL; D90002; BAA14055.1; ALT\_SEQ.  
DR PIR; J80389; WMBENA.  
SQ SEQUENCE 211 AA; 23551 MW; 217A4A569D95BB4B CRC64;

Query Match 85.3%; Score 29; DB 1; Length 211;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NAKTLTE 7  
Db 118 NAKTLIVE 124

RESULT 2  
UL45\_HSVMM  
ID UL45\_HSVMM STANDARD; PRT; 211 AA.  
AC P22653;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE UL45 homolog protein.  
UL45H.  
OS Marek's disease herpesvirus (strain Md5) (MDHV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Marek's disease-like viruses.  
OX NCBI\_TaxID=10389;

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RN SEQUENCE FROM N.A.
RP MEDLINE=90142542; PubMed=2559540;
RA Ihara T., Kato A., Ueda S., Ishihama A., Hirai K.;
RT "Comparison of the sequence of the secretory glycoprotein A (gA) gene
RL in MD5 and BC-1 strains of Marek's disease virus type 1.";
RL Virus Genes 3:127-140(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93389438; PubMed=8397281;
RA Yanagida N., Yoshida S., Nazerian K., Lee L.F.;
RT "Nucleotide and predicted amino acid sequences of Marek's disease
RT virus homologues of herpes simplex virus major tegument proteins.";
RL J. Gen. Virol. 74:1837-1845(1993).
CC -1- SIMILARITY: BELONGS TO THE UL45 FAMILY.
CC -----
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CC -----
DR EMBL; D90001; BAA14053.1; -
DR EMBL; L10283; AAA03152.1; -
DR PIR; B22818; WMBEMB.
DR PIR; JQ2207; JQ2207.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; CLECT; 1.
SQ SEQUENCE 211 AA; 23507 MW; FFDF3AA525AE38E0 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 211;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 118 NAKTLVE 124

RESULT 3
MUTH_ECOLI STANDARD; PRT; 228 AA.
AC P06722;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA mismatch repair protein muth.
GN MUTH OR MUTR OR PRV OR B2831.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RC STRAIN=K12;
RX MEDLINE=87174827; PubMed=3031619;
RA Grafstrom R.H., Hoess R.H.;
RT "Nucleotide sequence of the Escherichia coli muth gene.";
RL Nucleic Acids Res. 15:3073-3084(1987).
RN [2]
RP REVISIONS TO 82; 129-130 AND 135.
RC STRAIN=K12;
RA Feng G., Tsui H.T., Winkler M.E., Loh T.A., Marinus M.G.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

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RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RP MEDLINE=98151376; PubMed=9482749;
RA Ban C., Yang W.;
RT "Structural basis for Muth activation in E.coli mismatch repair and
RT relationship of Muth to restriction endonucleases.";
RL EMBO J. 17:1526-1534(1998).
CC -1- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED
CC GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR.
CC -1- MISCELLANEOUS: TWO INDEPENDENTLY ISOLATED TEMPERATURE SENSITIVE
CC ALLELES OF THE MUTH GENE HAVE BEEN SEQUENCED (TS AND TS28).
CC -----
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CC -----
DR EMBL; Y00113; CAA68292.1; ALT_SEQ.
DR EMBL; U16361; AAB59986.1; -
DR EMBL; U29581; AAB40478.1; -
DR EMBL; AE000367; AAC75870.1; -
DR PIR; A27506; MVECMH.
DR PDB; 1A20; 20-MAY-98.
DR PDB; 2A20; 20-MAY-98.
DR EcoGene; EG10624; muth.
DR InterPro; IPR004230; Muth.
DR Pfam; PF02976; Muth; 1.
KW DNA repair; Hydrolase; Endonuclease; 3D-structure; Complete proteome.
FT INIT MET 0
FT VARIANT 27 27 T -> L (IN TS7).
FT VARIANT 156 156 D -> N (IN TS28).
SQ SEQUENCE 228 AA; 25396 MW; 1F21EED4BB1A97A1 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 228;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 188 NAKALTE 194

RESULT 4
NK1R_MOUSE STANDARD; PRT; 407 AA.
ID NK1R_MOUSE
AC P30548;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
GN TACR1 OR TAC1R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=92137253; PubMed=1370937;
RA Sundelin J.B., Provvedini D.M., Wahlestedt C.R., Laurell H.,
RA Pohl J.S., Peterson P.A.;
RT "Molecular cloning of the murine substance K and substance P receptor
RT genes";
RL Eur. J. Biochem. 203:625-631(1992).
RN [2]
RP SEQUENCE OF 63-290 FROM N.A.
RC STRAIN=CBA; TISSUE=T-cell, and Brain;

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RX MEDLINE=94165478; PubMed=8120392;
RA Cook G.A., Elliott D., Metwali A., Blum A.M., Sandor M., Lynch R.,
RA Weinstein J.V.;
RT "Molecular evidence that granuloma T lymphocytes in murine
RT schistosomiasis mansoni express an authentic substance P (NK-1)
RT receptor.";
RL J. Immunol. 152:1830-1835(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
CC TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
CC -----
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CC -----
DR EMBL; X62934; CAA44707.1; -.
DR EMBL; L27828; AAA17892.1; -.
DR EMBL; L27826; AAA17891.1; -.
DR PIR; S20304; S20304.
DR MGD; MGI:98475; Tacrl.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 54 1 (POTENTIAL).
FT DOMAIN 55 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 128 3 (POTENTIAL).
FT DOMAIN 129 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 219 5 (POTENTIAL).
FT DOMAIN 220 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 308 7 (POTENTIAL).
FT DOMAIN 309 407 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 105 180 BY SIMILARITY.
FT LIPID 322 362 PALMITATE (POTENTIAL).
SQ SEQUENCE 407 AA; 46304 MW; 451B6D475A6659A0 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 407;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 391 NSKTWTE 397

RESULT 5
NKIR RAT STANDARD; PRT; 407 AA.
AC P1460;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

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DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).
GN TACR1 OR TAC1R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91154239; PubMed=1705552;
RA Hershey A.D., Dykema P.B., Krause J.E.;
RT "Organization, structure, and expression of the gene encoding the rat
RT substance P receptor.";
RL J. Biol. Chem. 266:4366-4374(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036822; PubMed=2478537;
RA Yokota Y., Sasai Y., Tanaka K., Fujiwara T., Tsuchida K.,
RA Shigemoto R., Kikizuka A., Ohkubo H., Nakanishi S.;
RT "Molecular characterization of a functional cDNA for rat substance P
RT receptor.";
RL J. Biol. Chem. 264:17649-17652(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=90161991; PubMed=2154852;
RA Hershey A.D., Krause J.E.;
RT "Molecular characterization of a functional cDNA encoding the rat
RT substance P receptor.";
RL Science 247:958-962(1990).
RN [4]
RP REVISION TO 213.
RC STRAIN=Sprague-Dawley;
RA Hershey A.D.;
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE
CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO
CC TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO OTHER TACHYKININS RECEPTORS.
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CC -----
EMBL; M64236; AAA42176.1; -.
EMBL; M64232; AAA42176.1; JOINED.
EMBL; M64233; AAA42176.1; JOINED.
EMBL; M64234; AAA42176.1; JOINED.
EMBL; M64235; AAA42176.1; JOINED.
EMBL; J05097; AAA42175.1; -.
EMBL; M31477; AAB59726.1; -.
PIR; A34357; A34357.
PIR; A38692; A38692.
PIR; A40089; A40089.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 54 1 (POTENTIAL).
FT DOMAIN 55 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 106 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 107 128 3 (POTENTIAL).
FT DOMAIN 129 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 219 5 (POTENTIAL).
FT DOMAIN 220 248 6 (POTENTIAL).
FT TRANSMEM 249 270 7 (POTENTIAL).
FT DOMAIN 271 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 308 7 (POTENTIAL).
FT DOMAIN 309 407 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 105 180 BY SIMILARITY.
FT LIPID 322 322 PALMITATE (POTENTIAL).
FT CONFLICT 73 73 N -> D (IN REF. 3).
SQ SEQUENCE 407 AA; 46366 MW; ADF885A0BF551C96 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 407;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 391 NSKTMTE 397

RESULT 6
LEU2_SULSO STANDARD; PRT; 416 AA.
AC Q97VY2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmaleate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmaleate isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEUC OR SSO2471.
OS Sulfobolus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate
CC and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmaleate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Heterodimer of leucC and leuD (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACNITASE/IPM ISOMERASE FAMILY. LEUC 2
CC SUBFAMILY.
CC
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CC -----
CC EMBL; AB006845; AAK42608.1; -.

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DR InterPro; IPR001030; Aconitase N.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR PROSITE; PS00450; ACONITASE_1; FALSE_NEG.
DR PROSITE; PS01244; ACONITASE_2; FALSE_NEG.
KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT METAL 299 299 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 357 357 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 360 360 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 416 AA; 45253 MW; 5A342E12C6B88796 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 416;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 3 SAKTLTE 9

RESULT 7
DCE_LYCES STANDARD; PRT; 502 AA.
AC P54767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15) (GAD) (ERT D1).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asterales; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ailsa Craig; TISSUE=Pericarp;
RX MEDLINE=95284363; PubMed=7766895;
RA Gallego P.P., Whotton L., Picton S., Grierson D., Gray J.E.;
RT "A role for glutamate decarboxylase during tomato ripening: the
RT characterisation of a cDNA encoding a putative glutamate
RL decarboxylase with a calmodulin-binding site."
RL Plant Mol. Biol. 27:1143-1151(1995).
CC -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY DIRECTLY
CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
CC BIOSYNTHESIS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC
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CC -----
CC EMBL; X80840; CAA56812.1; -.
DR InterPro; IPR002129; Pyridoxal dec.
DR Pfam; PF00282; Pyridoxal dec; 1.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Calmodulin-binding.
FT BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT DOMAIN 471 502 CALMODULIN-BINDING (BY SIMILARITY).
SQ SEQUENCE 502 AA; 56785 MW; 1CSF9BD0084272A6 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 502;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 NAKTLITE 7
DB 351 NAKVLITE 357

RESULT 8
GLYC_CAEEL STANDARD; PRT; 507 AA.
AC P50432; Q950X8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
DE (Glycine hydroxymethyltransferase) (SHMT) (Glycosylation related 1).
GN GLY-1 OR MEL-32 OR C05D11.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine +
CC H(2O) = tetrahydrofolate + L-serine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS,
CC HORMONES AND OTHER COMPONENTS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a and b (shown here); may be
CC produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE SHMT FAMILY.
CC
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CC
CC EMBL; U00048; AAB53830.1; -.
CC DR EMBL; U00048; AAL27228.1; -.
CC DR HSSP; P07511; 1CJ0.
CC DR WormPep; C05D11.11a; CE01130.
CC DR WormPep; C05D11.11b; CE29661.
CC DR InterPro; IPR001085; Gly_HyMettransf.
CC DR Pfam; PF00464; SHMT; 1.
CC DR PROSITE; PS00096; SHMT; 1.
KW Transferrase; Pyridoxal phosphate; One-carbon metabolism;
KW Alternative splicing.
FT BINDING 283 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT VARSPLIC 1 23 MISSING (IN ISOFORM A).
SQ SEQUENCE 507 AA; 55764 MW; 693B380E77BB07D8 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 507;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLITE 7
DB 359 NAKTLAE 365

RESULT 9
YAN4_SCHPO STANDARD; PRT; 601 AA.
ID YAN4_SCHPO
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OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OG Plasmid pUC122.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CNRZ 270;
RX MEDLINE=93247497; PubMed=8387149;
RA Huang D.C., Huang X.F., Novel G., Novel M.;
RT "Two genes present on a transposon-like structure in Lactococcus
RT lactis are involved in a Clp-family proteolytic activity.";
RL Mol. Microbiol. 7:957-965(1993).
CC -!- FUNCTION: COULD BE THE ATP-DEPENDENT SPECIFICITY COMPONENT OF AN
CC ATP-DEPENDENT PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE CLPA/CLPB FAMILY.
CC -----
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CC -----
DR EMBL; X62333; CAA44207.1; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR001270; Chaprinin_clpA/B.
DR Pfam; PF00004; AAA; 1.
DR PRINTS; PR00300; CLPPROTEASEA.
DR PRODOM; PD000739; GSPII_E; 1.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00870; CLPAB_1; FALSE NEG.
DR PROSITE; PS00871; CLPAB_2; FALSE NEG.
KW Chaperone; ATP-binding; Repeat; Plasmid.
FT DOMAIN 136 386
FT BIND 437 629
FT NP_BIND 181 188 ATP (POTENTIAL).
FT NP_BIND 511 518 ATP (POTENTIAL).
SQ SEQUENCE 763 AA; 86018 MW; E92CCF2F629D9C14 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 763;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 565 NAKTLTE 571

RESULT 11
RIMM_HELPJ
ID RIMM_HELPJ STANDARD; PRT; 181 AA.
AC Q9ZK65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probably 16S rRNA processing protein rimM.
GN RIMM OR JHF1076.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."

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RL Nature 397:176-180(1999).
CC -!- FUNCTION: ESSENTIAL FOR EFFICIENT PROCESSING OF 16S RNA. PROBABLY
CC PART OF THE 30S SUBUNIT PRIOR TO OR DURING THE FINAL STEP IN THE
CC PROCESSING OF 16S FREE 30S RIBOSOMAL SUBUNITS. IT COULD BE SOME
CC ACCESSORY PROTEIN NEEDED FOR EFFICIENT ASSEMBLY OF THE 30S
CC SUBUNIT. RIMM IS NEEDED IN A STEP PRIOR TO RBFA DURING THE
CC MATURATION OF 16S RNA. HAS AFFINITY FOR FREE RIBOSOMAL 30S
CC SUBUNITS BUT NOT FOR 70S RIBOSOMES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE RIMM FAMILY.
CC -----
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CC -----
DR EMBL; AE001535; AAD06656.1; -
DR InterPro; IPR002676; Rimm.
DR Pfam; PF01782; Rimm; 1.
KW rRNA processing; Complete proteome.
SQ SEQUENCE 181 AA; 20395 MW; DES6382F515B1E4A CRC64;

Query Match 82.4%; Score 28; DB 1; Length 181;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 173 NAKTLTE 179

RESULT 12
RIMM_HELPJ
ID RIMM_HELPJ STANDARD; PRT; 184 AA.
AC O25767;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probably 16S rRNA processing protein rimM.
GN RIMM OR HPI1149.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -!- FUNCTION: ESSENTIAL FOR EFFICIENT PROCESSING OF 16S RNA. PROBABLY
CC PART OF THE 30S SUBUNIT PRIOR TO OR DURING THE FINAL STEP IN THE
CC PROCESSING OF 16S FREE 30S RIBOSOMAL SUBUNITS. IT COULD BE SOME
CC ACCESSORY PROTEIN NEEDED FOR EFFICIENT ASSEMBLY OF THE 30S
CC SUBUNIT. RIMM IS NEEDED IN A STEP PRIOR TO RBFA DURING THE
CC MATURATION OF 16S RNA. HAS AFFINITY FOR FREE RIBOSOMAL 30S
CC SUBUNITS BUT NOT FOR 70S RIBOSOMES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE RIMM FAMILY.
CC -----

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DR EMBL; A5000621; AAD08193.1; -.  
DR TIGR; HP1149; -.  
DR InterPro; IPR002676; Rimm.  
DR Pfam; PF01782; Rimm; 1.  
KW rRNA processing; Complete proteome.  
SQ SEQUENCE 184 AA; 20792 MW; BB25C2A140488110 CRC64;  
  
Query Match 82.4%; Score 28; DB 1; Length 184;  
Best Local Similarity 85.7%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 NAKTLTE 7  
Db 176 NAKTLLE 182  
  
RESULT 13  
RS7\_THECE STANDARD; PRT; 215 AA.  
AC P29159;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 30S ribosomal protein S7P.  
GN RPS7P OR RPS7.  
OS Thermococcus celer.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=2264;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 2476;  
RX MEDLINE=92051399; PubMed=1840672;  
RA Klenk H.-P., Schwass V., Zillig W.;  
RT "Nucleotide sequence of the genes encoding the L30, S12 and S7  
RT equivalent ribosomal proteins from the archaeum Thermococcus celer.";  
RL Nucleic Acids Res. 19:6047-6047(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 2476;  
RX MEDLINE=93027167; PubMed=1408768;  
RA Klenk H.-P., Schwass V., Lottspeich F., Zillig W.;  
RT "Nucleotide sequence of the genes encoding the three largest subunits  
RT of the DNA-dependent RNA polymerase from the archaeum Thermococcus  
RT celer.";  
RL Nucleic Acids Res. 20:4659-4659(1992).  
RN [3]  
RP SEQUENCE OF 196-215 FROM N.A.  
RC STRAIN=DSM 2476;  
RX MEDLINE=93176822; PubMed=7916630;  
RA Klenk H.-P., Schwass V., Zillig W.;  
RT "Nucleotide sequence of the genes encoding proline tRNA (UGG) and  
RT threonine tRNA (GGU) and consensus promoter model of Thermococcus  
RT celer.";  
RL Biochim. Biophys. Acta 1172:236-238(1993).  
CC -!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF  
CC 16S RIBOSOMAL RNA (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.  
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-----  
DR EMBL; X60305; CAA42850.1; -.  
DR EMBL; X67313; CAA47728.1; -.  
DR EMBL; X68397; CAA48463.1; -.  
DR PIR; S18714; S18714.  
DR PIR; S29858; S29858.  
DR HSP; P17291; IRSS.  
DR InterPro; IPR00235; Ribosomal S7.  
DR Pfam; PF00177; Ribosomal S7; 1.  
DR ProDom; PD000817; Ribosomal S7; 1.  
DR TIGR; TIGR01028; S7\_S5\_E\_A; 1.  
DR PROSITE; PS00052; RIBOSOMAL\_S7; FALSE\_NEG.  
KW Ribosomal protein; rRNA-binding.  
FT CONFLICT 198 198 T -> S (IN REF. 2).  
FT CONFLICT 214 215 SR -> RA (IN REF. 2).  
SQ SEQUENCE 215 AA; 24393 MW; 6269A731ACE34230 CRC64;  
  
Query Match 82.4%; Score 28; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 AKTLTE 7  
Db 2 AKTLTE 7  
  
RESULT 14  
SAPR\_STRPU STANDARD; PRT; 296 AA.  
AC P11761;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-MAR-1992 (Rel. 21, Last annotation update)  
DE Spermact precursor (Sperm-activating peptide).  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=90241919; PubMed=2334699;  
RA Ramarao C.S., Burks D.J., Garbers D.L.;  
RT "A single mRNA encodes multiple copies of the egg peptide spermact.";  
RL Biochemistry 29:3383-3388(1990).  
RN [2]  
RP SEQUENCE OF SPERACT.  
RC TISSUE=Egg;  
RX MEDLINE=82142387; PubMed=7061446;  
RA Garbers D.L., Watkins H.D., Hansbrough J.R., Smith A., Misono K.S.;  
RT "The amino acid sequence and chemical synthesis of spermact and of  
RT spermact analogues.";  
RL J. Biol. Chem. 257:2734-2737(1982).  
RN [3]  
RP SEQUENCE OF SPERACT.  
RC TISSUE=Egg;  
RX MEDLINE=81094145; PubMed=6256397;  
RA Hansbrough J.R., Garbers D.L.;  
RT "Spermact. Purification and characterization of a peptide associated  
RT with eggs that activates spermatozoa.";  
RL J. Biol. Chem. 256:1447-1452(1981).  
CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY  
CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF  
CC CAMP, CGMP AND CLACTUM LEVELS IN SPERM CELLS, AND TRANSIENT  
CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF  
CC GUANYLATE CYCLASE.  
CC -!- SIMILARITY: SMALL TO A.PUNCTULATA RESACT.  
-----  
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DR EMBL; J02896; AAA30079.1; -  
 DR EMBL; J02896; AAA30080.1; ALT\_INIT.  
 DR PIR; A25724; A25724.  
 DR PIR; A34543; A34543.  
 FT PEPTIDE 135 144 SPERACT-LIKE (POTENTIAL).  
 FT PEPTIDE 191 200 SPERACT-LIKE (POTENTIAL).  
 FT PEPTIDE 202 211 SPERACT-LIKE.  
 FT PEPTIDE 213 222 SPERACT-LIKE.  
 FT PEPTIDE 224 233 SPERACT.  
 FT PEPTIDE 235 244 SPERACT.  
 FT PEPTIDE 246 255 SPERACT.  
 FT PEPTIDE 257 266 SPERACT.  
 FT PEPTIDE 268 277 SPERACT-LIKE.  
 FT PEPTIDE 279 288 SPERACT-LIKE.  
 SQ SEQUENCE 296 AA; 6B7F7484A255FDC4 CRC64;

Query Match 82.4%; Score 28; DB 1; Length 296;  
 Best Local Similarity 85.7%; Pred. No. 45;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKLTLE 7  
 ||| |||  
 Db 115 NAKELTE 121

RESULT 15  
 NK1R\_CAVPO  
 ID NK1R\_CAVPO STANDARD; PRT; 407 AA.  
 AC P30547;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Substance-P receptor (SPR) (NK-1 receptor) (NK-1R).  
 GN TACR1 OR TAC1R  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RX MEDLINE=92256498; PubMed=1374648;  
 RA Gorbulev V., Akhundova A., Luzius H., Fahrenholz F.;  
 RT "Molecular cloning of substance P receptor cDNA from guinea-pig  
 uterus.";  
 RL Biochim. Biophys. Acta 1131:99-102(1992).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHIKININ NEUROPEPTIDE  
 CC SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT  
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO  
 CC TACHIKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC HIGHEST TO OTHER TACHIKININS RECEPTORS.  
 CC -----  
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DR EMBL; X64323; CAA45608.1; -  
 DR PIR; S23510; S23510.  
 DR PIR; S19198; S19198.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 32 54 1 (POTENTIAL).  
 FT DOMAIN 55 64 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 65 86 2 (POTENTIAL).  
 FT DOMAIN 87 106 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 107 128 3 (POTENTIAL).  
 FT DOMAIN 129 148 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 149 169 4 (POTENTIAL).  
 FT DOMAIN 170 194 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 195 219 5 (POTENTIAL).  
 FT DOMAIN 220 248 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 249 270 6 (POTENTIAL).  
 FT DOMAIN 271 283 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 284 308 7 (POTENTIAL).  
 FT DOMAIN 309 407 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 105 180 BY SIMILARITY.  
 FT LIPID 322 322 PALMITATE (POTENTIAL).  
 SQ SEQUENCE 407 AA; 46257 MW; F8C5D31C4BB45E6B CRC64;

Query Match 82.4%; Score 28; DB 1; Length 407;  
 Best Local Similarity 71.4%; Pred. No. 62;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKLTLE 7  
 ||| |||  
 Db 391 NSKTVTE 397

RESULT 16  
 SR54\_MYCGE  
 ID SR54\_MYCGE STANDARD; PRT; 446 AA.  
 AC P47294;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Signal recognition particle protein (Fifty-four homolog).  
 GN FFH OR MG048.  
 OS Mycoplasma genitalium.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=96026346; PubMed=7569993;  
 RA Fraser C.M., Cocayne J.D., White O., Adams M.D., Clayton R.A.,  
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,  
 RA Nguyen D.T., Ufferback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
 RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,  
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  
 RT "The minimal gene complement of Mycoplasma genitalium.";  
 RL Science 270:397-403(1995).  
 CC -!- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC  
 CC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE  
 CC RIBOSOMES (BY SIMILARITY).  
 CC -!- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A SMALL  
 CC CYTOPLASMIC RNA (SC-RNA) MOLECULE AND PROTEIN FFH (BY SIMILARITY).  
 CC -!- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN  
 CC BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL  
 CC SEQUENCE.  
 CC -!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.  
 CC -----  
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Db 152 NSKVTTE 158
RESULT 19
Y422_MYCPN STANDARD; PRT; 839 AA.
AC F75175;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG422 homolog (C12_orf839).
GN MFN620 OR MF222.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelsreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
CC EMBL; A8000022; A8098870.1; --
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 839 AA; 99912 MW; 3E3523E18BCDFECC CRC64;
SQ
Query Match 82.4%; Score 28; DB 1; Length 839;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 NAKTLTE 7
DB 605 NATTLTE 611
RESULT 20
VNC5_AEDEV STANDARD; PRT; 849 AA.
AC P27454;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVp1).
GN NS1.
OS Aedes densovirus virus (strain GKV 002 002) (Aedes densovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Brevideovirus.
OX NCBI_TaxID=10808;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=92024090; PubMed=1833875;
RX Afanasiev B.N., Galyov E.E., Buchatsky L.P., Kozlov Y.V.;
RA "Nucleotide sequence and genomic organization of Aedes densovirus
RT virus."
RL Virology 185:323-336(1991).
CC -----
CC -!- FUNCTION: SEEMS NECESSARY FOR VIRAL DNA REPLICATION, PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF CAPSID GENE EXPRESSION. IT IS
CC COVALENTLY BOUND TO THE 5' TERMINI OF VIRAL DNA, AND CAN INFLUENCE
CC DNA PACKAGING. NS1 IS ALSO BELIEVED TO POSSESS THE TOPOISOMERASE I
CC TYPE NICKING ACTIVITY, AND CYTOTOXIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M37899; -- NOT ANNOTATED_CDS.
DR PIR; A40784; UYPVAD.
DR InterPro; IPR001257; Parvo_NSI.
DR Pfam; PF01057; Parvo_NSI; 1.
KW Nonstructural protein; Noncapsid protein; DNA replication;
KW ATP-binding.
FT NP BIND 624 631 ATP (POTENTIAL).
SQ SEQUENCE 849 AA; 97543 MW; D4FA0980B08E152E CRC64;
Query Match 82.4%; Score 28; DB 1; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 AKTLTE 7
DB 553 AKTLTE 558
RESULT 21
DPOM_ASCIM STANDARD; PRT; 1202 AA.
ID DPOM_ASCIM
AC P22374;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Probable DNA polymerase (EC 2.7.7.7).
OS Ascobolus immersus.
OG Mitochondrion.
OG Plasmid pA12.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
OC Pezizales; Ascobolaceae; Ascobolus.
OX NCBI_TaxID=5191;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=2/I;
RX MEDLINE=90066356; PubMed=2573821;
RA Kempken F., Meinhardt F., Esser K.;
RT "In organello replication and viral affinity of linear,
RT extrachromosomal DNA of the ascomycete Ascobolus immersus."
RL Mol. Gen. Genet. 218:523-530(1989).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -!- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. STRONG, TO
CC DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
CC -----
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CC -----
CC EMBL; X15982; CAA34106.1; --
DR PIR; S05362; S05362.
DR InterPro; IPR002064; DNA_pol_B.
DR Pfam; PF03175; DNA_pol_B_2; 1.
DR SMART; SM00486; POLB; 1.
DR PROSITE; PS00116; DNA POLYMERASE B; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Plasmid; Mitochondrion.
SQ SEQUENCE 1202 AA; 138279 MW; 51D41FCBBDF2CDE CRC64;
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Query Match      82.4%; Score 28; DB 1; Length 1202;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAKTLITE 7
      1:||||:
Db      174 NSKTLTD 180

RESULT 22
RL33 HELP
ID  RL33 HELPY      STANDARD;      PRT;      52 AA.
AC  P56055;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  50S ribosomal protein L33.
GN  RPL33 OR HP1204 OR JHP1204.
OS  Helicobacter pylori (Campylobacter pylori), and
OS  Helicobacter pylori J99 (Campylobacter pylori J99).
OC  Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC  Helicobacter.
OX  NCBI_TaxID=210, 85963;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=26695 / ATCC 700392;
RX  MEDLINE=97394467; PubMed=9252185;
RA  Fleischnmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA  Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA  Loftus B., Richardson D., Dodson R., Khairat H.G., Glodek A.,
RA  McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA  Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA  Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA  Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA  Venter J.C.;
RT  "The complete genome sequence of the gastric pathogen Helicobacter
RT  pylori.";
RL  Nature 388:539-547 (1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=J99;
RX  MEDLINE=99120557; PubMed=9923682;
RA  Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA  Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA  Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA  Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA  Trust T.J.;
RT  "Genomic sequence comparison of two unrelated isolates of the human
RT  gastric pathogen Helicobacter pylori.";
RL  Nature 397:176-180 (1999).
CC  -!- SIMILARITY: BELONGS TO THE L33P FAMILY OF RIBOSOMAL PROTEINS.
CC  -----
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CC  -----
DR  EMBL; AE000626; RAD08255.1; -
DR  EMBL; AE001541; RAD06710.1; -
DR  TIGR; HP1204; -
DR  InterPro; IPR001705; Ribosomal_L33.
DR  Pfam; PF00471; Ribosomal_L33; 1.
DR  ProDom; PD002595; Ribosomal_L33; 1.
DR  TIGRFAMs; TIGR01023; rplm33.bact; 1.
DR  PROSITE; PS00582; RIBOSOMAL_L33; 1.
KW  Ribosomal protein; Complete proteome.
SQ  SEQUENCE 52 AA; 6066 MW; 66BAC829C6859D6 CRC64;

Query Match      79.4%; Score 27; DB 1; Length 52;

Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKTLITE 7
      1:||||:
Db      22 NAKTNTE 28

RESULT 23
LEPU_BACSU
ID  LEPU_BACSU      STANDARD;      PRT;      187 AA.
AC  P42959;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Signal peptidase I U (EC 3.4.21.89) (Spase I) (Leader peptidase I).
GN  SPU.
OS  Bacillus subtilis.
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=1423;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RA  Akagawa E., Kurita K., Sugawara T., Nakamura K., Yamane K.;
RL  Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RX  MEDLINE=97124189; PubMed=8969502;
RA  Yamane K., Kumano M., Kurita K.;
RT  "The 25 degrees-36 degrees region of the Bacillus subtilis
RT  chromosome: determination of the sequence of a 146 kb segment and
RT  identification of 113 genes.";
RL  Microbiology 142:3047-3056 (1996).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RX  MEDLINE=98044033; PubMed=9384377;
RA  Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA  Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA  Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA  Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA  Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA  Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA  Enlart K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA  Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA  Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA  Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA  Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA  Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA  Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA  Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA  Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA  Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA  Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA  Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA  Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA  Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA  Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA  Sekiguchi J., Sekowska A., Seror S.J., Shin B.S., Soldo B.,
RA  Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA  Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA  Toesato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA  Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA  Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA  Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT  "The complete genome sequence of the Gram-positive bacterium Bacillus
RT  subtilis.";
RL  Nature 390:249-256 (1997).
CC  -!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
CC  secreted proteins precursor.
CC  -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC  -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S26; ALSO KNOWN AS TYPE
```

```
CC ----- I LEADER PEPTIDASE FAMILY. -----
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CC -----
CC EMBL; D38161; BAA07353.1; -
CC EMBL; D50453; BAA09032.1; -
CC EMBL; Z99106; CAB12209.1; -
CC HSP; P00803; IBI2.
CC MEROPS; S26.005; -
CC Subtilisin; BG11223; sipU.
CC InterPro; IPR000508; SigPase.
CC InterPro; IPR000223; SigPase_S26A.
CC Pfam; PF00461; Peptidase_S26; 1.
CC PRINTS; PR00727; LEADERPTASE.
CC PROSITE; PS00501; SPASE_I_1; 1.
CC PROSITE; PS00760; SPASE_I_2; 1.
CC PROSITE; PS00761; SPASE_I_3; 1.
CC Transmembrane; Hydrolase; Protease; Complete proteome.
CC DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 17 37 POTENTIAL.
CC DOMAIN 38 187 EXTRACELLULAR (POTENTIAL).
CC ACT_SITE 46 46 BY SIMILARITY.
CC ACT_SITE 88 88 BY SIMILARITY.
CC SEQUENCE 187 AA; 21183 MW; 31C48774CF6A849B CRC64;

Query Match 79.4%; Score 27; DB 1; Length 187;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTIT 6
DB 2 NAKTIT 7

RESULT 24
S3AG_BACSU STANDARD; PRT; 229 AA.
AC P49784;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stage III sporulation protein AG.
GN SPOIIIAG.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RA Guerout-Fleury A.M., Gonzy-Treboul G., Stragier P.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes."
RL Microbiology 142:3103-3111(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA MEDLINE=98044033; PubMed=9384377;
RA Kunat F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prieecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche M., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier J., Vassaretti A.,
RA Viati A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -----
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CC -----
CC EMBL; U35252; AAA76726.1; -
CC EMBL; D84432; BAA12566.1; -
CC EMBL; Z99116; CAB14368.1; -
CC Subtilisin; BG11414; spoIIIAG.
KW Sporulation; Transmembrane; Complete proteome.
FT TRANSMEM 30 50 POTENTIAL.
FT CONFLICT 14 14 F -> S (IN REF. 2).
SQ SEQUENCE 229 AA; 25549 MW; 110310C897BD8691 CRC64;

Query Match 79.4%; Score 27; DB 1; Length 229;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTIT 6
DB 58 NAKTIT 63

RESULT 25
HMUV_YERPE STANDARD; PRT; 266 AA.
AC Q56993;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemin transport system ATP-binding protein hmuV.
GN HMUV OR YPO0279.
OS Versinia pectis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM6;
RX MEDLINE=96386041; PubMed=9026634;
```

RA Hornung J.M., Jones H.A., Perry R.D.;  
 RT "the hmu locus of *Yersinia pestis* is essential for utilization of  
 RT free haemin and haem-protein complexes as iron sources.";   
 RL Mol. Microbiol. 20:725-739(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360;  
 RA ParKhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
 RA "Genome sequence of *Yersinia pestis*, the causative agent of plague.";   
 RL Nature 413:523-527(2001).  
 CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM  
 CC FOR HEMIN. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE  
 CC TRANSPORT SYSTEM.  
 CC -!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.  
 CC  
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 CC  
 CC EMBL; U60647; AAC64870.1; -;  
 CC EMBL; AJ414141; CAC89142.1; -;  
 CC InterPro: IPR003593; AAA ATPase.  
 CC InterPro: IPR003439; ABC\_transporter.  
 CC Pfam; PF00005; ABC\_tran; 1.  
 CC ProDom; PD000006; ABC\_transport; 1.  
 CC SMART; SM00382; AAA; 1.  
 CC PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
 CC Inner membrane; Iron transport; Transport; ATP-binding;  
 KW Complete proteome.  
 FT NP\_BIND 44 51 ATP (POTENTIAL).  
 FT SEQUENCE 266 AA; 29658 MW; 4A7DEB955383CB27 CRC64;  
 SQ  
 Query Match 79.4%; Score 27; DB 1; Length 266;  
 Best Local Similarity 71.4%; Pred. No. 68;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAKTLITE 7  
 Db 237 NAEITLQ 243  
 RESULT 26  
 ID ADT SCHPO STANDARD; PRT; 322 AA.  
 AC Q09188;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ADP.ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT).  
 GN ANCI1 OR SPBC530.10C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=96257204; PubMed=8675018;  
 RA Cousin N., Trezeguet V., Saux A.L., Lauquin G.J.M.;

RT "Cloning of the gene encoding the mitochondrial adenine nucleotide  
 RT carrier of Schizosaccharomyces pombe by functional complementation in  
 RT Saccharomyces cerevisiae.";   
 RL Genes 171:113-117(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Reinhardt R., Pohl T.M.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RL "The genome sequence of *Schizosaccharomyces pombe*.";   
 CC Nature 415:871-880(2002).  
 CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC  
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 CC  
 CC EMBL; Z49974; CAA90275.1; -;  
 CC EMBL; AL023634; CAA19176.1; -;  
 CC InterPro: IPR002067; Mit\_carrier.  
 CC InterPro: IPR001993; Mitoch\_carrier.  
 CC Pfam; PF00153; mito\_carr; 3.  
 CC PRINTS; PR00926; MITOCARRIER.  
 CC PROSITE; PS00215; MITOCH\_CARRIER; 2.  
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 28 48 1 (POTENTIAL).  
 FT TRANSMEM 93 111 2 (POTENTIAL).  
 FT TRANSMEM 131 151 3 (POTENTIAL).  
 FT TRANSMEM 197 217 4 (POTENTIAL).  
 FT TRANSMEM 222 242 5 (POTENTIAL).  
 FT TRANSMEM 289 309 6 (POTENTIAL).  
 FT SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;  
 SQ  
 Query Match 79.4%; Score 27; DB 1; Length 322;  
 Best Local Similarity 71.4%; Pred. No. 83;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 NAKTLITE 7  
 Db 15 NANTITE 21

## RESULT 27

FMRA\_CALPA STANDARD; PRT; 334 AA.  
AC Q01133;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Antho-RFamide neuropeptides precursor.  
OS Calliactis parasitica (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Hormathiidae; Calliactis.  
OX NCBI\_TaxID=6114;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91172845; PubMed=1706527;  
RA Darner D.; Schmutzler C.; Diekhoff D.; Gimmelikhuijzen C.J.P.;  
RT "Primary structure of the precursor for the sea anemone neuropeptide  
Antho-RFamide (<Glu-Gly-Arg-Phe-NH2>).";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).  
CC -!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT  
NEUROMUSCULAR SYNAPSES.  
CC -!- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.  
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CC  
CC EMBL; M59166; AAA27878.1; -;  
DR PIR; A39172; A39172.  
DR InterPro; IPR002544; FARP.  
DR Pfam; PF01581; FARP; 15.  
KW Neuropeptide; Amidation; Repeat; Signal.  
FT SIGNAL 1 26 POTENTIAL.  
FT PEPTIDE 117 120 ANTHO-RFAMIDE.  
FT PEPTIDE 126 129 ANTHO-RFAMIDE.  
FT PEPTIDE 135 138 ANTHO-RFAMIDE.  
FT PEPTIDE 143 146 ANTHO-RFAMIDE.  
FT PEPTIDE 152 155 ANTHO-RFAMIDE.  
FT PEPTIDE 161 164 ANTHO-RFAMIDE.  
FT PEPTIDE 170 173 ANTHO-RFAMIDE.  
FT PEPTIDE 179 182 ANTHO-RFAMIDE.  
FT PEPTIDE 188 191 ANTHO-RFAMIDE.  
FT PEPTIDE 197 200 ANTHO-RFAMIDE.  
FT PEPTIDE 206 209 ANTHO-RFAMIDE.  
FT PEPTIDE 215 218 ANTHO-RFAMIDE.  
FT PEPTIDE 224 227 ANTHO-RFAMIDE.  
FT PEPTIDE 234 237 ANTHO-RFAMIDE.  
FT PEPTIDE 243 246 ANTHO-RFAMIDE.  
FT PEPTIDE 253 256 ANTHO-RFAMIDE.  
FT PEPTIDE 263 266 ANTHO-RFAMIDE.  
FT PEPTIDE 272 275 ANTHO-RFAMIDE.  
FT PEPTIDE 281 284 ANTHO-RFAMIDE.  
FT MOD\_RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP).  
FT MOD\_RES 129 129 AMIDATION (G-130 PROVIDE AMIDE GROUP).  
FT MOD\_RES 138 138 AMIDATION (G-139 PROVIDE AMIDE GROUP).  
FT MOD\_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).  
FT MOD\_RES 155 155 AMIDATION (G-156 PROVIDE AMIDE GROUP).  
FT MOD\_RES 164 164 AMIDATION (G-165 PROVIDE AMIDE GROUP).  
FT MOD\_RES 173 173 AMIDATION (G-174 PROVIDE AMIDE GROUP).  
FT MOD\_RES 182 182 AMIDATION (G-183 PROVIDE AMIDE GROUP).  
FT MOD\_RES 191 191 AMIDATION (G-201 PROVIDE AMIDE GROUP).  
FT MOD\_RES 200 200 AMIDATION (G-210 PROVIDE AMIDE GROUP).  
FT MOD\_RES 209 209 AMIDATION (G-219 PROVIDE AMIDE GROUP).  
FT MOD\_RES 218 218 AMIDATION (G-228 PROVIDE AMIDE GROUP).  
FT MOD\_RES 227 227 AMIDATION (G-238 PROVIDE AMIDE GROUP).  
FT MOD\_RES 237 237 AMIDATION (G-247 PROVIDE AMIDE GROUP).  
FT MOD\_RES 246 246 AMIDATION (G-247 PROVIDE AMIDE GROUP).

FT MOD\_RES 256 256 AMIDATION (G-257 PROVIDE AMIDE GROUP).  
FT MOD\_RES 266 266 AMIDATION (G-267 PROVIDE AMIDE GROUP).  
FT MOD\_RES 275 275 AMIDATION (G-276 PROVIDE AMIDE GROUP).  
FT MOD\_RES 284 284 AMIDATION (G-285 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 334 AA; 39781 MW; 439E182C736EB583 CRC64;  
Query Match 79.4%; Score 27; DB 1; Length 334;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NAKTLTE 7  
DB 25 NAKTVTK 31  
RESULT 28  
CLPX\_VIBCH STANDARD; PRT; 426 AA.  
AC Q9KQ57;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE ATP-dependent Clp protease ATP-binding subunit clpX.  
GN CLPX OR VC1921.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=El Tor N16961 / Serotype O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L.;  
RA Dodson R.J.; Haft D.H.; Hickey E.K.; Peterson J.D.; Unayam L.A.;  
RA Gill S.R.; Nelson K.E.; Read T.D.; Tettelin H.; Dragoi I.; Sellers P.;  
RA Ermolaeva M.D.; Vamathevan J.; Bass S.; Qin H.; Rai S.; White O.;  
RA McDonald L.; Utterback T.; Fleischmann R.D.; Nierman W.C.; White O.;  
RA Salzberg S.L.; Smith H.O.; Colwell R.R.; Mekalanos J.J.; Venter J.C.;  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
cholerae.";  
RL Nature 406:477-483(2000).  
CC -!- FUNCTION: ATP-dependent specificity component of the Clp protease.  
It directs the protease to specific substrates. Can perform  
chaperone functions in the absence of clpP (By similarity).  
CC -!- SUBUNIT: Heterodimer of clpP and clpX (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY.  
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CC  
CC EMBL; AE004268; AAF95069.1; -;  
DR HSP; P32168; 1E94.  
DR TIGR; VC1921; -;  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR003959; AAA\_ATPase\_centre.  
DR InterPro; IPR004487; ClpX.  
DR Pfam; PF00004; AAA; 1.  
DR SMART; SM00382; AAA; 1.  
DR TIGRPFAMs; TIGR00382; clpX; 1.  
KW Chaperone; ATP-binding; Zinc-finger; Complete proteome.  
FT ZN FING 16 41 C4-TYPE.  
FT NP BIND 121 128 ATP (POTENTIAL).  
SQ SEQUENCE 426 AA; 46490 MW; 9EA336B942EFA9D4 CRC64;  
Query Match 79.4%; Score 27; DB 1; Length 426;  
Best Local Similarity 71.4%; Pred. No. 11e-02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NAKTLTE 7
Db 281 NSKLTSE 287

RESULT 29
FLGE_BORBU STANDARD; PRT; 442 AA.
AC Q44767; Q44899; Q44734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar hook protein flgE.
GN FLGE OR BB0283.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]_TaxID=139;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RA Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB19;
RA Old I.G.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kervavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA Van Vugt R., Palmer N.D., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
RN [4]
RP SEQUENCE OF 18-207 FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RA Limberger R.J., Slivinski L.L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS
CC FAMILY.
CC -----
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CC -----
CC EMBL; U19277; AAA64650.1; -
CC SEQUENCE 449 AA; 52510 MW; 3806354020A95E26 CRC64;

Query Match 79.4%; Score 27; DB 1; Length 449;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 244 NAETLTD 250

RESULT 31
SYN_ECOLI STANDARD; PRT; 572 AA.
AC P16659; O59430; P78272;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (PRORS)
DE (Global RNA synthesis factor).
DE PROS OR DRPA OR B0194.
GN Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-12.
RX MEDLINE=90370122; PubMed=2203971;
RA Erhani G., Delarue M., Poch O., Gangloff J., Moras D.;
RT "Partition of tRNA synthetases into two classes based on mutually
RT exclusive sets of sequence motifs.";
```

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RL Nature 347:203-206(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094229; PubMed=1688424;
RA Zhou Z., Syvanen M.;
RT "Identification and sequence of the drpA gene from Escherichia coli.";
RJ J. Bacteriol. 172:281-286(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / W3110;
RA Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
RA Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
RA Mizuno T., Makino K., Nakata A., Yura T., Sempel G., Mizobuchi K.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 4.0 - 6.0 min (189,987 - 281,416bp) region.";
RN Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
RA Davis R.W.;
RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-155 FROM N.A.
RX STRAIN=K12;
RA Miyamoto K.;
RT Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 1-12.
RX STRAIN=K12 / EMG2;
RX MEDLINE=97443775; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP +
CC diphosphate + L-prolyl-tRNA(Pro).
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; X55518; CAA39134.1; -
DR EMBL; M97858; AAA24420.1; -
DR EMBL; W32357; AAA23710.1; -
DR EMBL; A8000126; AAC73305.1; -
DR EMBL; D83536; BAA77870.1; -
DR EMBL; U70214; AAB08622.1; -
DR EMBL; D15061; BAA03654.1; -
DR PIR; JVO110; VPEC.
DR SWISS-2DPAGE; P16659; COLI.
DR EcoGene; EGI0770; PROS.
DR InterPro; IPR002106; AAErna_ligaseII.
DR InterPro; IPR004154; HGTP_anticonodon.
DR
DR InterPro; IPR004500; PROS_fam_II.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR002316; tRNA-synt_pro.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR Pfam; PF03129; HGTP_anticonodon; 1.
DR PRINTS; PR01046; TRNASYNTHPRO.
DR TIGRfams; TIGR00409; PROS_fam_II; 1.
DR PROSITE; PS00862; AA_TRNA_LIGASE_II.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT CONFLICT 26 27 ML -> IV (IN REF. 1 AND 4).
FT CONFLICT 127 128 QL -> HV (IN REF. 2).
FT CONFLICT 205 216 QASHEFOVLAOS -> RLPTNSRCWRR (IN REF. 2).
FT CONFLICT 205 205 O -> S (IN REF. 3 AND 5).
FT CONFLICT 516 517 PG -> RA (IN REF. 2).
FT CONFLICT 518 572 MISSING (IN REF. 2).
FT CONFLICT 568 572 KOIKG -> ETD (IN REF. 4).
SQ SEQUENCE 572 AA; 63733 MW; 2514448F3BC5FD3 CRC64;
Query Match 79.4%; Score 27; DB 1; Length 572;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NAKTLTE 7
DB 259 NAKTIAE 265
RESULT 32
SYN HAEIN
ID - SYP HAEIN STANDARD; PRT; 572 AA.
AC P43830.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (PRORS).
GN PROS OR HI0729.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_taxid=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Kleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP +
CC diphosphate + L-prolyl-tRNA(Pro).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY;
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CC -----
DR EMBL; U32756; AAC22388.1; -
DR TIGR; HI0729; -

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DR InterPro: IPR002106; AATRNA_ligaseII.
DR InterPro: IPR004154; HGRP_anticondon.
DR InterPro: IPR004500; ProS_fam_I.
DR InterPro: IPR002314; tRNA-synt_2b.
DR InterPro: IPR002316; tRNA-synt_pro.
DR Pfam: PF00587; tRNA-synt_2b; 1.
DR Pfam: PF03129; HGRP_anticondon; 1.
DR PRINTS: PRO1046; TRNASYNTHPRO.
DR TIGRFAMs: TIGR00409; ProS_fam_II; 1.
DR PROSITE: PS0862; AA TRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 572 AA; 63975 MW; 5BR0F81162368583 CRC64;

Query Match 79.4%; Score 27; DB 1; Length 572;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 258 NAKTIAE 264

RESULT 33
KICH_YEAST STANDARD; PRT; 582 AA.
AC P20485;
DT 01-FEB-1991 (Rel. 17, Last Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Choline kinase (EC 2.7.1.32).
GN CKII OR CKI OR YLR133W OR L3130 OR L9606.8.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89123268; PubMed=2536698;
RC STRAIN=S288c;
RA Delius H., Hebling U.;
RT "Cloning and characterization of the yeast CKI gene encoding choline
kinase and its expression in Escherichia coli.";
RL J. Biol. Chem. 264:2053-2059(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Delius H., Hebling U.;
RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RESPONSIBLE FOR PHOSPHATIDYLCHOLINE SYNTHESIS VIA THE
CC CDP-CHOLINE PATHWAY. ALSO EXHIBITS ETHANOLAMINE KINASE ACTIVITY
CC BUT AT 14% EFFICIENCY COMPARED WITH CHOLINE.
CC -!- CATALYTIC ACTIVITY: ATP + choline = ADP + O-phosphocholine.
CC -!- PATHWAY: CDP-CHOLINE AND CDP-ETHANOLAMINE PATHWAYS IN THE
CC SYNTHESIS OF PHOSPHOLIPIDS IN YEAST.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE CHOLINE/ETHANOLAMINE KINASES FAMILY.
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-----
DR EMBL: M61151; AAA22080.1; -.
DR InterPro: IPR002937; Amino oxidase.
DR InterPro: IPR000624; Glycosidase.
DR InterPro: IPR000205; NAD binding.
DR Pfam: PF01593; Amino oxidase; 1.
DR Pfam: PF02027; Ro1B_Ro1C; 1.
KW Oxidoreductase; Monooxygenase; Auxin biosynthesis; T-DNA; Plasmid.
SQ SEQUENCE 749 AA; 83178 MW; 8B7793970206F97B CRC64;

Query Match 79.4%; Score 27; DB 1; Length 749;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;

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-----
DR EMBL: J04454; AAA34499.1; -.
DR EMBL: X91258; CA62646.1; -.
DR EMBL: 273305; CAA97704.1; -.
DR EMBL: U53881; AAB82396.1; -.
DR PIR: A32034; A32034.
DR SGD: S0004123; CKII.
DR InterPro: IPR002573; Choline kinase.
DR Pfam: PF01633; Choline kinase; 1.
KW Transferase; Kinase; Phosphorylation.
FT MOD RES 30 30 PHOSPHORYLATION (POTENTIAL) .
FT MOD RES 85 85 PHOSPHORYLATION (POTENTIAL) .
FT ACT_SITE 328 328 BY SIMILARITY.
SQ SEQUENCE 582 AA; 66316 MW; 68C395B9CC120A0E CRC64;

Query Match 79.4%; Score 27; DB 1; Length 582;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 221 NSKTLTK 227

RESULT 34
TR2M_AGRH
ID TR2M_AGRH STANDARD; PRT; 749 AA.
AC Q09109;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN AUX1.
OS Agrobacterium rhizogenes.
OG Plasmid pRiA4.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A4;
RX MEDLINE=92033088; PubMed=1932811;
RA Camilleri C., Jouanin L.;
RT "The TR-DNA region carrying the auxin synthesis genes of the
Agrobacterium rhizogenes agropine-type plasmid pRiA4: nucleotide
sequence analysis and introduction into tobacco plants.";
RL Mol. Plant Microbe Interact. 4:155-162(1991).
CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.
CC -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
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-----
DR EMBL: M61151; AAA22080.1; -.
DR InterPro: IPR002937; Amino oxidase.
DR InterPro: IPR000624; Glycosidase.
DR InterPro: IPR000205; NAD binding.
DR Pfam: PF01593; Amino oxidase; 1.
DR Pfam: PF02027; Ro1B_Ro1C; 1.
KW Oxidoreductase; Monooxygenase; Auxin biosynthesis; T-DNA; Plasmid.
SQ SEQUENCE 749 AA; 83178 MW; 8B7793970206F97B CRC64;

Query Match 79.4%; Score 27; DB 1; Length 749;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 82 NAKSLTE 88

RESULT 35
SYAC_YEAST STANDARD; PRT; 958 AA.
ID _SYAC_YEAST
AC P40825;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.7) (Alanine--tRNA
ligase) (AlaRS).
GN ALAI OR YORJ35C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051586; PubMed=8896263;
RA Parle-Medemott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
RT "Sequence of 29 kb around the PDR10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I.";
RL Yeast 12:999-1004 (1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
CC diphosphate + L-alanyl-CRNA(Ala).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; U18672; AAC49007.1; -
DR EMBL; Z49821; CAA89980.1; -
DR EMBL; Z75243; CAA99658.1; -
DR SGD; S0005862; ALA1.
DR InterPro; IPR002106; AATRNA_ligaseII.
DR InterPro; IPR003156; DHAL1.
DR Pfam; PF01411; tRNA-synt_2c; 1.
DR Pfam; PF02272; DHAL1; 1.
DR PRINTS; PR00980; TRNASYNTHALA.
DR TIGRFAMs; TIGR00344; alas; 1.
DR PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT CONFLICT 136 136 R -> S (IN REF. 1).
FT CONFLICT 465 467 KQD -> RTK (IN REF. 1).
FT CONFLICT 840 841 FE -> LQ (IN REF. 1).
FT SEQUENCE 958 AA; 107277 MW; 50FD31C2E2D40F32 CRC64;

Query Match 79.4%; Score 27; DB 1; Length 958;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 858 NAKALTE 864

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLT 6
Db 449 NAKTIT 454

RESULT 36
RPB2_YEAST STANDARD; PRT; 1224 AA.
ID _RPB2_YEAST
AC P08518; Q12738;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DNA-directed RNA polymerase II 140 kDa polypeptide (EC 2.7.7.6) (B150)
DE (RNA polymerase II subunit 2).
GN RPB2 OR RPO22 OR RPB150 OR YOR151C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87147239; PubMed=3547406;
RA Sweetser D., Nonet M., Young R.A.;
RT "Prokaryotic and eukaryotic RNA polymerases have homologous core
RT subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1192-1196 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / FY1678;
RA Ayadi A., Bordonne R., Camasses A., Madania A., Poch O.,
RA Tatassov I.A., Winsor B., Martin R.P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -!- SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
CC THIS SUBUNIT IS THE SECOND LARGEST COMPONENT OF RNA POLYMERASE II.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND TRNA GENES.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC -----
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CC -----
DR EMBL; M15693; AAA68096.1; -
DR EMBL; U55020; AAC49637.1; -
DR EMBL; Z75059; CAA99357.1; -
DR PIR; A25884; A25884.
DR SGD; S0005677; RPB2.
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF00562; RNA_pol_B; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
KW Transferrase; DNA-directed RNA polymerase; Transcription; Zinc;
FT Zinc-finger; Nuclear protein.
FT ZN_FING 1163 1185 C4-TYPE (POTENTIAL).
FT CONFLICT 1003 1006 AEGI -> RRRY (IN REF. 1).
FT SEQUENCE 1224 AA; 138751 MW; BABD03212COA583E CRC64;

Query Match 79.4%; Score 27; DB 1; Length 1224;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6
Db 449 NAKTIT 454

RESULT 37
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RL33 BRUME
ID RL33 BRUME STANDARD; PRT; 55 AA.
AC Q8YC71;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L33.
GN RPMG OR BMEII0661.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RA MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kypides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
CC -!- SIMILARITY: BELONGS TO THE L33P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC
CC EMBL; V00778; CAA24155.1; -.
DR PIR; A01918; KVMK2.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION K2.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12581 MW; 4F41E3D40C539DEC CRC64;

Query Match 76.5%; Score 26; DB 1; Length 115;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NAKTLTE 7
DB 70 NAKTLAD 76

RESULT 39
CIB1 HUMAN
ID CIB1 HUMAN STANDARD; PRT; 218 AA.
AC Q07639;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN SCN1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93357746; PubMed=8394762;
RA McClatchey A.I., Cannon S.C., Slaughterhaupt S.A., Gusella J.F.;
RT "The cloning and expression of a sodium channel beta 1-subunit cDNA
RT from human brain.";
RL Hum. Mol. Genet. 2:745-749(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Heart;
RX MEDLINE=94171787; PubMed=8125980;
RA Makita N., Bennett P.B. Jr., George A.L. Jr.;
RT "Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult
RT human skeletal muscle, heart, and brain is encoded by a single
RT gene.";
RL J. Biol. Chem. 269:7571-7578(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154833; PubMed=7851891;
RA Makita N., Sloan-Brown K., Weghuis D.O., Ropers H.H.,
RA George A.L. Jr.;
```

"Genomic organization and chromosomal assignment of the human voltage-gated Na<sup>+</sup> channel beta 1 subunit gene (SCN1B)."; Genomics 23:628-634(1994).

[4] VARIANT GEF5+ TRP-121.

RX MEDLINE=98361163; PubMed=9697698;

RA Wallace R.H., Wang D.W., Singh R., Scheffer I.E., George A.L. Jr., Phillips H.A., Saar K., Reis A., Johnson E.W., Sutherland G.R., Bertovic S.P., Mulley J.C.;

RA "Fetile seizures and generalized epilepsy associated with a mutation in the Na(+)-channel beta-1 subunit gene SCN1B."; Nat. Genet. 19:366-370(1998).

CC -!- FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL MODULATION OF THE HETEROTRIMERIC COMPLEX OF THE SODIUM CHANNEL. THE BETA-1 SUBUNIT CAN MODULATE MULTIPLE ALPHA SUBUNIT ISOMERISMS FROM BRAIN, SKELETAL MUSCLE, AND HEART.

CC -!- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY DISULFIDE BONDS.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN SKELETAL MUSCLE, HEART AND BRAIN.

CC -!- DISEASE: DEFECTS IN SCN1B ARE A CAUSE OF GENERALIZED EPILEPSY WITH FEBRILE SEIZURES PLUS (GEFS+), A DISEASE CHARACTERIZED BY A HIGHLY VARIABLE PHENOTYPE COMBINING FEBRILE SEIZURES, GENERALIZED SEIZURES OFTEN PRECIPITATED BY FEVER AT AGE 6 YEARS OR MORE, AND PARTIAL SEIZURES, WITH A VARIABLE DEGREE OF SEVERITY.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

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DR EMBL; L10338; AAA60391.1; -.

DR EMBL; L16242; AAA61277.1; -.

DR EMBL; U12193; AAB97608.1; -.

DR EMBL; U12189; AAB97608.1; JOINED.

DR EMBL; U12190; AAB97608.1; JOINED.

DR EMBL; U12191; AAB97608.1; JOINED.

DR EMBL; U12192; AAB97608.1; JOINED.

DR Genbank; HGNC:10586; SCN1B.

DR MIM; 600235; -.

DR MIM; 604233; -.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003600; Ig\_Like.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00410; Ig\_Like; 1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Signal; Immunoglobulin domain; Disease mutation.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 218 SODIUM CHANNEL BETA-1 SUBUNIT.

FT DOMAIN 19 160 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 161 182 POTENTIAL.

FT DOMAIN 183 218 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 22 150 IG-LIKE C2-TYPE DOMAIN.

FT DISULFID 40 121 POTENTIAL.

FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 121 121 C -> W (IN GEFS+).

FT FTID=VAR 010165.

SQ SEQUENCE 218 AA; 24707 MW; 09B812F3F9E9018 CRC64;

Query Match 76.5%; Score 26; DB 1; Length 218;

Best Local Similarity 71.4%; Pred. No. 94;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||:|:|  
DB 50 NAEFTTE 56

RESULT 40

NIH3 AZOVI STANDARD; PRT; 275 AA.

ID PI6269;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nitrogenase iron protein 3 (EC 1.18.6.1) (Nitrogenase component II)

DE (Nitrogenase Fe protein 3) (Nitrogenase reductase).

GN ANFH.

OS Azotobacter vinelandii.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Azotobacter.

OX NCBI\_TaxID=354;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89123105; PubMed=2644222;

RA Joerges R.D., Jacobson M.R., Premakumar R., Wolfinger E.D., Bishop P.E.;

RT "Nucleotide sequence and mutational analysis of the structural genes (anFDGK) for the second alternative nitrogenase from Azotobacter vinelandii."; J. Bacteriol. 171:1075-1086(1989).

CC -!- FUNCTION: THE KEY ENZYMAIC REACTIONS IN NITROGEN FIXATION ARE CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE IRON PROTEIN (COMPONENT 2) AND A COMPONENT 1 WHICH IS EITHER A MOLYBDENUM-IRON PROTEIN, A VANADIUM-IRON, OR AN IRON-IRON PROTEIN.

CC -!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.

CC -!- COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.

CC -!- SUBUNIT: HOMODIMER.

CC -!- MISCELLANEOUS: THIS SUBUNIT IS ASSOCIATED WITH THE IRON-IRON NITROGENASE COMPONENT 2 (THE THIRD TYPE OF NITROGENASE).

CC -!- SIMILARITY: BELONGS TO THE NIFH / BCLH / CHLL FAMILY.

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DR EMBL; M23528; AAA82508.1; -.

DR PIR; A32057; A32057.

DR HSSP; P00459; IN2C.

DR InterPro; IPR000392; NitrogenaseII.

DR Pfam; PF00142; fer4\_NiH; 1.

DR PRINTS; PR00091; NITROGNASEII.

DR TIGRFAMs; TIGR01287; nifH; 1.

DR PROSITE; PS00692; NIFH\_FRXC\_2; 1.

DR PROSITE; PS00746; NIFH\_FRXC\_1; 1.

KW Oxidoreductase; Nitrogen fixation; Iron-sulfur; 4Fe-4S; ATP-binding.

FT NP BIND 9 16 ATP (POTENTIAL).

FT METAL 97 97 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

FT METAL 132 132 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

SQ SEQUENCE 275 AA; 29885 MW; 6D262472FE9258EB CRC64;

Query Match 76.5%; Score 26; DB 1; Length 275;

Best Local Similarity 71.4%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
||:|:|  
DB 223 NKKTVTE 229

Search completed: July 18, 2003, 15:07:19  
Job time : 5.34 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:40 ; Search time 18.06 Seconds  
(without alignments)  
79.863 Million cell updates/sec

Title: US-10-007-790-9  
Perfect score: 34  
Sequence: 1 NAKTLTE 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTRMBL\_21.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phase.\*
  - 10: sp\_plant.\*
  - 11: sp\_prodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_rvirus.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	94.1	2091	3 P78616	P78616 emericella
2	31	91.2	149	16 Q92BY8	Q92BY8 listeria in
3	31	91.2	149	16 Q8Y7B9	Q8Y7B9 listeria mo
4	31	91.2	714	4 Q9NYW8	Q9NYW8 homo sapien
5	30	88.2	1251	5 Q8SWP7	Q8SWP7 encephalito
6	29	85.3	106	2 Q9L643	Q9L643 prochloroco
7	29	85.3	229	16 Q8X6K2	Q8X6K2 escherichia
8	29	85.3	261	2 P77996	P77996 chermosaer
9	29	85.3	322	10 Q9FHQ6	Q9FHQ6 arabidopsis
10	29	85.3	351	16 Q9K701	Q9K701 bacillus ha
11	29	85.3	416	17 Q97VY2	Q97VY2 sulfolobus
12	29	85.3	468	16 Q8U5F8	Q8U5F8 agrobacteri
13	29	85.3	470	10 Q8S9A4	Q8S9A4 phaseolus a
14	29	85.3	472	16 Q8XIQ4	Q8XIQ4 clostridium
15	29	85.3	475	16 Q9CMS6	Q9CMS6 pasteurella
16	29	85.3	487	16 Q985E4	Q985E4 rhizobium 1

17	29	85.3	491	16 Q8YG44	Q8YG44 brucella me
18	29	85.3	493	16 Q8U858	Q8U858 agrobacteri
19	29	85.3	493	16 Q8XTA0	Q8XTA0 ralstonia s
20	29	85.3	494	16 Q8UGN0	Q8UGN0 agrobacteri
21	29	85.3	500	16 Q92R69	Q92R69 rhizobium m
22	29	85.3	507	5 Q95QX8	Q95QX8 caenorhabdi
23	29	85.3	715	16 O51542	O51542 borrelia bu
24	29	85.3	765	16 Q8Y153	Q8Y153 ralstonia s
25	29	85.3	841	5 Q9U5M9	Q9U5M9 manduca sex
26	29	85.3	942	16 Q8R523	Q8R523 fusobacteri
27	29	85.3	1817	11 O54952	O54952 rattus norv
28	28	82.4	131	16 Q92FX7	Q92FX7 rickettsia
29	28	82.4	166	16 Q9A1C0	Q9A1C0 streptococc
30	28	82.4	196	2 Q46622	Q46622 erwinia amy
31	28	82.4	223	10 Q9FKW3	Q9FKW3 arabidopsis
32	28	82.4	227	16 Q8Y237	Q8Y237 ralstonia s
33	28	82.4	236	16 P71631	P71631 mycobacteri
34	28	82.4	247	16 Q8UDG4	Q8UDG4 agrobacteri
35	28	82.4	268	16 O06542	O06542 mycobacteri
36	28	82.4	287	16 Q8YMR2	Q8YMR2 anabaena sp
37	28	82.4	293	2 Q9L5C1	Q9L5C1 leptospira
38	28	82.4	294	2 Q93QI0	Q93QI0 lactococcus
39	28	82.4	304	5 Q94382	Q94382 caenorhabdi
40	28	82.4	304	5 Q94383	Q94383 caenorhabdi
41	28	82.4	314	15 Q9ENI9	Q9ENI9 human immun
42	28	82.4	317	10 Q9C9K8	Q9C9K8 arabidopsis
43	28	82.4	320	10 Q9SFX4	Q9SFX4 arabidopsis
44	28	82.4	320	16 Q8XWH9	Q8XWH9 ralstonia s
45	28	82.4	328	16 Q9CE05	Q9CE05 lactococcus

ALIGNMENTS

RESULT 1

P78616

ID P78616 PRELIMINARY; PRT; 2091 AA.

AC P78616; TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Fatty acid synthase, beta subunit.

GN FASB.

OS Emericella nidulans (Aspergillus nidulans).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI\_TaxID=5072;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97121482; PubMed=8962148;

RA Brown D.W., Adams T.H., Keller N.P.;

RT "Aspergillus has distinct fatty acid synthases for primary and secondary metabolism.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:14873-14877(1996).

DR EMBL; U75347; AAB41494.1; -

DR InterPro; IPR001227; AC transferase.

DR InterPro; IPR003965; Fatty acid synth.

DR InterPro; IPR002539; MacC dehydratase.

DR Pfam; PF00698; Acyl\_transf; 1.

DR Pfam; PF01575; MacC dehydratase; 1.

DR PRINTS; PR01483; FASYNTHASE.

SQ SEQUENCE 2091 AA; 232284 MW; E3DCDE8640124BCC CRC64;

Query Match 94.1%; Score 32; DB 3; Length 2091;

Best Local Similarity 85.7%; Pred. No. 2.8e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NAKTLTE 7

Db 637 NAKTLTE 643

RESULT 2

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Q92BY8
ID Q92BY8 PRELIMINARY; PRT; 149 AA.
AC Q92BY8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein lin1404.
GN Lin1404.
OS Listeria innocua.
OC Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krett J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluer T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591978; CAC99445.1; -.
DR ListLib; LIN01404; -.
DR InterPro; IPR001669; Arg_repress.
DR Pfam; PF02863; Arg_repressor_C; 1.
DR ProDom; PD007402; Arg_repress; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 149 AA; 16811 MW; 364222B56ADDE1BF CRC64;

Query Match 91.2%; Score 31; DB 16; Length 149;
Best Local Similarity 85.7%; Pred.No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 137 NAKTLTD 143

RESULT 3
Q92BY8 PRELIMINARY; PRT; 149 AA.
AC Q92BY8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein lmo1367.
GN LMO1367.
OS Listeria monocytogenes.
OC Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGB-E / SEROVAR 1/2A;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krett J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
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RA Remmel B., Rose M., Schluer T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591978; CAC99445.1; -.
DR ListLib; LMO01367; -.
DR InterPro; IPR001669; Arg_repress.
DR Pfam; PF01316; Arg_repressor; 1.
DR Pfam; PF02863; Arg_repressor_C; 1.
DR ProDom; PD007402; Arg_repress; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 149 AA; 16778 MW; 25622476E092E1A1 CRC64;

Query Match 91.2%; Score 31; DB 16; Length 149;
Best Local Similarity 85.7%; Pred.No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 137 NAKTLTD 143

RESULT 4
Q9NYW8 PRELIMINARY; PRT; 714 AA.
AC Q9NYW8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RB-associated KRAB repressor.
GN RBK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20167201; PubMed=10702291;
RA Skapek S.X., Jansen D.B., Wei T.-F., McDermott T., Huang W.,
RA Olson E.N., Lee E.Y.H.P.;
RT "Cloning and Characterization of a Novel Kruppel-associated Box Family
RT Transcriptional Repressor That Interacts with the Retinoblastoma Gene
RT Product, RB.";
RL J. Biol. Chem. 275:7212-7223(2000).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF226869; AAF43389.1; -.
DR HSP; P08045; IZNF.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf-C2H2; 15.
DR PRINTS; PR00048; ZINC_FINGER.
DR ProDom; PD000003; Znf_C2H2; 11.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 14.
DR PROSITE; PS50805; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
KW SEQUENCE 714 AA; 82994 MW; 36D90A6206118F8B CRC64;

Query Match 91.2%; Score 31; DB 4; Length 714;
Best Local Similarity 85.7%; Pred.No. 16e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 106 NAKTLTD 112

RESULT 5
Q8SWP7 PRELIMINARY; PRT; 1251 AA.
ID Q8SWP7
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AC O8SWP7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein ECU01_0350.
GN ECU01_0350.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Harbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; ALJ91737; CAD24904.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1251 AA; 144573 MW; 2302875B5350DA11 CRC64;

Query Match 88.2%; Score 30; DB 5; Length 1251;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NAKTLTE 7
|||||
DB 1205 NAKTLSE 1211

RESULT 6
O9L643 PRELIMINARY; PRT; 106 AA.
AC O9L643;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE UreB.
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN UREB.
OS Prochlorococcus sp. (strain PCC 9511).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OX NCBI_TaxID=100363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 9511;
RX MEDLINE=20553173; PubMed=11101668;
RA Palinska K.A., Jahns T., Rippka R., Tandeau De Marsac N.;
RT "Prochlorococcus marinus strain PCC 9511, a picoplanktonic
RT cyanobacterium, synthesizes the smallest urease.";
RL Microbiology 146:3099-3107(2000).
DR EMBL; AF242489; AAF70249.1; -.
DR HSSP; FI8315; 1FWB.
DR InterPro; IPR002019; Urease beta.
DR Pfam; PF00699; Urease beta; 1.
DR ProDom; PD002326; Urease beta; 1.
DR TIGRFAMs; TIGR00192; urease_beta; 1.
SQ SEQUENCE 106 AA; 11678 MW; 39783E13202349D3 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NAKTLT 6
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DB 23 NAKTLT 28

RESULT 7
O8X6K2 PRELIMINARY; PRT; 229 AA.
AC O8X6K2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Methyl-directed mismatch repair.
GN MUTH OR Z4149 OR ECS3688.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005512; AAG57943.1; -.
DR EMBL; AP002563; BAB37111.1; -.
DR InterPro; IPR004230; Muth.
DR Pfam; PF02976; Muth; 1.
KW Complete proteome.
SQ SEQUENCE 229 AA; 25499 MW; 20D2BD945E962CED CRC64;

Query Match 85.3%; Score 29; DB 16; Length 229;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NAKTLTE 7
|||||
DB 189 NAKALTE 195

RESULT 8
P77996 PRELIMINARY; PRT; 261 AA.
AC P77996;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RNA polymerase sigma factor.
GN SIGA.
OS Thermoanaerobacter thermosulfurogenes (Clostridium
OS Thermosulfurogenes).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacterales; Thermoanaerobacteriaceae;
OC Thermoanaerobacterium.
OX NCBI_TaxID=33950;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EM1;

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RA Matuschek M., Sahn K., Bahl H.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
DR EMBL; U50951; AAB08043.1; -.
DR HSSP; P00579; 1SIG.
DR InterPro; IPR000943; Sigma_70.
DR Pfam; PF00140; sigma70; 1.
DR PRINTS; PR00046; SIGMA70FECT.
DR PROSITE; PS00715; SIGMA70.1; 1.
DR PROSITE; PS00716; SIGMA70.2; 1.
KW DNA-binding; DNA-directed RNA polymerase; Sigma factor;
KW Transcription regulation.
SQ SEQUENCE 261 AA; 30627 MW; A99F6038F2842242 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 261;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 217 NLKTLTE 223

RESULT 9
Q9FH06 PRELIMINARY; PRT; 322 AA.
AC Q9FH06;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polyubiquitin.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=9397451; PubMed=10470850;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
RT Sequence features of the regions of 1,011,550 bp covered by seventeen
RT P1 and TAC clones.";
RL DNA Res. 6:183-195(1999).
DR EMBL; AB018107; BAB08310.1; -.
DR HSSP; P02248; 1UBI.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 4.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00213; UBQ; 4.
DR PROSITE; PS00299; UBIQUITIN 1; 2.
DR PROSITE; PS50053; UBIQUITIN 2; 4.
SQ SEQUENCE 322 AA; 36256 MW; 8E1D215E50085A99 CRC64;

Query Match 85.3%; Score 29; DB 10; Length 322;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 6 HAKTLTE 12

RESULT 10
Q9K701 PRELIMINARY; PRT; 351 AA.
AC Q9K701;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BH3573.
GN BH3573.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]_TaxID=86665;
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07292.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 351 AA; 40308 MW; 39688EA2CCD5A9A7 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 351;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 110 NASTLITE 116

RESULT 11
Q97VY2 PRELIMINARY; PRT; 416 AA.
AC Q97VY2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-isopropylmalate dehydratase, large subunit (isopropylmalate
DE isomerase) (alpha IPM isomerase) (IPMI) (leuc) (EC 4.2.1.33).
GN LEUC OR SSO2471.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]_TaxID=2287;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006845; AAK42608.1; -.
DR InterPro; IPR001030; Aconitase N.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 416 AA; 45253 MW; 5A342E12C6B88796 CRC64;

Query Match 85.3%; Score 29; DB 17; Length 416;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 3 SAKTLITE 9
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RESULT 12
Q8U5F8
ID Q8U5F8 PRELIMINARY; PRT; 468 AA.
AC Q8U5F8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE AGR_C 1849P.
GN AGR_C 1849.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorllo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AB008031; AAK86815.1; -.
SQ SEQUENCE 468 AA; 51681 MW; 5CD479AF05DFD15F CRC64;

Query Match 85.3%; Score 29; DB 16; Length 468;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 266 NAKTLTD 272

RESULT 13
Q8S9A4
ID Q8S9A4 PRELIMINARY; PRT; 470 AA.
AC Q8S9A4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Glucosyltransferase-5.
GN ADGT-5.
OS Phaseolus angularis (Adzuki bean) (Vigna angularis).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3914;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=HYPOCOTYL;
RA Xu Z.;
RT "Glucosyltransferase-like genes from adzuki bean hypocotyls.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB070748; BAB86923.1; -.
KW Transferase.
SQ SEQUENCE 470 AA; 51740 MW; F2EB79037605ABE1 CRC64;

Query Match 85.3%; Score 29; DB 10; Length 470;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 128 NPKTLTE 134

RESULT 14
Q985E4
ID Q985E4 PRELIMINARY; PRT; 487 AA.
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Q8XIQ4
ID Q8XIQ4 PRELIMINARY; PRT; 472 AA.
AC Q8XIQ4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Probable glutamate gamma-aminobutyrate antiporter.
GN CPE2060.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003192; BAB81766.1; -.
DR InterPro; IPR002293; AA/rel_protase1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51056 MW; CF8FB1C27533FE99 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 6
Db 8 NAKTLTD 13

RESULT 15
Q9CMS6
ID Q9CMS6 PRELIMINARY; PRT; 475 AA.
AC Q9CMS6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical protein PM0735.
GN PM0735.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006111; AAK02819.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 475 AA; 52905 MW; BB781D8A893B957E CRC64;

Query Match 85.3%; Score 29; DB 16; Length 475;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 202 NAKTLVE 208

RESULT 16
Q985E4
ID Q985E4 PRELIMINARY; PRT; 487 AA.
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AC Q98584;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE AMP nucleosidase.
GN MLL7714.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303059;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR ENBL; AF003012; BAB54118.1; -.
DR InterPro; IPR000845; PNP_UDP.
DR Pfam; PF01048; PNP_UDP_1; 1.
KW Complete proteome.
SQ SEQUENCE 487 AA; 54277 MW; A8928E4C2B1529A1 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 487;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 285 NAKTIID 291

RESULT 17
Q8YG44
ID Q8YG44 PRELIMINARY; PRT; 491 AA.
AC Q8YG44;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AMP nucleosidase (EC 3.2.2.4).
GN BME11318.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kaprat V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR ENBL; AE009569; AAL52499.1; -.
DR InterPro; IPR000845; PNP_UDP.
DR Pfam; PF01048; PNP_UDP_1; 1.
KW Hydrolase; Glycosidase; Complete proteome.
SQ SEQUENCE 491 AA; 54760 MW; 7AE3118EFCC17FB0 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 491;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

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Db 289 NAKTIID 295

RESULT 18
Q8U858
ID Q8U858 PRELIMINARY; PRT; 493 AA.
AC Q8U858;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Aldehyde dehydrogenase.
GN DHAS OR ATU4241 OR AGR_L 1241.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Doan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58 ";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Houello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Hummel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR ENBL; AE009353; AAL45035.1; -.
DR EMBL; AE008260; AAK89198.1; -.
KW Complete proteome.
SQ SEQUENCE 493 AA; 52866 MW; 3AD4B8D13BCC7467 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 493;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 85 NAKTLAE 91

RESULT 19
Q8XTAO
ID Q8XTAO PRELIMINARY; PRT; 493 AA.
AC Q8XTAO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable AMP nucleosidase protein (EC 3.2.2.4).
GN AMN OR RSP0214 OR RS05213
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cumnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646077; CAD17365.1; -;
DR InterPro; IPR002106; AAKNA_ligaseII.
DR InterPro; IPR000845; PNP_UDP.
DR Pfam; PF01048; PNP_UDP_1; 1.
DR PROSITE; PS00339; AA TRNA LIGASE II 2; UNKNOWN 1.
KW Hydrolase; Glycosidase; Plasmid; Complete proteome.
SQ SEQUENCE 493 AA; 55209 MW; 6E9C8134E889D4E4 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 493;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 292 NAKTITD 298

RESULT 20
QBUGNO PRELIMINARY; PRT; 494 AA.
AC Q8UGNO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AMP nucleosidase.
GN AMN OR ATU1006.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Okura V.K., Zhou Y., Chen L., Wood J.A., Karp P.D., Bovee D. Sr.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Kutayavin T., Levy R., Li M.-J., McLelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AF009065; AAL42020.1; -;
KW Complete proteome.
SQ SEQUENCE 494 AA; 54526 MW; 51B9B1AD99DE830B CRC64;

Query Match 85.3%; Score 29; DB 16; Length 494;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 292 NAKTITD 298

RESULT 21
Q92R69
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ID Q92R69 PRELIMINARY; PRT; 500 AA.
AC Q92R69;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable AMP nucleosidase protein (EC 3.2.2.4).
GN AMN OR R01042 OR SMC02386.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boislard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puhler A., Fournelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591785; CAC45614.1; -;
DR InterPro; IPR000845; PNP_UDP.
DR Pfam; PF01048; PNP_UDP_1; 1.
KW Hydrolase; Glycosidase; Complete proteome.
SQ SEQUENCE 500 AA; 55385 MW; 0B4C31860A6A4538 CRC64;

Query Match 85.3%; Score 29; DB 16; Length 500;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
DB 298 NAKTITD 304

RESULT 22
Q95QX8 PRELIMINARY; PRT; 507 AA.
AC Q95QX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 55.8 kDa protein.
GN C05D11.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Du Z.;
RT "The sequence of C. elegans cosmid C05D11.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00048; AAL27228.1; -;
DR InterPro; IPR001085; Gly_HyMetransf.
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DR Pfam; PF00464; SHMT; 1.
DR PROSITE; PS00096; SHMT; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 507 AA; 55764 MW; 693B380E77BB07D8 CRC64;

Query Match      85.3%; Score 29; DB 5; Length 507;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
   |||||
Db 359 NAKTLAE 365

RESULT 23
OS1542 PRELIMINARY; PRT; 715 AA.
ID OS1542;
AC OS1542;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Methyl-accepting chemotaxis protein (MCP-2).
GN BB0396.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Karlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Matthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
DR EMBL; AE001161; AAC66955.1; -.
DR TIGR; BB0596; -.
DR InterPro; IPR004089; Chmtaxis_transd.
DR InterPro; IPR003660; HAMP.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; NA; 1.
KW Complete proteome.
SQ SEQUENCE 715 AA; 80469 MW; 9A9E3157396F9BD1 CRC64;

Query Match      85.3%; Score 29; DB 16; Length 715;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
   |||||
Db 248 NPKTLTE 254

RESULT 24
OSV153 PRELIMINARY; PRT; 765 AA.
ID OSV153;
AC OSV153;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable bacteriophage-related protein.
GN RSC0839 OR RS04987.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.

OX NCBI_TaxID=305;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billaut A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguiet P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502(2002).
DR EMBL; AL646061; CAD14541.1; -.
KW Complete proteome.
SQ SEQUENCE 765 AA; 84779 MW; 0AB174490618272E CRC64;

Query Match      85.3%; Score 29; DB 16; Length 765;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKTLT 6
   |||||
Db 696 NAKTLT 701

RESULT 25
Q9USM9 PRELIMINARY; PRT; 841 AA.
ID Q9USM9;
AC Q9USM9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Vacuolar ATPase subunit a (EC 3.6.1.35).
GN MVA.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Spingioidea; Spingidae; Spinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=MIDGUT;
RX MEDLINE=20483512; PubMed=11030595;
RA Merzendorfer H., Reineke S., Zhao X.F., Jacobmeier B., Harvey W.R.,
RA Wiczorek H.;
RT "The multi-gene family of the tobacco hornworm V-ATPase: novel subunits
a, C, D, H and putative isoforms."
RL Biochim. Biophys. Acta 1467:369-379(2000).
DR EMBL; AJ249390; CAB55500.1; -.
DR InterPro; IPR002490; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_sub_a; 1.
KW Hydrolase.
SQ SEQUENCE 841 AA; 95873 MW; 5C914CB3A3A18A2E CRC64;

Query Match      85.3%; Score 29; DB 5; Length 841;
Best Local Similarity 85.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
   |||||
Db 486 NAKTLTE 492

RESULT 26
Q8R5Z3 PRELIMINARY; PRT; 942 AA.
ID Q8R5Z3;
AC Q8R5Z3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA/RNA helicase (DEAD/DEAH box family).
GN FN1974.
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OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Resnik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasteva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010499; AAL94064.1; -.
KW Helicase; Complete proteome.
SQ SEQUENCE 942 AA; 110580 MW; B3F40B0AAE05C0B2 CRC64;

Query Match      85.3%; Score 29; DB 16; Length 942;
Best Local Similarity 85.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKTLTE 7
DB      173 NUKTLTE 179
      | | | | |
RESULT 27
O54952 PRELIMINARY; PRT; 1817 AA.
AC O54952; P97951;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE Breast cancer type 1 susceptibility protein (Breast and ovarian cancer
DE susceptibility protein).
GN BRCA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=99111388; PubMed=9892727;
RA Bennett L.M., Brownlee H.A., Hagavik S., Wiseman R.W.;
RT "Sequence analysis of the rat brca1 homolog and its promoter region.";
RL Mamm. Genome 10:19-25(1999).
RN [2]
RP SEQUENCE OF 8-222 FROM N.A.
RC STRAIN=WISTAR-KYOTO; TISSUE=SPLEEN;
RX MEDLINE=96358532; PubMed=8761410;
RA Chen K.S., Shepel L.A., Haag J.D., Heil G.M., Gould M.N.;
RT "Cloning, genetic mapping and expression studies of the rat Brca1
RT gene.";
RL Carcinogenesis 17:1561-1566(1996).
CC -!- FUNCTION: NOT KNOWN, MAY REGULATE GENE EXPRESSION. MAY PLAY A ROLE
CC -!- IN CELL PROLIFERATION AND DIFFERENTIATION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; AF036760; AAC36493.1; -.
DR EMBL; S82504; -; NOT ANNOTATED CDS.
DR EMBL; S82502; -; NOT ANNOTATED_CDS.
DR EMBL; U60523; AAB40387.1; -.
DR EMBL; S82500; AAB37501.1; -.
DR InterPro; IPR001357; BRCT.
DR InterPro; IPR002378; Brst_cancer1.
DR Pfam; PF00533; BRCT; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PR00493; BRSTCANCER1.
DR SMART; SM00292; BRCT; 2.

DR SMART; SM00184; RING; 1.
DR PROSITE; PS50172; BRCT; 2.
DR PROSITE; PS00518; ZF_RING_1; 1.
KW Zinc-finger; DNA-binding; Nuclear protein; Anti-oncogene.
FT ZN_FING 24 64 C3HC4-TYPE.
FT DOMAIN 497 503 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT CONFLICT 38 38 Q -> K (IN REF. 2).
FT CONFLICT 192 192 A -> M (IN REF. 2).
SQ SEQUENCE 1817 AA; 199876 MW; C0B4760F0E349A01 CRC64;

Query Match      85.3%; Score 29; DB 11; Length 1817;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKTLTE 7
DB      981 NRKTLTE 987
      | | | | |
RESULT 28
Q92FX7 PRELIMINARY; PRT; 131 AA.
AC Q92FX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similarity to type I' restriction enzyme M subunit.
GN RC1350.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008681; AAL03888.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003356; N6_DNA_Mtase.
DR Pfam; PF02384; N6_Mtase; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 131 AA; 14721 MW; 0112B8788C13FEA3 CRC64;

Query Match      82.4%; Score 28; DB 16; Length 131;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NAKTLTE 7
DB      14 NGKTLTE 20
      | | | | |
RESULT 29
Q9A1C0 PRELIMINARY; PRT; 166 AA.
AC Q9A1C0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SPY0357.
GN SPY0357.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferreretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006499; AAK33403.1; -.
DR InterPro; IPR003607; ME_Plpase_HDC.
DR SMART; SM00471; HDC; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 166 AA; 20033 MW; 0A82100E7C8A3904 CRC64;

Query Match 82.4%; Score 28; DB 16; Length 166;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 95 NAKLUTE 101

RESULT 30
Q46622
ID Q46622 PRELIMINARY; PRT; 196 AA.
AC Q46622;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE hrpE.
DE HRP.
GN hrpE.
OS Erwinia amylovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=552;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EA321;
RA Kim J.-H.F., Wei Z.-M., Beer S.V.;
RT "Complementation groups II and III of the Erwinia amylovora hrp gene
RT cluster are required for secretion of harpin.";
RL Phytopathology 85:1163-1163(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EA321;
RX MEDLINE=97197534; PubMed=9045830;
RA Kim J.F., Wei Z.M., Beer S.V.;
RT "The hrpA and hrpC operons of Erwinia amylovora encode components of a
RT type III pathway that secretes harpin.";
RL J. Bacteriol. 179:1690-1697(1997).
DR EMBL; U56662; AAB49176.1; -.
SQ SEQUENCE 196 AA; 22351 MW; EA3B3BC587279A5 CRC64;

Query Match 82.4%; Score 28; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKTLTE 7
Db 125 AKTLTE 130

RESULT 31
Q9FKW3
ID Q9FKW3 PRELIMINARY; PRT; 223 AA.
AC Q9FKW3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chalcone isomerase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferreretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006499; AAK33403.1; -.
DR InterPro; IPR003607; ME_Plpase_HDC.
DR SMART; SM00471; HDC; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 166 AA; 20033 MW; 0A82100E7C8A3904 CRC64;

Query Match 82.4%; Score 28; DB 10; Length 223;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 63 NAKELTE 69

RESULT 32
Q8Y237
ID Q8Y237 PRELIMINARY; PRT; 227 AA.
AC Q8Y237;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative phosphoglycerate mutase 2 protein (EC 5.4.2.1).
GN GPMB OR RSC0499 OR RS05023.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646059; CAD14027.1; -.
DR InterPro; IPR001345; PG/BPGM_mutase.
DR Pfam; PF00300; PGAM; 1.
DR PROSITE; PS00175; PG_MUTASE; 1.
KW Isomerase; Complete Proteome.
SQ SEQUENCE 227 AA; 25127 MW; 3C2B273B4272D491 CRC64;

Query Match 82.4%; Score 28; DB 16; Length 227;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7
Db 176 NAKTLTE 182

RESULT 33
P71631
ID P71631 PRELIMINARY; PRT; 236 AA.
AC P71631;

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DT 01-FEB-1997 (TREMELrel. 02, Created)  
 DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE Hypothetical protein RV2821c.  
 GN RV2821C OR MTGV16B7.21 OR MT2888.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OSHKOSH;  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RL Science 294:2317-2323(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Guallo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,  
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328(2001).  
 DR EMBL; AE009166; AAL43151.1; -;  
 DR EMBL; AE008132; AAK87907.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 247 AA; 26115 MW; 48A246AA52426B15 CRC64;  
 Query Match 82.4%; Score 28; DB 16; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AKLTLE 7  
 DB 183 AKLTLE 188  
 RESULT 35  
 O06542 PRELIMINARY; PRT; 268 AA.  
 AC O06542;  
 DT 01-JUL-1997 (TREMELrel. 04, Created)  
 DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE Hypothetical 27.6 kDa protein (Enoyl-CoA hydratase/isomerase family  
 DE protein).  
 GN ECHA10 OR RV1142C OR MTCI65.09C OR MT1175.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OSHKOSH;  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

DR EMBL; Z95584; CAB09030.1; --  
 DR EMBL; AB006996; AAK45434.1; --  
 DR TIGR; MT1175; --  
 DR Tuberculist; Rv1142c; --  
 DR InterPro; IPR001753; EnCoA\_hydratase.  
 DR Pfam; PF00378; ECH; 1.  
 KW Hypothetical protein; Isomerase; Complete proteome.  
 SQ SEQUENCE 268 AA; 27649 MW; 8EFA8FF161FD8DC0 CRC64;

Query Match 82.4%; Score 28; DB 16; Length 268;  
 Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

Db 223 NAKTLTE 229

# RESULT 36

Q8YMR2 PRELIMINARY; PRT; 287 AA.  
 AC Q8YMR2;  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Hypothetical protein All4871.  
 GN All4871.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL; AF003597; BAB76570.1; --  
 DR InterPro; IPR002123; Acyltransferase.  
 DR Pfam; PF01553; Acyltransferase; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 287 AA; 31891 MW; 7625C0A12CC3B82A CRC64;

Query Match 82.4%; Score 28; DB 16; Length 287;  
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

Db 223 NAKTLTE 229

# RESULT 37

Q915C1 PRELIMINARY; PRT; 293 AA.  
 AC Q915C1;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE 5,10 methylene tetrahydrofolate reductase.  
 GN METF.  
 OS Leptospira interrogans.  
 OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.  
 OX NCBI\_TaxID=173;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VERDUN;  
 RA MEDLINE=20480680; PubMed=11024273;  
 RX Bourhy P., Saint Girons I.;

RT "Localization of the Leptospira interrogans metF gene on the CII  
 secondary chromosome.";  
 RL FEMS Microbiol. Lett. 191:259-263(2000).  
 DR EMBL; AF233051; AAF64321.1; --  
 DR HSSP; P00394; IBST.  
 DR InterPro; IPR003171; Mehdyrof\_redctse.  
 DR Pfam; PF02219; MTHFR; 1.  
 SQ SEQUENCE 293 AA; 32610 MW; B997A57B4DD3F4A2 CRC64;

Query Match 82.4%; Score 28; DB 2; Length 293;  
 Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7

Db 156 NAKTLTE 162

# RESULT 38

Q93Q10 PRELIMINARY; PRT; 294 AA.  
 AC Q93Q10;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Integral membrane protein.  
 GN OPIC.  
 OS Lactococcus lactis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OX NCBI\_TaxID=1358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MG1363;  
 RA Sanz Y., Lanfermeijer F.C., Hellendoorn M., Kok J., Konings W.N.,  
 RA Poolman B.;  
 RT "Two homologous oligopeptide binding protein genes (oppA) in  
 Lactococcus lactis MG1363.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF245305; AAK58894.1; --  
 DR InterPro; IPR000515; BPD\_transp.  
 DR Pfam; PF00528; BPD\_transp; 1.  
 SQ SEQUENCE 294 AA; 33003 MW; B3AB6171C614F4B2 CRC64;

Query Match 82.4%; Score 28; DB 2; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKTLTE 7

Db 173 AKTLTE 178

# RESULT 39

Q94382 PRELIMINARY; PRT; 304 AA.  
 AC Q94382;  
 DT 01-FEB-1997 (TRENBLrel. 02, Created)  
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE ZC47.3a protein.  
 GN ZC47.3a.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurray A.A.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;

RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z81141; CAB03491.1; -.  
DR InterPro; IPR002900; DUF38.  
DR InterPro; IPR001810; F-box.  
DR Pfam; PF01827; DUF38; 1.  
DR Pfam; PF00646; F-box; 1.  
DR SMART; SM00256; FBOX; 1.  
DR PROSITE; PS50181; FBOX; 1.  
SQ SEQUENCE 304 AA; 35542 MW; OBEC3888A963909B CRC64;

Query Match 82.4%; Score 28; DB 5; Length 304;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 162 NAKTLRE 168

## RESULT 40

Q94383  
ID Q94383 PRELIMINARY; PRT; 304 AA.  
AC Q94383;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ZC47.3b protein.  
GN ZC47.3B.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McMurray A.A.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z81141; CAB03492.1; -.  
DR InterPro; IPR002900; DUF38.  
DR InterPro; IPR001810; F-box.  
DR Pfam; PF01827; DUF38; 1.  
DR Pfam; PF00646; F-box; 1.  
DR SMART; SM00256; FBOX; 1.  
DR PROSITE; PS50181; FBOX; 1.  
SQ SEQUENCE 304 AA; 35621 MW; 98914D432857D778 CRC64;

Query Match 82.4%; Score 28; DB 5; Length 304;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAKTLTE 7  
Db 162 NAKTLRE 168

Search completed: July 18, 2003, 15:09:48  
Job time : 19.06 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:01:44 ; Search time 30.42 Seconds  
(without alignments)  
39.423 Million cell updates/sec

Title: US-10-007-790-10

Perfect score: 58

Sequence: 1 QHHYGFPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	9	21	AA1987662 Murine PIP3 recogn
2	58	100.0	107	16	AA1987971 Light chain variab
3	58	100.0	107	21	AA1987656 Murine PIP3 recogn
4	54	93.1	99	18	AA1987656 Anti-DNA antibody
5	54	93.1	99	18	AA1987656 Anti-DNA antibody
6	54	93.1	99	18	AA1987656 Anti-DNA antibody
7	54	93.1	99	18	AA1987656 Anti-DNA antibody
8	54	93.1	107	18	AA1987439 Anti-DNA antibody
9	54	93.1	243	15	AA1985348 VH and VL of Mab P
10	50	86.2	256	23	AA19872864 P4-15 single chain

11	50	86.2	503	23	AA19872873	3B10xP5-2 bispecif
12	49	84.5	109	19	AA19872873	8019 VK antibody.
13	46	79.3	9	21	AA19872873	Murine 15B8 light
14	46	79.3	107	21	AA19872873	Murine 15B8 light
15	44	75.9	113	21	AA19872873	Amino acid sequenc
16	44	75.9	128	17	AA19872873	Anti-human gp39 MA
17	44	75.9	135	10	AA19872873	Predicted sequence
18	44	75.9	171	17	AA19872873	Humanised MAB 39-1
19	44	75.9	271	13	AA19872873	Sequence of the sh
20	43	74.1	126	12	AA19872873	Mouse Mab 2G12 L c
21	43	74.1	127	12	AA19872873	Light (kappa) chai
22	43	74.1	268	21	AA19872873	Recombinant mouse
23	42	72.4	9	23	AA19872873	Murine MC-1 antibo
24	42	72.4	92	23	AA19872873	Murine MC-1 antibo
25	42	72.4	107	23	AA19872873	Murine MC-1 antibo
26	42	72.4	495	23	AA19872873	Murine CCR5xCD3 bi
27	40	69.0	9	19	AA19872873	Mouse anti-HM1.24
28	40	69.0	9	19	AA19872873	Chimeric L chain V
29	40	69.0	9	20	AA19872873	Artificial CDR (3)
30	40	69.0	9	20	AA19872873	Mouse humanised an
31	40	69.0	9	21	AA19872873	Antibody H chain V
32	40	69.0	9	22	AA19872873	Amino acid sequenc
33	40	69.0	9	22	AA19872873	Amino acid sequenc
34	40	69.0	9	22	AA19872873	Anti-PTHrP AB VL C
35	40	69.0	9	22	AA19872873	Human PTHrP mouse
36	40	69.0	9	22	AA19872873	Human PTHrP mouse
37	40	69.0	9	22	AA19872873	Human PTHrP mouse
38	40	69.0	9	23	AA19872873	Human joint diseas
39	40	69.0	105	17	AA19872873	Variable light cha
40	40	69.0	105	18	AA19872873	Anti-human FasL an
41	40	69.0	107	12	AA19872873	Anti-placental alk
42	40	69.0	107	12	AA19872873	Human anti-placent
43	40	69.0	107	17	AA19872873	Humanised 1D10 ant
44	40	69.0	119	15	AA19872873	Sequence of the co
45	40	69.0	126	19	AA19872873	HM1.24 antibody li

#### ALIGNMENTS

RESULT 1  
AA1987662  
ID AAY87662 standard; Protein; 9 AA.  
AC AAY87662;  
XX  
XX  
XX  
DT 11-AUG-2000 (first entry)  
XX  
DE Murine PIP3 recognizing Mab variable region light chain CDR3 region.  
XX  
KW PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR3;  
KW immunogen; antibody; light chain; complementarity determining region.  
XX  
OS Mus sp.  
XX  
PN JP2000083664-A.  
XX  
PD 28-MAR-2000.  
XX  
PF 07-SEP-1998; 98JP-0252921.  
XX  
PR 07-SEP-1998; 98JP-0252921.  
XX  
PA (FUKU/) FUKUI Y.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
XX  
DR WPI; 2000-353334/31.  
XX  
PT A monoclonal antibody recognizing  
PT phosphatidylinositol-3,4,5-triphosphate  
XX  
PS Claim 12; Page 13; 15pp; Japanese.  
XX

CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region light  
 CC chain complementarity determining region, CDR3 described in the method of  
 CC the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 |||||  
 Db 1 QHHYGTPT 9

RESULT 2  
 AAR78971  
 ID AAR78971 standard; Protein; 107 AA.

AC AAR78971;

XX 21-DEC-1995 (first entry)

XX Light chain variable region for monoclonal antibody 2D5.

XX Monoclonal antibody; heavy metal; mercury; variable region;  
 KW light chain.

XX Synthetic.

XX WO9520607-A.

XX 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.

XX 27-JAN-1994; 94US-0187407.

XX (BION-) BIONEERASKA INC.

XX Lopez O, Wagner FW, Wylie DE;

XX WPI; 1995-275415/36.

XX N-PSDB; AAQ97509.

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals

XX Claim 23; Page 69; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of  
 CC BALB/c mouse that had received multiple injections of mercuric ions  
 CC reacted with glutathione to produce a mercuric ion coordinate  
 CC covalent compound which was covalently bound to keyhole limpet  
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5C4, 23F8, 2D5,  
 CC 5B6 and 3E8) were producing MAb that were strongly positive  
 CC against glutathione-mercuric ions but negative against glutathione  
 CC without mercuric ions. RNA was isolated from hybridoma cells with  
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed  
 CC by MvL reverse transcriptase. The primers used for cDNA synthesis  
 CC were complementary to the 5' end of the CHI domain of the heavy  
 CC chain expressed by the hybridoma of interest, or to the 5' and of  
 CC the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the

CC variable region of a particular antibody polypeptide was also used  
 CC for PCR amplification of that variable region, in conjunction with  
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518  
 CC was used to amplify the MAb 2D5 and 5B6 heavy chains. The sequences  
 CC of the PCR amplified nucleotides were determined. These are given  
 CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &  
 CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45  
 CC and in the claims are different from the descriptions in the  
 CC sequence listings. The descriptions in the sequence listings are  
 CC used here.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 58; DB 16; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 |||||  
 Db 89 QHHYGTPT 97

RESULT 3  
 AAY87656  
 ID AAY87656 standard; Protein; 107 AA.

AC AAY87656;

XX 11-AUG-2000 (first entry)

XX Murine PIP3 recognizing Mab variable region light chain protein.  
 DE PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;  
 KW immunogen; antibody; light chain.

XX Mus sp.

XX JP2000083664-A.

XX 28-MAR-2000.

XX 07-SEP-1998; 98JP-0252921.

XX 07-SEP-1998; 98JP-0252921.

XX (FUKU/) FUKUI Y.  
 PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.

XX N-PSDB; AAY87656.

XX A monoclonal antibody recognizing  
 PT phosphatidylinositol-3,4,5-triphosphate -

XX Claim 6; Page 12; 15pp; Japanese.

XX This invention describes a novel antibody specifically recognizing.  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region light  
 CC chain described in the method of the invention.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 58; DB 21; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 QHHYGTPT 9
Db 89 QHHYGTPT 97

RESULT 4
AAW04587
ID AAW04587 standard; Protein; 99 AA.
XX AC AAW04587;
XX DT 12-AUG-1997 (first entry)
XX DE Anti-DNA antibody 15d8 light chain variable region.
XX KW Light chain; variable region; anti-DNA; monoclonal; antibody;
KW MAb 15d8; hairpin; diagnosis; inflammatory glomerulonephritis;
KW systemic lupus erythematosus; screening; treatment; prevention;
KW SLE; disease.
XX OS Mus spp.
XX FH Key Location/Qualifiers
FT Region 1..15 /label= framework_I
FT Region 16..26 /label= CDR_I
FT Region 27..41 /label= framework_II
FT Region 42..48 /label= CDR_II
FT Region 49..80 /label= framework_III
FT Region 81..89 /label= CDR_III
FT Region 90..99 /label= J_region
XX PN WO9636361-A1.
XX PD 21-NOV-1996.
XX PF 16-MAY-1996; 96WO-US07113.
XX PR 18-MAY-1995; 95US-0443540.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Glick GD, Swanson PC;
XX DR WPI; 1997-011854/01.
XX DR N-PSDB; AAT43739.
XX PT Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus
XX PS Example; Fig 8; 102pp; English.
XX CC The present sequence is the light chain variable region of the
CC anti-DNA monoclonal antibody (MAb) 15d8, which has a high affinity
CC for single stranded DNA, low or no affinity for double stranded DNA
CC and specifically binds a DNA hairpin. The MAb can be used to diagnose
CC disorders associated with the pathological complexation of DNA,
CC e.g. inflammatory glomerulonephritis and systemic lupus
CC erythematosus. It can also be used to generate reagents to screen
CC for pharmaceutical agents, and treat and/or prevent an above
CC disorder.
CC Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
CC from which were then fused with Sp2/0 myeloma cells to give
CC hybridomas producing the anti-DNA MAb. 15d8 was found to react
CC strongly with single stranded DNA and poly(dT), and weakly with
CC poly(dG).

XX SQ Sequence 99 AA;
Query Match 93.1%; Score 54; DB 18; Length 99;
Best Local Similarity 88.9%; Pred No. 0.074; 0; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

QY 1 QHHYGTPT 9
Db 81 QHHYGTPT 89

RESULT 5
AAW04596
ID AAW04596 standard; Protein; 99 AA.
XX AC AAW04596;
XX DT 12-AUG-1997 (first entry)
XX DE Anti-DNA antibody 9f11 light chain variable region.
XX KW Light chain; variable region; anti-DNA; monoclonal; antibody;
KW MAb 9f11; hairpin; diagnosis; inflammatory glomerulonephritis;
KW systemic lupus erythematosus; screening; treatment; prevention;
KW SLE; disease.
XX OS Mus spp.
XX FH Key Location/Qualifiers
FT Region 1..22 /label= framework_I
FT Region 23..27 /label= CDR_I
FT Region 28..41 /label= framework_II
FT Region 42..58 /label= CDR_II
FT Region 59..90 /label= framework_III
FT Region 91..102 /label= CDR_III
FT Region 103..115 /label= J_region
XX PN WO9636361-A1.
XX PD 21-NOV-1996.
XX PF 16-MAY-1996; 96WO-US07113.
XX PR 18-MAY-1995; 95US-0443540.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Glick GD, Swanson PC;
XX DR WPI; 1997-011854/01.
XX DR N-PSDB; AAT43741.
XX PT Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus
XX PS Example; Fig 8; 102pp; English.
XX CC The present sequence is the light chain variable region of the
CC anti-DNA monoclonal antibody (MAb) 9f11, which has a high affinity
CC for single stranded DNA, low or no affinity for double stranded DNA
CC and specifically binds a DNA hairpin. The MAb can be used to diagnose
CC disorders associated with the pathological complexation of DNA,
CC e.g. inflammatory glomerulonephritis and systemic lupus
CC erythematosus. It can also be used to generate reagents to screen

```

CC for pharmaceutical agents, and treat and/or prevent an above  
 CC disorder.  
 CC Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells  
 CC from which were then fused with Sp2/0 myeloma cells to give  
 CC hybridomas producing the anti-DNA MAb. 9f11 was found to react  
 CC strongly with single stranded DNA and poly(dT), and weakly with  
 CC poly(dG).  
 XX  
 SQ Sequence 99 AA;  
 Query Match 93.1%; Score 54; DB 18; Length 99;  
 Best Local Similarity 88.9%; Pred. No. 0.074;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QHHYGTPTT 9  
 Db 81 QHHYGTPTT 89  
 RESULT 6  
 AAW04597  
 ID AAW04597 standard; Protein; 99 AA.  
 XX AC  
 XX AAW04597;  
 XX  
 DT 12-AUG-1997 (first entry)  
 DE Anti-DNA antibody 15b10 light chain variable region.  
 XX  
 KW Light chain; variable region; anti-DNA; monoclonal; antibody;  
 KW MAb 15b10; hairpin; diagnosis; inflammatory glomerulonephritis;  
 KW systemic lupus erythematosus; screening; treatment; prevention;  
 KW SLE; disease.  
 XX  
 OS Mus spp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..22 /label= framework\_I  
 FT Region 23..27 /label= CDR\_I  
 FT Region 28..41 /label= framework\_II  
 FT Region 42..58 /label= CDR\_II  
 FT Region 59..90 /label= framework\_III  
 FT Region 91..102 /label= CDR\_III  
 FT Region 103..115 /label= J\_region  
 XX WO9636361-A1.  
 PN 21-NOV-1996.  
 XX 16-MAY-1996; 96WO-US07113.  
 XX 18-MAY-1995; 95US-0443540.  
 XX (UNMI ) UNIV MICHIGAN.  
 XX Glick GD, Swanson PC;  
 XX WPI; 1997-011854/01.  
 XX N-PSDB; AAT43742.  
 XX Anti-DNA antibody which specifically binds DNA hairpin - useful to  
 PT develop prods. for diagnosis and treatment of disorders, e.g.  
 PT glomerulonephritis or systemic lupus erythematosus  
 XX Example; Fig 8; 102pp; English.  
 PS

CC The present sequence is the light chain variable region of the  
 CC anti-DNA monoclonal antibody (MAb) 15b10, which has a high affinity  
 CC for single stranded DNA, low or no affinity for double stranded DNA  
 CC and specifically binds a DNA hairpin. The MAb can be used to diagnose  
 CC disorders associated with the pathological complexation of DNA,  
 CC e.g. inflammatory glomerulonephritis and systemic lupus  
 CC erythematosus. It can also be used to generate reagents to screen  
 CC for pharmaceutical agents, and treat and/or prevent an above  
 CC disorder.  
 CC Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells  
 CC from which were then fused with Sp2/0 myeloma cells to give  
 CC hybridomas producing the anti-DNA MAb. 15b10 was found to react  
 CC strongly with single stranded DNA and poly(dT), and weakly with  
 CC poly(dG).  
 XX  
 SQ Sequence 99 AA;  
 Query Match 93.1%; Score 54; DB 18; Length 99;  
 Best Local Similarity 88.9%; Pred. No. 0.074;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QHHYGTPTT 9  
 Db 81 QHHYGTPTT 89  
 RESULT 7  
 AAW04598  
 ID AAW04598 standard; Protein; 99 AA.  
 XX AC  
 XX AAW04598;  
 XX  
 DT 12-AUG-1997 (first entry)  
 DE Anti-DNA antibody 5f3 light chain variable region.  
 XX  
 KW Light chain; variable region; anti-DNA; monoclonal; antibody;  
 KW MAb 5f3; hairpin; diagnosis; inflammatory glomerulonephritis;  
 KW systemic lupus erythematosus; screening; treatment; prevention;  
 KW SLE; disease.  
 XX  
 OS Mus spp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..22 /label= framework\_I  
 FT Region 23..27 /label= CDR\_I  
 FT Region 28..41 /label= framework\_II  
 FT Region 42..58 /label= CDR\_II  
 FT Region 59..90 /label= framework\_III  
 FT Region 91..102 /label= CDR\_III  
 FT Region 103..115 /label= J\_region  
 XX WO9636361-A1.  
 PN 21-NOV-1996.  
 XX 16-MAY-1996; 96WO-US07113.  
 XX 18-MAY-1995; 95US-0443540.  
 XX (UNMI ) UNIV MICHIGAN.  
 XX Glick GD, Swanson PC;  
 XX WPI; 1997-011854/01.  
 XX N-PSDB; AAT43743.  
 XX

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XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 8; 102pp; English.
XX
CC The present sequence is the light chain variable region of the
CC anti-DNA monoclonal antibody (MAB) 5f3, which has a high affinity
CC for single stranded DNA, low or no affinity for double stranded DNA
CC and specifically binds a DNA hairpin. The MAB can be used to diagnose
CC disorders associated with the pathological complexation of DNA,
CC e.g. inflammatory glomerulonephritis and systemic lupus
CC erythematosus. It can also be used to generate reagents to screen
CC for pharmaceutical agents, and treat and/or prevent an above
CC disorder.
CC
CC Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
CC from which were then fused with Sp2/0 myeloma cells to give
CC hybridomas producing the anti-DNA MAB.
XX
XX SQ Sequence 99 AA;
XX
XX Query Match 93.1%; Score 54; DB 18; Length 99;
XX Best Local Similarity 88.9%; Pred.No. 0.074;
XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QHHYGTPT 9
XX | | | | | | |
XX 81 QHHYGTPT 89
XX
XX RESULT 8
XX AA07439
XX ID ID AA07439 standard; Protein; 107 AA.
XX AC AA07439;
XX
XX 12-AUG-1997 (first entry)
XX
XX Anti-DNA antibody 9f11 group light chain variable region.
XX
XX Light chain; variable region; anti-DNA; monoclonal; antibody;
XX 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis;
XX systemic lupus erythematosus; screening; treatment; prevention;
XX SLE; disease; consensus; putative.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..23
XX FT /label= framework_I
XX Region 24..34
XX FT /label= CDR_I
XX Region 35..49
XX FT /label= framework_II
XX Region 50..56
XX FT /label= CDR_II
XX Region 57..88
XX FT /label= framework_III
XX Region 89..97
XX FT /label= CDR_III
XX Region 98..107
XX FT /label= J_region
XX
XX WO9636361-A1.
XX
XX 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
XX 18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.

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XX WPI; 1994-151334/18.
DR N-PSDB; AAQ64476.
XX
PT Monoclonal antibody specific for prostate cells - used in the
PT diagnosis and treatment of conditions involving abnormal growth
PT of prostate cells, esp prostate cancer.
XX
PS Example 3; Fig 1; 64pp; English.
XX
CC This sequence is encoded by the PE38KDEL fragment of the plasmid
CC pULI40 and represents the heavy chain and light chain variable regions
CC (VH and VL) of the monoclonal antibody (Mab) PR1. The cDNA encoding
CC this sequence was derived by PCR amplification of reverse transcribed
CC PR1-hybridoma RNA using the primer sequences given in AAQ64477-81. The
CC VH and VL complementarity determining regions (CDRs) are used in the
CC construction of the Mab of the invention which competes with PR1
CC for binding to a prostate cell associated antigen. The Mab of the
CC invention can be used for targeting a drug, cytotoxin or radioisotope
CC to prostate cells of a patient suffering from prostate cancer. It can
CC also be used for diagnosing the presence of prostate cancer in an
CC individual and for the diagnosis and treatment of other conditions
CC involving abnormal growth of prostate cells, eg. benign prostate
CC hyperplasia. The Mab reacts strongly with prostate cancer cells but
CC only weakly with a few other normal human tissues. The effect of
CC therapy on normal prostate cells does not threaten the overall health
CC of the patient.
XX
SQ Sequence 243 AA;
Query Match 93.1%; Score 54; DB 15; Length 243;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 222 QHHYGTPT 230

RESULT 10
AAU72864
ID AAU72864 standard; Protein; 256 AA.
XX
AC AAU72864;
XX
DT 26-FEB-2002 (first entry)
XX
DE P4-15 single chain Fv.
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14;
KW P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23.
XX
OS Homo sapiens.
XX
PN WO200171005-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-EP03414.
XX
PR 24-MAR-2000; 2000EP-0106467.
XX
PA (KUFE/) KUFE P.
XX
PI Kufer P, Riethmüller G, Lutterbues R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;

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XX WPI; 2002-055119/07.
DR N-PSDB; AAS97138.
XX
PT Multifunctional polypeptides comprising binding sites that specifically
PT recognise extracellular groups of the NKG2D receptor complex and
PT domains which function as receptors or ligands, useful for treating
PT cancers and infectious diseases -
XX
PS Example 7; Fig 16; 114pp; English.
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
CC receptor and the polypeptides of the invention.
XX
SQ Sequence 256 AA;
Query Match 86.2%; Score 50; DB 23; Length 256;
Best Local Similarity 88.9%; Pred. No. 0.96;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 226 QHHYGTPT 234

RESULT 11
AAU72873
ID AAU72873 standard; Protein; 503 AA.
XX
AC AAU72873;
XX
DT 26-FEB-2002 (first entry)
XX
DE 3B10XP5-2 bispecific single chain Fv.
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10XP4-3; 3B10XP4-14;
KW P53 tetramerisation domain; 3B10XP5-2; 3B10XP5-23.
XX
OS Homo sapiens.
XX
PN WO200171005-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-EP03414.
XX
PR 24-MAR-2000; 2000EP-0106467.
XX
PA (KUFE/) KUFE P.
XX
PI Kufer P, Riethmüller G, Lutterbues R, Borschert K, Kischel R;

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PI Mayer M, Hofmeister R;  
 XX WPI; 2002-055119/07.  
 DR N-PSDB; AAS97147.  
 XX  
 PT Multifunctional polypeptides comprising binding sites that specifically  
 PT recognise extracellular groups of the NKG2D receptor complex and  
 PT domains which function as receptors or ligands, useful for treating  
 PT cancers and infectious diseases -  
 XX  
 XX Example 5; Fig 16; 114pp; English.  
 PS  
 CC The invention relates to a multifunctional polypeptide comprising a  
 CC domain with a binding site that specifically recognises an extracellular  
 CC group of the NKG2D receptor complex and a second domain which functions  
 CC as a receptor or ligand. The polypeptide and its associated  
 CC polynucleotide are used for the preparation of a pharmaceutical  
 CC composition for the treatment of cancer, infections and/or autoimmune  
 CC conditions. The cancer may be a tumour of the head and neck, stomach,  
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,  
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,  
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.  
 CC The infectious diseases can be caused by viruses, bacteria, fungi,  
 CC protozoa or helminths. The autoimmune diseases include multiple  
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior  
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent  
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and  
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D  
 CC receptor and the polypeptides of the invention.  
 XX  
 XX Sequence 503 AA;  
 SQ

Query Match 86.2%; Score 50; DB 23; Length 503;  
 Best Local Similarity 88.9%; Pred. No. 2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OHHYGTPYT 9  
 DB 473 OHHYGTPLT 481  
 |||||  
 |||||

RESULT 12  
 AAW46483  
 ID AAW46483 standard; protein; 109 AA.  
 AC  
 AC AAW46483;  
 XX  
 XX 24-JUN-1998 (first entry)  
 DT  
 XX  
 DE 8019 VK antibody.  
 XX  
 XX Diagnosis; photoaffinity compound; therapeutic; antibody; SIC5; 8019;  
 KW antigen; immuno-conjugate.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO9803870-A1.  
 PN  
 XX 29-JAN-1998.  
 PD  
 XX 22-JUL-1997; 97WO-US12223.  
 PF  
 XX 23-JUL-1996; 96US-0681432.  
 PR  
 XX (KENT ) UNIV KENTUCKY RES FOUND.  
 PA  
 XX Haley BE, Kohler H, Pavlinkova G, Rajogopalan K;  
 PI WPI; 1998-120935/11.  
 XX  
 XX Conjugates formed by site-specific attachment of nucleic  
 PT photo-affinity agents to antibodies - useful as immunoassay reagents  
 PT for detecting antigen, also immuno-therapeutic complex also

PT containing cytotoxin for treating cancer, infection or genetic  
 PT disease  
 XX  
 PS Disclosure; Figure 12c; 75pp; English.  
 XX  
 CC This is the amino acid sequence of 8019 VK antibody. The invention  
 CC relates to the site-specific photo-attachment of a nucleic  
 CC photoaffinity compound to an antibody which comprises reacting them  
 CC under conditions that promote attachment of the photoaffinity  
 CC compound to at least 1 nucleotide binding site in the antibody. Also  
 CC claimed are: photoaffinity compound-antibody conjugates produced this  
 CC way, and immuno-conjugates comprising cytotoxic or therapeutic agent  
 CC site-specifically attached to the photoaffinity compound in the  
 CC conjugate. When the conjugate is labelled it is used for detection or  
 CC quantitation of an antigen (Ag) by any standard immunoassay format,  
 CC while immuno-conjugates are used therapeutically, e.g. in cases of  
 CC tumours, infections or genetic diseases, or as imaging agents. The  
 CC photoaffinity compounds are attached under mild, physiological  
 CC conditions, particularly a single 2-5 minute photoactivation results in  
 CC almost 100% attachment (contrast conditions usually required to attach  
 CC molecules to antibodies.  
 XX  
 XX Sequence 109 AA;  
 SQ

Query Match 84.5%; Score 49; DB 19; Length 109;  
 Best Local Similarity 77.8%; Pred. No. 0.58;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OHHYGTPYT 9  
 DB 89 OHHFGTPWT 97  
 |||||  
 |||||

RESULT 13  
 AAY92163  
 ID AAY92163 standard; Peptide; 9 AA.  
 XX  
 AC AAY92163;  
 XX  
 DT 01-AUG-2000 (first entry)  
 DE  
 DE Murine 15B8 light chain variable region CDR 3.  
 XX  
 KW Light chain; variable region; complementarity determining region; CDR 3;  
 KW anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic;  
 KW vascular-general; proliferative; antiischemic; cerebroprotective;  
 KW cardiant; agonist; antibody inhibition.  
 XX  
 OS Mus musculus.  
 XX  
 XX WO200018804-A1.  
 PN  
 XX 06-APR-2000.  
 PD  
 XX 28-SEP-1999; 99WO-US22428.  
 PF  
 XX 28-SEP-1998; 98US-0102098.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Holmes SD, Erickson-miller CL, Winkler JD;  
 DR WPI; 2000-293114/25.  
 XX  
 XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in  
 PT patients suffering from strokes and myocardial infarctions  
 PT  
 PS Claim 14; Page 41; 50pp; English.  
 XX  
 CC AAY92161-63 are light chain CDR (complementarity determining regions)  
 CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal  
 CC antibody 15B8. Tie2 is a single-transmembrane, tyrosine kinase receptor

CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and  
CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2  
CC antibodies may be administered to enhance angiogenesis in mammals  
CC suffering from ischemic disease, myocardial infarction or cerebral stroke  
CC or other vascular diseases such as diabetes. It may also be used to  
CC enhance endothelial cell survival and to promote haematopoietic or  
CC megakaryocyte cell proliferation (claimed).

XX  
SQ Sequence 9 AA;

Query Match 79.3%; Score 46; DB 21; Length 9;  
Best Local Similarity 77.8%; Pred. No. 7.8e+05;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
DB 1 QHHYSIPT 9

RESULT 14  
AAAY92157  
ID AAAY92157 standard; Protein; 107 AA.  
XX AC  
XX AC AAAY92157;  
XX DT 01-AUG-2000 (first entry)  
XX DE Murine 1598 light chain variable region.  
XX light chain; variable region; anti-Tie2 kinase receptor; agonist;  
XX monoclonal antibody; 15B8; Angiogenic; vascular-general; proliferative;  
XX antiischemic; cardiac; cerebroprotective; antibody inhibition.  
XX  
XX Mus musculus.  
XX WO200018804-A1.  
XX 06-APR-2000.  
XX 28-SEP-1999; 99WO-US22428.  
XX 28-SEP-1998; 98US-0102098.  
XX (SMIK) SMITHKLINE BEECHAM CORP.  
XX (SMIK) SMITHKLINE BEECHAM PLC.  
XX Holmes SD, Erickson-miller CL, Winkler JD;  
XX WPI: 2000-293114/25.  
XX N-PSDB; AAA09016.  
XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in  
XX patients suffering from strokes and myocardial infarctions  
XX Claim 10; Page 38; 50pp; English.  
XX This is a murine anti-Tie2 kinase receptor agonist monoclonal antibody  
XX 1598 light chain variable region. Tie2 is a single-transmembrane,  
XX tyrosine kinase receptor ('Tie' stands for tyrosine kinase receptor with  
XX immunoglobulin and endothelial growth factor (EGF) homology domain(s)).  
XX Anti-Tie2 antibodies may be administered to enhance angiogenesis in  
XX mammals suffering from ischemic disease, myocardial infarction or  
XX cerebral stroke or other vascular diseases such as diabetes. It may also  
XX be used to enhance endothelial cell survival and to promote  
XX haematopoietic or megakaryocyte cell proliferation (claimed).

XX  
SQ Sequence 107 AA;

Query Match 79.3%; Score 46; DB 21; Length 107;  
Best Local Similarity 77.8%; Pred. No. 1.8;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9

CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and  
CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2  
CC antibodies may be administered to enhance angiogenesis in mammals  
CC suffering from ischemic disease, myocardial infarction or cerebral stroke  
CC or other vascular diseases such as diabetes. It may also be used to  
CC enhance endothelial cell survival and to promote haematopoietic or  
CC megakaryocyte cell proliferation (claimed).

XX  
SQ Sequence 9 AA;

Query Match 75.9%; Score 44; DB 21; Length 113;  
Best Local Similarity 77.8%; Pred. No. 4.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
DB 95 QQYGTPT 103

RESULT 16  
AAAW03721  
ID AAW03721 standard; Protein; 128 AA.  
XX

DB 89 QHHYSIPT 97

RESULT 15  
AAB18865  
ID AAB18865 standard; Protein; 113 AA.  
XX AC AAB18865;  
XX 08-FEB-2001 (first entry)  
XX DE Amino acid sequence of anti-p53 antibody light chain clone 163.9.  
XX p53; antibody; immune response; vaccine; gene therapy; cancer;  
XX rheumatoid arthritis; coronary heart disease.  
XX Homo sapiens.  
XX WO2000056770-A1.  
XX 28-SEP-2000.  
XX 15-MAR-2000; 2000WO-AU00189.  
XX 19-MAR-1999; 99AU-0009321.  
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.  
XX Ward RL, Coomber DWJ;  
XX WPI: 2000-638249/61.  
XX N-PSDB; AAA96142.  
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide  
XX fragments, useful in treatment and diagnosis of cancer, rheumatoid  
XX arthritis and coronary heart disease  
XX Claim 30; Page 140; 163pp; English.  
XX The present sequence represents the light chain of an antibody reactive  
XX against p53. The antibody is obtained from a vertebrate host expressing  
XX an immune response against a naturally occurring disease. The antibodies  
XX are useful in pharmaceutical compositions, which additionally contain  
XX chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes  
XX or gadolinium. The polypeptide components of the antibodies are useful in  
XX vaccines, for inducing an immune response against a disease in a  
XX vertebrate, for treatment and/or prophylaxis of disease and for detection  
XX purposes. The nucleic acid sequences can be used to detect a disease as  
XX well as for gene therapy and recombinant production of the polypeptides.  
XX In particular, the following can be treated cancer, rheumatoid arthritis  
XX and coronary heart disease. Cancers include carcinogenic tumours, tumours  
XX of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,  
XX head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,  
XX gastric cancer, brain cancer, bladder cancer, prostate cancer and  
XX urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,  
XX e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX  
SQ Sequence 113 AA;

Query Match 75.9%; Score 44; DB 21; Length 113;  
Best Local Similarity 77.8%; Pred. No. 4.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
DB 95 QQYGTPT 103

RESULT 16  
AAAW03721  
ID AAW03721 standard; Protein; 128 AA.  
XX

AAW03721;  
 02-APR-1997 (first entry)  
 Anti-human gp39 MAB 39-1.106 light chain variable region.  
 Light chain; variable region; murine; mouse; anti-human; disease;  
 glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
 diagnosis; inhibition; B-cell; activation; treatment; disorder;  
 immune; autoimmune; allergic reaction; organ rejection; drug;  
 graft versus host; cell imaging; tumour; targeted; delivery;  
 targeted.  
 OS Mouse musculus.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= sig\_peptide  
 FT Peptide 21..128  
 FT /label= mat\_peptide  
 FT Region 44..54  
 FT /note= "complementarity determining region 1"  
 FT Region 70..76  
 FT /note= "complementarity determining region 2"  
 FT Region 109..117  
 FT /note= "complementarity determining region 3"  
 XX WO9623071-A2.  
 XX  
 XX  
 XX 01-AUG-1996. 96WO-US01119.  
 XX  
 XX 26-JAN-1996; 96WO-US01119.  
 XX  
 XX 26-JAN-1995; 95US-0379057.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;  
 PI Harris LJ, Hollenbaugh D, Siadak AW;  
 XX WPI; 1996-362694/36.  
 XX N-PSDB; AAT35973.  
 XX  
 XX Monoclonal antibodies specific for different epitope(s) on human  
 FT gp39 - used for inhibiting B cell activation and for the diagnosis  
 FT of various disorders, e.g. cancer, psoriasis etc..  
 XX  
 XX Claim 89; Fig 6A; 167pp; English.  
 XX  
 XX The present sequence is the light chain variable region of the  
 CC murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAB)  
 CC 39-1.106 (a member of the murine kappa V subfamily). The MAB was  
 CC prep'd. by immunising a 6-8 week old BALB/c mouse with a gp39-CD8  
 CC fusion protein, and 3 days later harvesting and fusing spleen and  
 CC lymph cells to mouse melanoma cells, to produce an anti-human gp39  
 CC MAB producing hybridoma. The MAB may be useful for diagnosing  
 CC disease states, inhibiting B-cell activation and for treating  
 CC immunological disorders, e.g. autoimmune disorders, allergic  
 CC responses, organ rejection and graft versus host disease. It may  
 CC also be used for imaging cells which express gp39 on their surface,  
 CC e.g. tumour cells, and to target therapeutic agents to such cells.  
 CC The MAB inhibits the CD40/gp39 interaction, therefore limiting both  
 CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.  
 CC specific to these antigens. A typical compsn. for intramuscular  
 CC injection pref. contains 50 mg of MAB in 1 ml of sterile buffered  
 CC water.  
 XX  
 XX Sequence 128 AA;

Query Match 75.9%; Score 44; DB 17; Length 128;  
 Best Local Similarity 77.8%; Pred. No. 4.9;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 DB 109 QHHYNTPLT 117  
 RESULT 17  
 AAP90835  
 ID AAP90835 standard; protein; 135 AA.  
 XX  
 XX AAP90835;  
 XX  
 XX 28-JUN-1990 (first entry)  
 XX  
 XX Predicted sequence of variable light (VL) region of B72.3  
 DE monoclonal antibody (MAB) from CDNA clones PBH41 & PBH52.  
 DE  
 XX Mouse monoclonal antibody B72.3; humanised antibody molecule;  
 KW TAG-72 antigen; antigen binding site; complementarity determining region;  
 KW VL domain; light chain CDNA.  
 XX  
 XX Mouse.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /note= "signal peptide"  
 FT Protein 21..134  
 FT Protein 135  
 FT /note= "human C region"  
 XX  
 XX WO901783-A.  
 XX  
 XX 09-MAR-1989.  
 XX  
 XX 05-SEP-1988; 88WO-GB00731.  
 XX  
 XX 05-SEP-1988; 88WO-GB00731, GB-020833.  
 XX  
 XX (CLLT ) CELLTech LTD.  
 XX  
 XX Bodmer MW, Adair JR, Whittle NR;  
 PI  
 XX WPI; 1989-085403/11.  
 XX N-PSDB; AAN90672.  
 XX  
 XX Recombinant humanised antibody specific for TAG-72 -  
 PT having complementary determining regions of variable domains  
 PT from mouse antibody and the remainder from human immunoglobulin  
 XX  
 XX Fig 1B; page 1/13; 49pp; English.  
 XX  
 XX A chimeric mouse-human light chain gene was constructed from  
 CC B72.3 light chain clone (see AAN90672) and an M13-derived vector contg.  
 CC the human C-kappa gene. Heavy and light chimeric genes as well as  
 CC mouse heavy and light chain CDNA clones were  
 CC inserted separately into plasmid pEE6. The 4 expression constructs  
 CC were used singly or in heavy/light chain gene pairs to transfect  
 CC COS-1 cells. Transfection of COS cells with both the chimeric  
 CC heavy and light chain genes generated a complete  
 CC chimeric Ab molecule with TAG-72 antigen binding specificity. Humanising  
 CC the B72.3 does not adversely affect its binding activity and this  
 CC produces a humanised antibody molecule (HAM) which is useful in both  
 CC therapy and diagnosis of certain carcinomas, eg solid tumours  
 CC expressing TAG-72.  
 XX  
 XX Sequence 135 AA;  
 XX  
 XX Query Match 75.9%; Score 44; DB 10; Length 135;  
 Best Local Similarity 77.8%; Pred. No. 5.1;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 DB 109 QHFWGTPT 117

## RESULT 18

AAW03725 ID AAW03725 standard; Protein; 171 AA.

XX AC AAW03725;

XX DT 02-APR-1997 (first entry)

XX DE Humanised MAb 39-1.106 light chain variable region.

XX KW Light chain; variable region; murine; mouse; anti-human; disease;  
KW Glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
KW diagnosis; inhibition; B-cell; activation; treatment; disorder;  
KW immune; autoimmunity; allergic response; organ rejection; drug;  
KW graft versus host; cell imaging; tumour; targeted; delivery;  
KW targeted; humanised.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Misc-difference 2 /note= "corresponding codon TAG"

FT Misc-difference 11

FT Misc-difference 157 /note= "corresponding codon TAA"

FT Misc-difference 165 /note= "corresponding codon TAA"

FT Misc-difference 165 /note= "corresponding codon TAA"

XX PN WO9623071-A2.

XX PD 01-AUG-1996.

XX PF 26-JAN-1996; 96WO-US011119.

XX PR 26-JAN-1995; 95US-0379057.

XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PI Aruffo AA, Bajorath J, Gilliland LK, Gordon MB;  
PI Harris LJ, Hollenbaugh D, Siadak AW;

XX DR WPI; 1996-362694/36.

XX DR N-PSDB; AAT36018.

XX Monoclonal antibodies specific for different epitope(s) on human  
PT gp39 - used for inhibiting B cell activation and for the diagnosis  
PT of various disorders, e.g. cancer, psoriasis etc..

XX Example 13; Fig 16; 167pp; English.

XX The present sequence is the light chain variable region of the  
CC humanised murine anti-human glycoprotein (gp) 39 monoclonal  
CC antibody (Mab) 39-1.106. The Mab may be useful for diagnosing  
CC disease states, inhibiting B-cell activation and for treating  
CC immunological disorders, e.g. autoimmune disorders, allergic  
CC responses, organ rejection and graft versus host disease. It may  
CC also be used for imaging cells which express gp39 on their surface,  
CC e.g. tumour cells, and to target therapeutic agents to such cells.  
CC The Mab inhibits the CD40/gp39 interaction, therefore limiting both  
CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.  
CC specific to these antigens. A typical compen. for intramuscular  
CC injection pref. contains 50 mg of Mab in 1 ml of sterile buffered  
CC water.

XX SQ Sequence 171 AA;

Query Match 75.9%; Score 44; DB 17; Length 171;

Best Local Similarity 77.8%; Pred. No. 6.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 OHHYGTPYT 9  
Db 131 OHYNTPLT 139

## RESULT 19

AAR20185 ID AAR20185 standard; peptide; 271 AA.

XX AC AAR20185;

XX DT 15-APR-1992 (first entry)

XX DE Sequence of the shortened hinge version of the B72.3 single  
DE chain Fv hinge.

XX KW Fv fragment; in vivo diagnosis; therapy; antibody.

XX OS Homo sapiens.

XX PN WO9119739-A.

XX PD 26-DEC-1991.

XX PF 11-JUN-1991; 91WO-GB00935.

XX PR 11-JUN-1990; 90GB-0012995.

XX PA (CELL-) CELLTECH LTD.

XX PI King DJ, Mountain A, Owens RJ, Yarranton GT;

XX DR WPI; 1992-024365/03.

XX DR N-PSDB; AAQ20381.

XX New multivalent antigen-binding proteins - comprise Fv fragment  
PT linked to at least 1 other Fv fragment spacer and useful for  
PT in-vivo diagnosis or therapy

XX Example; Fig 5; 54pp; English.

XX The bivalent antigen-binding protein B72.3 Fv (AAR20184) is an example  
CC of the antigen-binding proteins of the invention. They comprise a  
CC first Fv fragment bound to at least one other Fv fragment by a  
CC linker which keeps the Fv fragment apart. The connecting structure  
CC of AAR20184 comprises a joining sequence derived from a human IgG1  
CC domain linked to a complete human IgG4 hinge region. AAR20185 is the  
CC sequence of the shortened hinge version of the B72.3 single chain Fv  
CC hinge.

XX SQ Sequence 271 AA;

Query Match 75.9%; Score 44; DB 13; Length 271;

Best Local Similarity 77.8%; Pred. No. 11;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 OHHYGTPYT 9  
Db 111 OHFWGTPYT 119

## RESULT 20

AAR12235 ID AAR12235 standard; Protein; 126 AA.

XX AC AAR12235;

XX DT 19-AUG-1991 (first entry)

XX DE Mouse MAb 2G12 L chain V region.

XX KW HIV-1; chimera.

```

OS Mus sp.
XX WO9107494-A.
XX 30-MAY-1991.
XX 13-NOV-1990; 90WO-US06627.
XX 13-NOV-1989; 89US-0433703.
XX (XOMA-) XOMA CORP.
XX
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX WPI; 1991-178106/24.
XX N-PSDB; AAQ12015.
XX New chimeric mouse human antibodies - used in treatment, diagnosis
XX and prophylaxis of HIV infections.
XX
XX Disclosure; Fig 8; 108pp; English.
XX
XX The mouse VL gene product may be used to produce chimeric mouse-
XX human Abs against HIV-1 comprising human Ig constant regions and
XX murine variable regions. These novel sequence are useful in
XX treatment, diagnosis and prophylaxis of HIV infections, and may be
XX produced by a bacterial, yeast or mammalian expression system.
XX
XX Sequence 126 AA;

Query Match 74.1%; Score 43; DB 12; Length 126;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9
DB 109 QHHYGAPPT 117

RESULT 21
AAR12357
ID AAR12357 standard; Protein; 127 AA.
XX
XX AAR12357;
XX
XX 15-AUG-1991 (first entry)
XX Light (kappa) chain variable region of murine 2G12 immuno-
XX globulin.
XX
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
XX Mus musculus.
XX
XX WO9107493-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1990; 90WO-US06615.
XX
XX 13-NOV-1989; 89US-0433730.
XX
XX (XOMA-) XOMA CORP.
XX (GREC ) GREEN CROSS CORP.
XX
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX WPI; 1991-178044/24.
XX N-PSDB; AAQ12059.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and
XX remove HIV-1 antigen from sample

```

```

PS Disclosure; fig 8; 107pp; English.
XX
XX This is the light(kappa)-chain variable (V) region of a mouse
XX monoclonal antibody (MAB), 2G12, and is specific for an HIV-1
XX viral antigen. It is used in the construction of a chimeric
XX MAB comprising heavy and light chains having murine V regions
XX and human C regions. The chimeric MABs are more effective than
XX murine MAB 2G12 since they have an increased compatibility in
XX humans. The heavy and light chain V-regions are joined by
XX manipulating their respective joining (J) regions, to generate
XX restriction enzyme recognition sites. The chimeric MABs can be
XX used as immunoconjugates, in association with e.g. toxins for HIV
XX treatment. They can also be used in diagnosis of HIV.
XX See also AAQ12056-58 and AAQ12060-63.
XX
XX Sequence 127 AA;

Query Match 74.1%; Score 43; DB 12; Length 127;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9
DB 109 QHHYGAPPT 117

RESULT 22
AAY44972
ID AAY44972 standard; Protein; 268 AA.
XX
XX AAY44972;
XX
XX 23-MAY-2000 (first entry)
XX Recombinant mouse anti-rotavirus antibody (Clone 11).
XX
XX Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;
XX VH; light chain variable region; VL; pCANTAB SE vector; treatment;
XX probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;
XX immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.
XX
XX Synthetic.
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Region 6..116
XX /label= Mouse_Heavy_chain_variable_region
XX Region 117..151
XX /label= Linker_region
XX Region 152..250
XX /label= Mouse_light_chain_variable_region
XX Domain 254..266
XX /label= E tag domain
XX /note= Enables immunodetection and immunoaffinity
XX purification of the recombinant antibody"
XX
XX WO200006764-A1.
XX
XX 10-FEB-2000.
XX
XX 29-JUL-1999; 99WO-US17296.
XX
XX 30-JUL-1998; 98US-0094697.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Fahl WE, Letchworth GJ, Mueller GC, Savage AK, Loo D;
XX WPI; 2000-195315/17.
XX N-PSDB; AA250508.
XX
XX Composition for supplementing or replacing an immune response against
XX gastrointestinal pathogens in e.g. newborn infants, comprises probiotic
XX microorganisms expressing antibodies specific for the gastrointestinal

```



CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
CC renal diseases and inflammatory bowel diseases and graft versus host  
CC and transplant rejections. The present sequence is murine MC-1 antibody  
CC light chain variable domain (VL) (1). This antibody is specific for  
CC human chemokine receptor 5 (CCR5).

XX  
SQ Sequence 92 AA;

Query Match 72.4%; Score 42; DB 23; Length 92;  
Best Local Similarity 77.8%; Pred. No. 7.5;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 81 QHHYDTPRT 89

RESULT 25  
AAE22189  
ID AAE22189 standard; Protein; 107 AA.  
XX  
AC AAE22189;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Murine MC-1 antibody light chain variable domain (VL) (1) #1.  
XX  
KW Chemokine construct; human immunodeficiency virus 1; allergic disease;  
KW skin disease; immunological disorder; autoimmune disease; psoriasis;  
KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
KW inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;  
KW MC-1 antibody; VL; light chain variable domain; chemokine receptor 5.  
XX  
OS Mus sp.  
XX  
PN WO200220615-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-EPI0433.  
XX  
PR 08-SEP-2000; 2000EP-0119694.  
PR 05-SEP-2001; 2001US-0948004.  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Mack M, Schloendorff D, Spring M;  
XX  
DR WPI; 2002-362240/39.  
DR N-PSDB; AAD35248.  
XX  
PT Use of an antibody and/or chemokine construct that binds to a chemokine  
PT receptor, for eliminating cells latently infected with primate  
PT immunodeficiency virus, or treating, preventing and alleviating immune  
PT disorders -  
XX  
PS Example 2; Page 49; 117pp; English.  
XX  
CC The invention relates to the use of an antibody and/or chemokine  
CC construct that binds a chemokine receptor for preparing a pharmaceutical  
CC composition for eliminating cells latently infected with a primate  
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They  
CC are used in gene therapy and as vaccines. The antibody and/or chemokine  
CC construct is also used for preparing a pharmaceutical composition for  
CC treating, preventing and/or alleviating immunological disorders  
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes  
CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin  
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
CC renal diseases and inflammatory bowel diseases and graft versus host  
CC and transplant rejections. The present sequence is murine MC-1 antibody

CC light chain variable domain (VL) (1). This antibody is specific for  
CC human chemokine receptor 5 (CCR5).

XX  
SQ Sequence 107 AA;

Query Match 72.4%; Score 42; DB 23; Length 107;  
Best Local Similarity 77.8%; Pred. No. 8.8;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 89 QHHYDTPRT 97

RESULT 26  
AAE22193  
ID AAE22193 standard; Protein; 495 AA.  
XX  
AC AAE22193;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Murine CCR5xCD3 bispecific single chain antibody construct.  
XX  
KW Chemokine construct; human immunodeficiency virus 1; allergic disease;  
KW skin disease; immunological disorder; autoimmune disease; psoriasis;  
KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;  
KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;  
KW inflammatory renal disease; HIV-1; transplant rejection; CCR5xCD3;  
KW antibody; chemokine receptor 5; CD3 antigen; chimeric; murine.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Unidentified.  
XX  
PN WO200220615-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-EPI0433.  
XX  
PR 08-SEP-2000; 2000EP-0119694.  
PR 05-SEP-2001; 2001US-0948004.  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Mack M, Schloendorff D, Spring M;  
XX  
DR WPI; 2002-362240/39.  
DR N-PSDB; AAD35252.  
XX  
PT Use of an antibody and/or chemokine construct that binds to a chemokine  
PT receptor, for eliminating cells latently infected with primate  
PT immunodeficiency virus, or treating, preventing and alleviating immune  
PT disorders -  
XX  
PS Claim 29; Page 52; 117pp; English.  
XX  
CC The invention relates to the use of an antibody and/or chemokine  
CC construct that binds a chemokine receptor for preparing a pharmaceutical  
CC composition for eliminating cells latently infected with a primate  
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They  
CC are used in gene therapy and as vaccines. The antibody and/or chemokine  
CC construct is also used for preparing a pharmaceutical composition for  
CC treating, preventing and/or alleviating immunological disorders  
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes  
CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin  
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases  
CC such as inflammatory joint diseases (chronic arthritis), inflammatory  
CC renal diseases and inflammatory bowel diseases and graft versus host  
CC and transplant rejections. The present sequence is CCR5xCD3 bispecific  
CC single chain antibody construct. This antibody construct comprises  
CC light chain variable domain (VL) and heavy chain variable (VH) domains  
CC of murine MC-1 antibody specific for human chemokine receptor 5 (CCR5)

CC and VH and VL domains of an antibody specific for a CD3 antigen joined  
 CC by a peptide linker.

SQ Sequence 495 AA;  
 Query Match 72.4%; Score 42; DB 23; Length 495;  
 Best Local Similarity 77.8%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QHHYGTPT 9  
 |||||  
 Db 89 QHHYGTPT 97

RESULT 27  
 AAW62191  
 ID AAW62191 standard; peptide; 9 AA.  
 XX AAW62191;  
 AC AAW62191;  
 XX 21-SEP-1998 (first entry)  
 DT Mouse anti-HM1.24 antibody L chain V region CDR 3.  
 XX  
 DE Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR; CDR;  
 KW framework region; complementarity determining region; antigenicity.  
 KW  
 XX Mus sp.  
 OS  
 XX WO9814580-A1.  
 PN  
 XX 09-APR-1998.  
 PD  
 XX 03-OCT-1997; 97WO-JP03553.  
 PF  
 XX 04-OCT-1996; 96JP-0264756.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Koishihara Y, Kosaka M, Ohtomo T, Ono K, Tsuchiya M;  
 PI Yoshimura Y;  
 XX WPI; 1998-286421/25.

DR Humanised anti-HM1.24 antibody - for treatment of myeloma  
 XX  
 XX Claim 10; Page 103; 210pp; Japanese.  
 PS  
 XX A humanised anti-HM1.24 antibody has been developed which comprises  
 CC human L and H chain C regions, and L and/or H chain V regions  
 CC containing material originating in mouse anti-HM1.24 antibody. The V  
 CC regions contain framework (FR) regions of human origin and  
 CC complementarity determining regions (CDR) of mouse origin, leading to  
 CC a reshaped humanised antibody. The C regions are human Ck (L-chain) and  
 CC human C gamma (especially C gamma 1) (H-chain). The FR regions of the  
 CC L chain V region are derived from human subtype HSG1 (e.g. from human  
 CC antibody RE1) and the FR regions of the H chain V region are derived  
 CC from human subtype HSG1 (e.g. FR1-3 from human antibody HG3 and FR4  
 CC from human antibody JH6). The present sequence represents mouse L chain  
 CC V region CDR 3 from the present invention. The antibodies are used for  
 CC the treatment of myeloma, especially by injection, intravenously,  
 CC intramuscularly or subcutaneously. The antibodies are used at 0.01-1000  
 CC (especially 5-100) mg/kg body weight. The humanised antibody has low  
 CC antigenicity and is therefore effective therapeutically in humans.  
 XX  
 SQ Sequence 9 AA;

Query Match 69.0%; Score 40; DB 19; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QHHYGTPT 9  
 |||||  
 Db 1 QHHYGTPT 97

Db 1 QHHYSTPFT 9  
 RESULT 28  
 AAW57579  
 ID AAW57579 standard; peptide; 9 AA.  
 XX AAW57579;  
 AC AAW57579;  
 XX 03-SEP-1998 (first entry)  
 DT Chimeric L chain V region CDR-3 for an antibody against hTPRP.  
 DE  
 XX Chimeric; antibody; human parathormone related peptide; hTPRP; mouse;  
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;  
 KW hypophosphemia; pathogen; vitamin D resistance; V region; C region;  
 KW humanised.  
 XX  
 XX Synthetic.  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 OS  
 XX WO9813388-A1.  
 PN  
 XX 02-APR-1998.  
 PD  
 XX 24-SEP-1997; 97WO-JP03382.  
 PF  
 XX 24-JUL-1997; 97JP-0214168.  
 PR  
 XX 26-SEP-1996; 96JP-0255196.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Sato K, Wakahara Y, Yabuta N;  
 PI WPI; 1998-230640/20.

DR New chimeric antibodies against human parathormone related  
 XX peptide(s) - useful for, e.g. treatment of hypercalcaemia and other  
 PT disorders caused by malignant neoplasm(s)  
 PT  
 XX Claim 9; Page 124; 182pp; Japanese.  
 PS  
 XX New antibodies have been developed which are specific for human  
 CC parathormone related peptides (hTPRP). The antibodies comprise chimeric  
 CC L and/or H chains, where the C region is of human and L region of mouse,  
 CC an antibody of the invention. Host cells, transformed with vectors  
 CC containing DNA encoding antibodies of the invention, can be used to  
 CC produce the antibodies. The antibodies may be used to treat  
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of  
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,  
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They  
 CC may also be used for treatment of hypophosphemia such as that due to  
 CC pathogens or to vitamin D resistance.  
 XX  
 SQ Sequence 9 AA;

Query Match 69.0%; Score 40; DB 19; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QHHYGTPT 9  
 |||||  
 Db 1 QHHYSTPFT 9

RESULT 29  
 AAY02549  
 ID AAY02549 standard; Peptide; 9 AA.  
 XX AAY02549;  
 AC AAY02549;  
 XX

DT 16-JUL-1999 (first entry)  
XX Artificial CDR(3) of L chain V region of antiHm1.24 antibody.  
DE  
XX  
KW Reconstituted human antibody; peptide antigen Hm1.24; framework region;  
KW complementary determining region; CDR; anti-Hm1.24 antibody; myeloma.  
XX  
OS Synthetic.  
XX  
XX WO9918212-A1.  
XX  
XX 15-APR-1999.  
XX  
XX 02-OCT-1998; 98WO-JP04469.  
XX  
XX 03-OCT-1997; 97JP-0271726.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Tsuchiya M;  
XX  
XX WPI; 1999-277273/23.  
XX  
XX Reconstituted human antibody useful in the treatment of myeloma  
XX  
XX Disclosure; Page 83; 256pp; Japanese.  
XX  
XX The specification describes a reconstituted human antibody recognizing  
CC the peptide antigen Hm1.24. This human antibody contains natural human  
CC framework regions modified by amino acid substitutions to provide  
CC homogeneity with a previously designed framework region (which may  
CC arise from a human or non-human source); and complementary determining  
CC regions (CDR) derived from a non-human anti-Hm1.24 antibody. The  
CC reconstituted antibody is useful in the treatment of diseases in which  
CC the surface antigen Hm1.24 is implicated such as myeloma. The present  
CC sequence is used in the creation of the antibodies of the invention.  
XX  
XX  
SQ Sequence 9 AA;  
Query Match 69.0%; Score 40; DB 20; Length 9;  
Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 9  
Db |||||  
1 QQHYSTPFT 9  
RESULT 30  
AAW89631  
ID AAW89631 standard; peptide; 9 AA.  
XX  
XX AAW89631;  
AC  
XX  
XX 14-APR-1999 (first entry)  
DT  
XX Mouse humanised antibody #23-57-137-1 light chain CDS3 peptide.  
DE  
XX Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;  
KW inhibitor; humanised.  
KW  
XX Mus sp.  
OS  
XX Synthetic.  
XX  
XX WO9851329-A1.  
PN  
XX 19-NOV-1998.  
XX  
XX 13-MAY-1998; 98WO-JP02116.  
XX  
XX PF  
XX 18-JUL-1997; 97JP-0194445.  
PR  
XX 15-MAY-1997; 97JP-0125505.  
PR  
XX

PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Ishii K, Sato K, Tunesari T;  
XX  
XX WPI; 1999-070101/06.  
XX  
XX Inhibitors of binding of parathyroid hormone related peptide to its  
PT receptor - useful for, e.g. treatment of cachexia arising from  
PT cancer or other diseases  
XX  
XX Example 2; Page 85; 125pp; Japanese.  
XX  
XX The present invention describes compositions for the treatment of  
CC cachexia containing a substance which inhibits the binding of a  
CC parathyroid hormone related peptide (PTHrP) to its receptor, as an  
CC active component. This substance may be an antagonist to the receptor,  
CC or an antibody (preferably monoclonal) or antibody fragment, or  
CC recognising PTHrP. The antibody is preferably humanised or chimeric.  
CC The present invention also describes a humanised antibody prepared  
CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for  
CC the treatment of cachexia arising in connection with diseases such as  
CC cancer, thereby improving the quality of life of the patient. The  
CC present sequence represents mouse humanised antibody light chain CDS3  
XX from #23-57-137-1 from the present invention.  
XX  
XX Sequence 9 AA;  
Query Match 69.0%; Score 40; DB 20; Length 9;  
Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 9  
Db |||||  
1 QQHYSTPFT 9  
RESULT 31  
AAW77517  
ID AAW77517 standard; peptide; 9 AA.  
XX  
XX AAW77517;  
AC  
XX  
XX 26-APR-2000 (first entry)  
DT  
XX  
XX Antibody H chain V region CDR3 peptide seq ID No: 61.  
DE  
XX Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.  
KW  
XX Homo sapiens.  
OS  
XX WO200000219-A1.  
PN  
XX 06-JAN-2000.  
PD  
XX  
XX 25-JUN-1999; 99WO-JP03433.  
PF  
XX  
XX 26-JUN-1998; 98JP-0180143.  
PR  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
PA  
XX  
XX Sato K, Tunesari T;  
PI  
XX  
XX WPI; 2000-117115/10.  
DR  
XX  
XX Treatment of hypercalcemic crisis with a substance inhibiting binding  
PT of parathyroid hormone related peptide to its receptor  
PT  
XX  
XX Example 2; Page 100; 120pp; Japanese.  
PS  
XX  
XX The invention relates to a method of treatment of hypercalcemic crisis.  
CC A composition for the treatment of hypercalcemic crisis contains as  
CC active component a substance which inhibits the binding of parathyroid  
CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used

CC for the treatment of hypercalcemic crisis, such as that associated with  
 CC a malignant tumour.

XX Sequence 9 AA;

Query Match 69.0%; Score 40; DB 21; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
 Db 1 QHHYSTPFT 9

# RESULT 32

AAG67115  
 ID AAG67115 standard; peptide; 9 AA.

XX AC AAG67115;

DT 13-NOV-2001 (first entry)

DE Amino acid sequence of a human peptide.

XX Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;  
 KW septicemia; injury; muscular dystrophy; cytokine; interleukin-6;  
 KW granulocyte colony stimulating factor; interleukin-11;  
 KW leukemia inhibitory factor; weight loss.

XX OS Homo sapiens.

XX PN WO200164249-A1.

XX PD 07-SEP-2001.

XX PF 30-AUG-2000; 2000WO-JP05886.

XX PR 28-FEB-2000; 2000JP-0052414.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Saito H, Tsunenari T, Onuma E, Sato K;

XX DR WPI; 2001-550131/61.

XX Tissue decomposition inhibitor that prevents parathyroid hormone  
 PT associated proteins from binding to its receptor

XX PS Disclosure; Page 109; 132pp; Japanese.

XX The specification describes a tissue decomposition inhibitor, which  
 CC comprises a substance that inhibits peptides associated with  
 CC parathyroid hormone (PTH) from binding with their receptor. The method  
 CC is used to inhibit tissue decomposition caused by cancer cachexia,  
 CC septicemia, heavy external injury or muscular dystrophy, and for  
 CC treating patients with elevated cytokine (interleukin-6, granulocyte  
 CC colony stimulating factor, interleukin-11 and leukemia inhibitory  
 CC factor) levels. It may also be used for preventing weight loss caused  
 CC by cancer cachexia. The present sequence represents a peptide, which is  
 CC used in the course of the invention.

XX Sequence 9 AA;

Query Match 69.0%; Score 40; DB 22; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
 Db 1 QHHYSTPFT 9

# RESULT 33

## AAG63397

ID AAG63397 standard; peptide; 9 AA.

XX AC AAG63397;

DT 15-OCT-2001 (first entry)

DE Amino acid sequence of a human peptide.

XX Parathyroid hormone-associated peptide; PTHrP; dental disease.

XX OS Homo sapiens.

XX PN WO200154725-A1.

XX PD 02-AUG-2001.

XX PF 14-DEC-2000; 2000WO-JP08875.

XX PR 25-JAN-2000; 2000JP-0083034.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Kato A, Suzuki M, Sugimoto T;

XX DR WPI; 2001-465459/50.

XX Parathyroid hormone-associated peptide binding inhibitors useful for  
 PT treating dental disease

XX PS Disclosure; Page 116; 140pp; Japanese.

XX The specification describes a treatment for dental diseases. The  
 CC treatment comprises a substance that inhibits binding between  
 CC parathyroid hormone-associated peptide and its receptor. The  
 CC present sequence represents a human peptide, which is used in the  
 CC course of the invention.

XX Sequence 9 AA;

Query Match 69.0%; Score 40; DB 22; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
 Db 1 QHHYSTPFT 9

## RESULT 34

AAG64779  
 ID AAG64779 standard; peptide; 9 AA.

XX AC AAG64779;

DT 08-OCT-2001 (first entry)

DE Anti-PTHrP Ab VL CDR3, SEQ ID NO:61.

XX Parathyroid hormone-related peptide; PTHrP; antagonist; antibody;  
 KW calcium regulation disorder; serum calcium concentration; light chain;  
 KW humoral hypercalcaemia of malignancy; cytostatic; analgesic; CDR;  
 KW complementarity determining region.

XX OS Homo sapiens.

XX PN WO200147554-A1.

XX PD 05-JUL-2001.

XX PF 27-DEC-2000; 2000WO-JP09339.

XX PR 28-DEC-1999; 99JP-0375203.



CC cytostatic, antithyroid, eating-disorders and cardiovascular activities.  
 CC (1) is used for treatment and prevention of disorders associated with PTH  
 CC or PTHrP, including: pain; immune suppression; disturbances of the  
 CC digestive system, protein metabolism, sugar metabolism, lipid metabolism,  
 CC appetite, blood chemistry, thyroid function, and electrolyte balance;  
 CC central nervous system disorders such as sleep disturbance, neurological  
 CC disturbances, brain function disturbance, brain circulation disturbance  
 CC and autonomic nervous system disturbance; and disorders caused by PTH or  
 CC PTHrP associated cytokine cascade including blood poisoning, dropsy,  
 CC inflammation, blood disease, calcium disturbance and autoimmune disease.  
 CC Treatment and prevention of disorders other than hypercalcaemia which  
 CC are associated with PTH or PTHrP, especially those associated with  
 CC malignant tumours, and thereby ameliorating the quality of life of these  
 CC patients. AAF69141 to AAF69196 and AAB76988 to AAB76916 represent  
 CC sequences used in the exemplification of the present invention.

XX  
 SQ Sequence 9 AA;  
 Query Match 69.0%; Score 40; DB 22; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 | ||| :|  
 Db 1 QOHYSTPFT 9

RESULT 37  
 AAB76931  
 ID AAB76931 standard; Peptide; 9 AA.

XX  
 AC AAB76931;

DT 17-APR-2001 (first entry)

DE Human PTHrP mouse Mab L chain V region CDR3 SEQ ID NO:61.

XX Human; mouse; drug-resistant hyperglycaemia; PTHrP; cardiovascular;  
 KW parathyroid hormone related peptide; gastrointestinal; cancer;  
 KW central nervous system; calcium-antagonist; bone resorption inhibitor;  
 KW bisphosphonate; calcitonin; calcium elimination promoter;  
 KW intestinal calcium absorption inhibitor.

XX Homo sapiens.

XX WO200102012-A1.

PD 11-JAN-2001.

XX 06-JUL-2000; 2000WO-JP04523.

PR 06-JUL-1999; 99JP-0192270.

XX (CHUS ) CHUGAI SEIVAKU KK.

PI Saito H, Tsunenari T, Onuma E;

DR WPI; 2001-123066/13.

PT Agents inhibiting binding of parathyroid hormone related peptide to its  
 receptor for treatment of drug-resistant hyperglycemia

PS Example; Page 97; 118pp; Japanese.

XX The present invention describes an agent (I) for the treatment of  
 CC drug-resistant hyperglycaemia. (I) contains as an active component a  
 CC substance which inhibits the binding of parathyroid hormone related  
 CC peptide (PTHrP) to its receptor. (I) is a calcium-antagonist. (I) can  
 CC be used for treatment of drug-resistant hyperglycaemia e.g. associated  
 CC with cancer. The hyperglycaemia is resistant to treatment with other  
 CC drugs including bone resorption inhibitors (such as bisphosphonate or  
 CC calcitonin), calcium elimination promoters and intestinal calcium  
 CC absorption inhibitors. AAF69197 to AAF69252 and AAB76917 to AAB76935

CC represent sequences used in the exemplification of the present  
 CC invention.

SQ Sequence 9 AA;

Query Match 69.0%; Score 40; DB 22; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 | ||| :|  
 Db 1 QOHYSTPFT 9

RESULT 38

ABB95191  
 ID ABB95191 standard; Peptide; 9 AA.

XX  
 AC ABB95191;

DT 17-JUN-2002 (first entry)

DE Human joint disease related peptide SEQ ID NO 61.

XX Joint disease; PTH; PTHrP; parathyroid hormone-related peptide;  
 KW parathyroid hormone; osteopathic; rheumatoid arthritis; arthritis.

XX Homo sapiens.

XX WO200213865-A1.

PD 21-FEB-2002.

PF 15-AUG-2001; 2001WO-JP07044.

XX 16-AUG-2000; 2000JP-0247013.

XX (CHUS ) CHUGAI SEIVAKU KK.

XX Yoshikawa H;

XX WPI; 2002-257551/30.

XX Agents for ameliorating symptoms caused by joint diseases relating to  
 PT PTH or PTHrP e.g. chronic rheumatoid arthritis, containing inhibitors  
 PT on receptor binding of parathyroid hormone-related peptide

PS Disclosure; Page 92; 112pp; Japanese.

XX The invention relates to agents for ameliorating symptoms causing joint  
 CC diseases, containing a substance inhibiting the binding of a parathyroid  
 CC hormone-related peptide to its receptor as active ingredient. The agents  
 CC have osteopathic activity are useful for ameliorating symptoms caused by  
 CC joint diseases relating to PTH or PTHrP e.g. chronic rheumatoid arthritis  
 CC and arthritis deformans. The agents particularly improve the lowering of  
 CC bone amount or suppression of bone reduction. The present sequence is  
 CC that of a joint disease related protein peptide; useful to the invention.

SQ Sequence 9 AA;

Query Match 69.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 | ||| :|  
 Db 1 QOHYSTPFT 9

RESULT 39

AAW00832  
 ID AAW00832 standard; Protein; 105 AA.

XX

```

AAW00832;
29-MAY-1997 (first entry)
Variable light chain of anti-human Fas ligand antibody NOK-5.
Variable region; light chain; human; Fas ligand; monoclonal;
antibody; NOK-5; hybridoma; inhibition; apoptosis; assay;
diagnosis; disease; hepatitis; infectious mononucleosis;
systemic lupus erythematosus.
Mus musculus.
WO9629350-Al.
26-SEP-1996.
21-MAR-1996; 96WO-JP00734.
27-OCT-1995; 95JP-0303492.
20-MAR-1995; 95JP-0087420.
(SUME ) SUMITOMO ELECTRIC IND CO.
Kayagaki N, Nakata M, Okumura K, Yagita H;
WPI; 1996-443140/44.
N-PSDB; AAT39558.
Monoclonal antibody specifically recognising the Fas ligand - useful
for the detection of Fas ligands either on cell surface or in
solution
Claim 28; Page 91; 133pp; Japanese.
The present sequence is the light chain variable region of the
anti-human Fas ligand monoclonal antibody (MAB) NOK-5 is
produced by the hybridoma NOK-5 (FERM BP-5048), which was prepared
by immunising mice with transformed human Fas ligand expressing COS
cells, and fusing spleen cells isolated from the mice with myeloma
P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human
Fas ligand on the cell surface or in solution, and can be used to
inhibit the apoptosis inducing cell surface Fas ligand/Fas
reaction. The MAB can also be used for a Fas ligand assay in
biological samples (e.g. human blood), especially for disease
diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
lupus erythematosus.
SQ Sequence 105 AA;
Query Match 69.0%; Score 40; DB 17; Length 105;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
DB 89 QQHYSSPT 97
RESULT 40
AAW19018
ID AAW19018 standard; Protein; 105 AA.
XX
AC AAW19018;
XX
DT 14-JAN-1998 (first entry)
XX
DE Anti-human FasL antibody (NOK5) light chain variable region.
XX
KW Light chain; variable region; mouse; murine; human; Fas ligand;
KW FasL; monoclonal antibody; MAB; hybridoma; treatment; hepatitis;
KW hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis;
KW liver cell; glutamate oxaloacetate; pyruvate transaminase.

```

```

XX Mus sp.
OS WO9715326-Al.
XX
PN 01-MAY-1997.
XX
PD 24-OCT-1996; 96WO-JP03089.
XX
PF 27-OCT-1995; 95JP-0303491.
XX
PA (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI Kayagaki N, Nakata M, Okumura K, Seino K, Yagita H;
XX
DR WPI; 1997-258767/23.
XX
DR N-PSDB; AAT69542.
XX
PT Anti-human Fas Ligand antibody to treat hepatitis - controls
PT apoptosis in liver cells and improves liver function
XX
PS Claim 6; Page 41; 51pp; Japanese.
XX
CC The present sequence is the light chain variable region of the
CC murine anti-human Fas ligand (FasL) monoclonal antibody (MAB) NOK5,
CC which is expressed by the hybridoma NOK5 (FERM BP-5044). The MAB
CC can be used in the preparation of a composition for the effective
CC oral or parenteral treatment of hepatitis, including hepatitis
CC caused by hepatitis B or C virus. The composition controls apoptosis
CC in liver cells caused by the binding of FasL to Fas expressing liver
CC cells, and improves liver function by improving blood glutamate
CC oxaloacetate and pyruvate transaminase levels. The composition is
CC given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day.
CC Spleen cells from mice immunised with FasL expressing COS cells
CC were fused with mouse myeloma cells to produce hybridomas. The
CC hybridomas were screened for anti-FasL activity, and the active
CC clones NOK1-5 isolated.
XX
SQ Sequence 105 AA;
Query Match 69.0%; Score 40; DB 18; Length 105;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
DB 89 QQHYSSPT 97

```

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Job time : 31.42 secs



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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:46 ; Search time 10.44 Seconds  
(without alignments)  
25.365 Million cell updates/sec

Title: US-10-007-790-10  
Perfect score: 58  
Sequence: 1 QHHYGTPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	9	4	US-09-357-069-10
2	58	100.0	107	2	US-08-888-366-24
3	58	100.0	107	4	US-09-257-069-4
4	54	93.1	99	3	US-08-881-037-32
5	54	93.1	99	3	US-08-881-037-33
6	54	93.1	99	3	US-08-881-037-34
7	54	93.1	99	3	US-08-881-037-35
8	54	93.1	107	3	US-08-881-037-69
9	54	93.1	107	3	US-08-881-037-70
10	54	93.1	107	3	US-08-881-037-71
11	54	93.1	107	3	US-08-881-037-72
12	54	93.1	243	1	US-07-958-140-2
13	54	93.1	243	5	PCT-US93-09166-2
14	49	84.5	227	1	US-08-681-432-2
15	46	79.3	9	4	US-09-406-532-10
16	46	79.3	107	4	US-09-406-532-4
17	44	75.9	108	2	US-08-379-057-27
18	44	75.9	108	2	US-08-379-057-28
19	44	75.9	128	2	US-08-379-057-12
20	44	75.9	135	6	5219996-19
21	44	75.9	271	2	US-08-400-115-4
22	43	74.1	108	2	US-08-378-939-20
23	40	69.0	105	3	US-09-065-059-17
24	40	69.0	107	3	US-08-397-411-1
25	40	69.0	107	3	US-08-397-411-2
26	40	69.0	119	4	US-08-477-347-11
27	40	69.0	214	3	US-08-397-411-5

28	39	67.2	94	3	US-08-881-037-68	Sequence 68, Appl
29	39	67.2	264	4	US-08-564-164A-4	Sequence 4, Appl
30	38	65.5	9	2	US-08-765-783A-83	Sequence 83, Appl
31	38	65.5	9	4	US-09-416-557-83	Sequence 83, Appl
32	38	65.5	126	2	US-08-765-783A-73	Sequence 73, Appl
33	38	65.5	126	2	US-08-765-783A-77	Sequence 77, Appl
34	38	65.5	126	3	US-08-921-100-73	Sequence 73, Appl
35	38	65.5	126	3	US-08-921-100-77	Sequence 77, Appl
36	38	65.5	126	3	US-08-880-142-73	Sequence 73, Appl
37	38	65.5	126	3	US-08-880-142-77	Sequence 77, Appl
38	38	65.5	126	3	US-08-902-201-73	Sequence 73, Appl
39	38	65.5	126	3	US-08-902-201-77	Sequence 77, Appl
40	38	65.5	126	4	US-09-416-557-73	Sequence 73, Appl
41	38	65.5	126	4	US-09-416-557-77	Sequence 77, Appl
42	38	65.5	127	2	US-08-765-783A-27	Sequence 27, Appl
43	38	65.5	127	3	US-08-921-100-27	Sequence 27, Appl
44	38	65.5	127	3	US-08-880-142-27	Sequence 27, Appl
45	38	65.5	127	3	US-08-902-201-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-09-257-069-10  
; Sequence 10, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; TITLE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; CURRENT FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-10

Query Match 100.0%; Score 58; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QHHYGTPT 9  
| | | | | | | |  
Db 1 QHHYGTPT 9

RESULT 2  
US-08-888-366-24  
; Sequence 24, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-24

Query Match      100.0%; Score 58; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
DB      89 QHHYGTPT 97

RESULT 3
US-09-257-069-4
; Sequence 4, Application US/09257069
; Patent No. 6348580
; GENERAL INFORMATION:
; APPLICANT: Medical & Biological Laboratories Co., Ltd.
; TITLE OF INVENTION: Monoclonal Antibody Specific for
; TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate
; FILE REFERENCE: M3-008-US
; CURRENT APPLICATION NUMBER: US/09/257,069
; CURRENT FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: JP 1998-252921
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-257-069-4

Query Match      100.0%; Score 58; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
DB      89 QHHYGTPT 97

RESULT 4

```

```

US-08-881-037-32
; Sequence 32, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-32

Query Match      93.1%; Score 54; DB 3; Length 99;
Best Local Similarity 88.9%; Pred. No. 0.034;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
DB      81 QHHYGTPT 89

RESULT 5
US-08-881-037-33
; Sequence 33, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-33

Query Match 93.1%; Score 54; DB 3; Length 99;  
Best Local Similarity 88.9%; Pred. No. 0.034;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OHHYGTPT 9  
DB 81 OHHYGTPT 89

## RESULT 6

US-08-881-037-34  
Sequence 34, Application US/08881037  
Patent No. 6080588

GENERAL INFORMATION:  
APPLICANT: Glick, Gary D.  
APPLICANT: Swanson, Patrick C.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-35

LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-34  
Query Match 93.1%; Score 54; DB 3; Length 99;  
Best Local Similarity 88.9%; Pred. No. 0.034;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OHHYGTPT 9  
DB 81 OHHYGTPT 89

## RESULT 7

US-08-881-037-35  
Sequence 35, Application US/08881037  
Patent No. 6080588

GENERAL INFORMATION:  
APPLICANT: Glick, Gary D.  
APPLICANT: Swanson, Patrick C.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-35

Query Match 93.1%; Score 54; DB 3; Length 99;  
Best Local Similarity 88.9%; Pred. No. 0.034;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OHHYGTPT 9  
DB 81 OHHYGTPT 89

## RESULT 8

US-08-881-037-69  
Sequence 69, Application US/08881037  
Patent No. 6080588

```
;
; GENERAL INFORMATION:
; APPLICANT: Klick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-69
;
; Query Match 93.1%; Score 54; DB 3; Length 107;
; Best Local Similarity 88.9%; Pred. No. 0.036;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 OHHYGTPYT 9
Db 89 OHHYGTPFT 97

;
; RESULT 9
; US-08-881-037-70
; Sequence 70, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Klick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-71
;
; Query Match 93.1%; Score 54; DB 3; Length 107;
; Best Local Similarity 88.9%; Pred. No. 0.036;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 OHHYGTPYT 9
Db 89 OHHYGTPFT 97

;
; RESULT 10
; US-08-881-037-71
; Sequence 71, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Klick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-70
;
; Query Match 93.1%; Score 54; DB 3; Length 107;
; Best Local Similarity 88.9%; Pred. No. 0.036;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 OHHYGTPYT 9
Db 89 OHHYGTPFT 97
```

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; TOPOLOGY: linear
US-08-881-037-71
;
; Query Match 93.1%; Score 54; DB 3; Length 107;
; Best Local Similarity 88.9%; Pred. No. 0.036;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 89 QHHYGTPT 97

RESULT 11
US-08-881-037-72
; Sequence 72, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5500
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-72
;
; Query Match 93.1%; Score 54; DB 3; Length 107;
; Best Local Similarity 88.9%; Pred. No. 0.036;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 89 QHHYGTPT 97

RESULT 12
US-07-958-140-2
; Sequence 2, Application US/07958140
; Patent No. 5489525
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS

; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,140
; FILING DATE: 19921008
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-958-140-2
;
; Query Match 93.1%; Score 54; DB 1; Length 243;
; Best Local Similarity 88.9%; Pred. No. 0.084;
; Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 222 QHHYGTPT 230

RESULT 13
PCT-US93-09166-2
; Sequence 2, Application PC/TUS9309166
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-09166-2

Query Match          93.1%; Score 54; DB 5; Length 243;
Best Local Similarity 88.9%; Pred. No. 0.084;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 222 QHHYGTPT 230

RESULT 14
US-08-681-432-2
; Sequence 2, Application US/08681432
; Patent No. 5800991
; GENERAL INFORMATION:
; APPLICANT: HALEY, Boyd E.
; APPLICANT: KOHLER, Heinz
; APPLICANT: RAJAGOPALAN, Krishnan
; APPLICANT: PAVLINKOVA, Gabriela
; TITLE OF INVENTION: NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY
; TITLE OF INVENTION: COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND
; TITLE OF INVENTION: THERAPEUTICS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURN, DOANE, SWECKER & MATHIS
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,432
; FILING DATE: 23-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,822
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 028750-132.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-432-2

Query Match          84.5%; Score 49; DB 1; Length 227;
Best Local Similarity 77.8%; Pred. No. 0.51;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 89 QHHFGTPT 97

;
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-09166-2

Query Match          93.1%; Score 54; DB 5; Length 243;
Best Local Similarity 88.9%; Pred. No. 0.084;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 222 QHHYGTPT 230

RESULT 15
US-09-406-532-10
; Sequence 10, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(9)
; OTHER INFORMATION: 15B8 light chain CDR 3
US-09-406-532-10

Query Match          79.3%; Score 46; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 1 QHHYSIPT 9

RESULT 16
US-09-406-532-4
; Sequence 4, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-406-532-4

Query Match          79.3%; Score 46; DB 4; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.74;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 89 QHHYSIPT 97

RESULT 17
US-08-379-057-27
; Sequence 27, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
```

```
/ APPLICANT: Gilliland, Lisa K.
/ APPLICANT: Gordon, Marcia L.
/ APPLICANT: Bajorath, Jurgen
/ APPLICANT: Aruffo, Alejandro A.
/ TITLE OF INVENTION: Monoclonal Antibodies Specific For
/ TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
/ TITLE OF INVENTION: In diagnosis and Therapy
/ NUMBER OF SEQUENCES: 57
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bristol-Myers Squibb Company
/ STREET: 3005 First Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,057
/ FILING DATE: 26-JAN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Poor, Brian W.
/ REGISTRATION NUMBER: 32,928
/ REFERENCE/DOCKET NUMBER: ON0133-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 727-3670
/ TELEFAX: (206) 727-3601
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-379-057-27

Query Match 75.9%; Score 44; DB 2; Length 108;
Best Local Similarity 77.8%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9
Db 89 QHHYNTPLT 97

RESULT 18
US-08-379-057-28
; Sequence 28, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-379-057-27
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,057
/ FILING DATE: 26-JAN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Poor, Brian W.
/ REGISTRATION NUMBER: 32,928
/ REFERENCE/DOCKET NUMBER: ON0133-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 727-3670
/ TELEFAX: (206) 727-3601
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-08-379-057-28

Query Match 75.9%; Score 44; DB 2; Length 108;
Best Local Similarity 77.8%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9
Db 89 QHHYNTPLT 97

RESULT 19
US-08-379-057-12
; Sequence 12, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-379-057-12
Query Match 75.9%; Score 44; DB 2; Length 128;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 109 QHHYNTPLT 117

RESULT 20
5219996-19
; Patent No. 5219996
; APPLICANT: BODMER, MARK W.; ADAIR, JOHN R.; WHITTLE, NIGEL R.
; LYONS, ALAN H.; OWENS, RAYMOND J.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND METHODS FOR
; THEIR PRODUCTION IN WHICH SURFACE RESIDUES ARE ALTERED TO
; CYSTEINE RESIDUES FOR ATTACHMENT OF EFFECTOR OR RECEPTOR
; MOLECULES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/353,634
; FILING DATE: 05-SEP-1988
; SEQ ID NO: 19
; LENGTH: 135
5219996-19
Query Match 75.9%; Score 44; DB 6; Length 135;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 109 QHFWGTPT 117

RESULT 21
US-08-400-115-4
; Sequence 4; Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040283/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-400-115-4
Query Match 75.9%; Score 44; DB 2; Length 271;
Best Local Similarity 77.8%; Pred. No. 4.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 111 QHFWGTPT 119

RESULT 22
US-08-378-939-20
; Sequence 20; Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-20
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Query Match 74.1%; Score 43; DB 2; Length 108;  
Best Local Similarity 77.8%; Pred. No. 2.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
Db 89 QHNYGTPLT 97

RESULT 23  
US-09-065-059-17  
; Sequence 17, Application US/09065059  
; Patent No. 6068841  
; GENERAL INFORMATION:  
; APPLICANT: SEINO, Ken-ichiro  
; APPLICANT: KAYAGAKI, No. 6068841uhiko  
; APPLICANT: YAGITA, Hideo  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/065,059  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca Ph.D., Daniel  
; REGISTRATION NUMBER: P-42,368  
; REFERENCE/DOCKET NUMBER: 50356-151  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-518-5100  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-065-059-17

Query Match 59.0%; Score 40; DB 3; Length 105;  
Best Local Similarity 66.7%; Pred. No. 7;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
Db 89 QHYSPT 97

RESULT 24  
US-08-397-411-1  
; Sequence 1, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; B-Cell Lymphoma and Cell Line

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-1

Query Match 69.0%; Score 40; DB 3; Length 107;  
Best Local Similarity 75.0%; Pred. No. 7.1;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 8  
Db 89 QHHYNSY 96

RESULT 25  
US-08-397-411-2  
; Sequence 2, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-2

Query Match 59.0%; Score 40; DB 3; Length 107;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
Db 89 QHHYGSY 96

RESULT 26
US-08-477-347-11
; Sequence 11, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jack
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid

Query Match 69.0%; Score 40; DB 3; Length 107;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
Db 89 QHHYGSY 96

RESULT 27
US-08-397-411-5
; Sequence 5, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: TSO, J. Yun
; TITLE OF INVENTION: Bispesic Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-5

Query Match 69.0%; Score 40; DB 3; Length 214;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
Db 89 QHHYGSY 96

RESULT 28
US-08-881-037-68
; Sequence 68, Application US/08881037
; Patent No. 6080588
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```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-347-11

Query Match 69.0%; Score 40; DB 4; Length 119;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9
Db 87 QHHYSTPFT 95

RESULT 27
US-08-397-411-5
; Sequence 5, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: TSO, J. Yun
; TITLE OF INVENTION: Bispesic Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-5

Query Match 69.0%; Score 40; DB 3; Length 214;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8
Db 89 QHHYGSY 96

RESULT 28
US-08-881-037-68
; Sequence 68, Application US/08881037
; Patent No. 6080588
```

```

; GENERAL INFORMATION:
; APPLICANT:  Click, Gary D.
; APPLICANT:  Swanson, Patrick C.
; TITLE OF INVENTION:  DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES:  113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Morrison & Foerster
; STREET:  755 Page Mill Road
; CITY:  Palo Alto
; STATE:  CA
; COUNTRY:  USA
; ZIP:  94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/881,037
; FILING DATE:  23-JUN-1997
; CLASSIFICATION:  530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 08/443,540
; FILING DATE:  18-MAY-1995
; CLASSIFICATION:  530
; ATTORNEY/AGENT INFORMATION:
; NAME:  Kanski, Antoinette F.
; REGISTRATION NUMBER:  34,202
; REFERENCE/DOCKET NUMBER:  203442110710
; TELEPHONE:  (650) 813-5600
; TELEFAX:  (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-68

Query Match      67.2%; Score 39; DB 3; Length 94;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QHHYGT 6
        |||||
Db      89 QHHYGT 94

RESULT 29
US-08-564-164A-4
; Sequence 4, Application US/08564164A
; Patent No. 6159947
; GENERAL INFORMATION:
; APPLICANT:  Schweighofer, Fabien
; APPLICANT:  Tocque, Bruno
; TITLE OF INVENTION:  Intracellular Binding Proteins and Use
; TITLE OF INVENTION:  Thereof
; NUMBER OF SEQUENCES:  17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Rhone-Poulenc Rorer Inc.
; STREET:  500 Arcola Road, 3C43
; CITY:  Collegeville
; STATE:  PA
; COUNTRY:  USA
; ZIP:  19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER:  US/08/564,164A
; FILING DATE:  28-DEC-1995
; CLASSIFICATION:  424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  WO PCT/FR94/00714
; FILING DATE:  15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  FR 93/07241
; FILING DATE:  16-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:  Savitzky, Martin F.
; REGISTRATION NUMBER:  29,699
; REFERENCE/DOCKET NUMBER:  ST93030-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (610)454-3816
; TELEFAX:  (610)454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-564-164A-4

Query Match      67.2%; Score 39; DB 4; Length 264;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 HHYGTPT 8
        |||||
Db      232 HHYGTPT 238

RESULT 30
US-08-765-783A-83
; Sequence 83, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT:  Matsushima, Kouji
; APPLICANT:  Matsumoto, Yoshihiro
; APPLICANT:  Yamada, Yoshiki
; APPLICANT:  Sato, Koh
; APPLICANT:  Tsuchiya, Masayuki
; APPLICANT:  Yamazaki, Tatsumi
; TITLE OF INVENTION:  Reshaped Human Antibody to
; TITLE OF INVENTION:  Interleukin-8
; NUMBER OF SEQUENCES:  105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  MORRISON & FOERSTER
; STREET:  2000 Pennsylvania Avenue, NW, suite 5500
; CITY:  Washington
; STATE:  DC
; COUNTRY:  USA
; ZIP:  20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Diskette
; COMPUTER:  IBM Compatible
; OPERATING SYSTEM:  DOS
; SOFTWARE:  FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/765,783A
; FILING DATE:  07-MAR-1997
; CLASSIFICATION:  530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:  Murashige, Kate H
; REGISTRATION NUMBER:  29,959
; REFERENCE/DOCKET NUMBER:  35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  202-887-1500
; TELEFAX:  202-822-0168

```

```

;
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-08-765-783A-83

Query Match      65.5%; Score 38; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. NO. 2e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 OHHFGTPPT 9
Db      1 OHHFGPPT 9

RESULT 31
US-09-416-557-83
; Sequence 83, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,557
; FILING DATE: 12-October-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,783
; FILING DATE: 7-March-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
;
US-09-416-557-83

Query Match      65.5%; Score 38; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. NO. 2e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 OHHFGTPPT 9
Db      1 OHHFGPPT 9

RESULT 32
US-08-765-783A-73
; Sequence 73, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
;
US-08-765-783A-73

Query Match      65.5%; Score 38; DB 2; Length 126;
Best Local Similarity 66.7%; Pred. NO. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 OHHFGTPPT 9
Db      108 OHHFGPPT 116

RESULT 33
US-08-765-783A-77
; Sequence 77, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji

```

APPLICANT: Matsumoto, Yoshihiro  
APPLICANT: Yamada, Yoshiaki  
APPLICANT: Sato, Koh  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,783A  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Signal Sequence  
LOCATION: 1..19  
OTHER INFORMATION:  
US-08-765-783A-77  
Query Match 65.5%; Score 38; DB 2; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 9  
Db 108 QHHFGFPRT 116  
RESULT 34  
US-08-921-100-73  
Sequence 73, Application US/08921100  
Patent No. 6024956  
GENERAL INFORMATION:  
APPLICANT: MATSUSHIMA, KOUJI  
APPLICANT: MATSUMOTO, YOSHIHIRO  
APPLICANT: YAMADA, YOSHIKI  
APPLICANT: SATO, KOH  
APPLICANT: TSUCHIYA, MASSAYUKI  
APPLICANT: YAMAZAKI, TATUMI  
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/921,100  
FILING DATE: 29-AUG-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/437,323  
FILING DATE: 09-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 15580-0001.02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-921-100-73  
Query Match 65.5%; Score 38; DB 3; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QHHYGTPT 9  
Db 108 QHHFGFPRT 116  
RESULT 35  
US-08-921-100-77  
Sequence 77, Application US/08921100  
Patent No. 6024956  
GENERAL INFORMATION:  
APPLICANT: MATSUSHIMA, KOUJI  
APPLICANT: MATSUMOTO, YOSHIHIRO  
APPLICANT: YAMADA, YOSHIKI  
APPLICANT: SATO, KOH  
APPLICANT: TSUCHIYA, MASSAYUKI  
APPLICANT: YAMAZAKI, TATUMI  
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/921,100  
FILING DATE: 29-AUG-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/437,323

;; FILING DATE: 09-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 15580-0001.02  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 887-0763  
;; TELEX: 90-4030  
;; INFORMATION FOR SEQ ID NO: 77:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 126 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-921-100-77

Query Match 65.5%; Score 38; DB 3; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 108 QHHFGPRT 116

RESULT 36  
US-08-880-142-73  
; Sequence 73, Application US/08880142  
; Patent No. 6048972  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATUMI  
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-JUN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/345,145  
; FILING DATE: 28-NOV-1994  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-JUN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/345,145  
; FILING DATE: 28-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 15580-0001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-880-142-73

Query Match 65.5%; Score 38; DB 3; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 108 QHHFGPRT 116

RESULT 37  
US-08-880-142-77  
; Sequence 77, Application US/08880142  
; Patent No. 6048972  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI  
; APPLICANT: MATSUMOTO, YOSHIHIRO  
; APPLICANT: YAMADA, YOSHIKI  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUCHIYA, MASSAYUKI  
; APPLICANT: YAMAZAKI, TATUMI  
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-JUN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/345,145  
; FILING DATE: 28-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 15580-0001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-880-142-77

Query Match 65.5%; Score 38; DB 3; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 108 QHHFGPRT 116

RESULT 38  
US-08-902-201-73  
; Sequence 73, Application US/08902201  
; Patent No. 6068840  
; GENERAL INFORMATION:  
; APPLICANT: MATSUSHIMA, KOUJI

APPLICANT: MATSUMOTO, YOSHIHIRO  
APPLICANT: YAMADA, YOSHIKI  
APPLICANT: SATO, KOH  
APPLICANT: TSUCHIYA, MASSAYUKI  
APPLICANT: YAMAZAKI, TATUMI  
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,201  
FILING DATE: 29-JUL-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/437,328  
FILING DATE: 09-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 15580-0001.01  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-201-73

Query Match 65.5%; Score 38; DB 3; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
|||:|  
Db 108 QHHFGPRT 116

RESULT 39  
US-08-902-201-77  
Sequence 77, Application US/08902201  
Patent No. 6068840  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, KOUJI  
APPLICANT: MATSUMOTO, YOSHIHIRO  
APPLICANT: YAMADA, YOSHIKI  
APPLICANT: SATO, KOH  
APPLICANT: TSUCHIYA, MASSAYUKI  
APPLICANT: YAMAZAKI, TATUMI  
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. NW, Suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,201  
FILING DATE: 29-JUL-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/437,328  
FILING DATE: 09-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 15580-0001.01  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-201-77

Query Match 65.5%; Score 38; DB 3; Length 126;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
|||:|  
Db 108 QHHFGPRT 116

RESULT 40  
US-09-416-557-73  
Sequence 73, Application US/09416557  
Patent No. 6245894  
GENERAL INFORMATION:  
APPLICANT: Matsushima, Kouji  
APPLICANT: Matsumoto, Yoshihiro  
APPLICANT: Yamada, Yoshiki  
APPLICANT: Sato, Koh  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/416,557  
FILING DATE: 12-October-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,783  
FILING DATE: 7-March-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.10  
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-09-416-557-73

Query Match 65.5%; Score 38; DB 4; Length 126;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 108 QHHFGPPT 116

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Search completed: July 18, 2003, 15:11:51  
Job time : 10.44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:09:56 ; Search time 23.22 Seconds  
(without alignments)  
46.031 Million cell updates/sec

Title: US-10-007-790-10

Perfect score: 58

Sequence: 1 QHHYGTPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*  
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5: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB pep.\*  
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10: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep1.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep2.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep3.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	93.1	106	15	US-10-096-246-15
2	54	93.1	108	15	US-10-096-246-19
3	47	81.0	101	15	US-10-096-246-18
4	44	75.9	110	15	US-10-096-246-14
5	44	75.9	235	10	US-09-799-777-43
6	43	74.1	12	15	US-10-322-142-9
7	43	74.1	107	15	US-10-322-142-32
8	40	69.0	9	11	US-09-423-800-61
9	40	69.0	9	12	US-09-269-921-5
10	40	69.0	9	12	US-09-509-098-7
11	40	69.0	9	14	US-10-218-253-5
12	40	69.0	9	15	US-10-182-018-61
13	40	69.0	9	15	US-10-169-003-61
14	40	69.0	106	12	US-09-509-098-133
15	40	69.0	107	12	US-09-509-098-130
16	40	69.0	107	12	US-09-509-098-134

17	40	69.0	119	11	US-09-800-908-11	Sequence 11, Appl
18	40	69.0	126	10	US-09-760-723-6	Sequence 6, Appl
19	40	69.0	126	10	US-09-355-925-6	Sequence 6, Appl
20	40	69.0	126	12	US-09-269-921-106	Sequence 106, Appl
21	40	69.0	126	12	US-09-269-921-107	Sequence 107, Appl
22	40	69.0	126	12	US-09-509-098-12	Sequence 12, Appl
23	40	69.0	126	12	US-09-509-098-14	Sequence 14, Appl
24	40	69.0	126	14	US-10-218-253-106	Sequence 106, Appl
25	40	69.0	126	14	US-10-218-253-107	Sequence 107, Appl
26	40	69.0	126	15	US-10-315-125-6	Sequence 6, Appl
27	40	69.0	131	12	US-09-269-921-104	Sequence 104, Appl
28	40	69.0	131	12	US-09-509-098-2	Sequence 2, Appl
29	40	69.0	131	14	US-10-218-253-104	Sequence 104, Appl
30	39	67.2	175	15	US-10-221-558-2	Sequence 2, Appl
31	39	67.2	518	11	US-09-816-248-17	Sequence 17, Appl
32	38.5	66.4	110	15	US-10-096-246-16	Sequence 16, Appl
33	38	65.5	9	10	US-09-730-857-83	Sequence 83, Appl
34	38	65.5	126	10	US-09-730-857-73	Sequence 73, Appl
35	38	65.5	126	10	US-09-730-857-77	Sequence 77, Appl
36	38	65.5	127	10	US-09-730-857-27	Sequence 27, Appl
37	37	63.8	250	11	US-09-887-853-2	Sequence 2, Appl
38	36	62.1	100	10	US-09-899-896-8	Sequence 8, Appl
39	36	62.1	237	12	US-09-880-748-2110	Sequence 2110, Appl
40	36	62.1	912	11	US-09-987-482-2	Sequence 2, Appl
41	36	62.1	1070	15	US-10-001-486B-2	Sequence 32, Appl
42	36	62.1	2843	8	US-08-681-219-32	Sequence 1, Appl
43	36	62.1	2843	11	US-09-987-482-1	Sequence 1, Appl
44	35	60.3	21	12	US-09-939-126-11	Sequence 11, Appl
45	35	60.3	47	15	US-10-001-879-151	Sequence 151, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-096-246-15  
; Sequence 15, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R E

; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leslie

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor

; FILE OF INVENTION: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/096,246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version.3.1

; SEQ ID NO 15

; LENGTH: 106

; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A4A1

US-10-096-246-15

Query Match 93.1%; Score 54; DB 15; Length 106;

Best Local Similarity 88.9%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 1;

QY 1 QHHYGTPT 9

Db 89 QHHYGTPT 97

#### RESULT 2

US-10-096-246-19

; Sequence 19, Application US/10096246

; Publication No. US20030100060A1

; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R E

; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-19

Query Match 93.1%; Score 54; DB 15; Length 108;  
Best Local Similarity 88.9%; Pred. No. 0.094; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 89 QHHYGTPT 97

RESULT 3  
US-10-096-246-18  
; Sequence 18, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-18

Query Match 81.0%; Score 47; DB 15; Length 101;  
Best Local Similarity 88.9%; Pred. No. 1.2; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 82 QHHYGTPT 90

RESULT 4  
US-10-096-246-14  
; Sequence 14, Application US/10096246  
; Publication No. US20030100060A1  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/096,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 110  
; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-096-246-14

Query Match 75.9%; Score 44; DB 15; Length 110;  
Best Local Similarity 77.8%; Pred. No. 3.9; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 89 QHHYGTPT 97

RESULT 5  
US-09-799-777-43  
; Sequence 43, Application US/09799777  
; Patent No. US20020091244A1  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; Hillman, Jennifer L.  
; Corley, Neil C.  
; Guegler, Karl J.  
; Baugh, Mariah  
; Sather, Susan  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/799,777  
; FILING DATE: 06-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,485  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BILLINGS, LUCY J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0459 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT04  
; CLONE: 1969426  
; SEQUENCE DESCRIPTION: SEQ ID NO: 43 :  
US-09-799-777-43

Query Match 75.9%; Score 44; DB 10; Length 235;  
Best Local Similarity 87.5%; Pred. No: 8.1; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8  
Db 70 QSHYGTPT 77

## RESULT 6

US-10-322-142-9  
; Sequence 9, Application US/10322142  
; Publication No. US20030113322A1  
; GENERAL INFORMATION:  
; APPLICANT: BES, CEDRIC  
; APPLICANT: BRIANT-LONGUET, LAURENCE  
; APPLICANT: CERUTTI, MARTINE  
; APPLICANT: CHARDES, THIERRY  
; APPLICANT: DEVAUCHELLE, GERARD  
; APPLICANT: DEVAUX, CHRISTIAN  
; APPLICANT: GRANIER, CLAUDE  
; APPLICANT: MAWAS, CLAUDE  
; APPLICANT: OLIVE, DANIEL  
; APPLICANT: PAU, BERNARD  
; TITLE OF INVENTION: CDR-H1-DERIVED PETIDE CB11, PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: MADE THEREFROM AND METHODS OF TREATING DISORDERS IN  
; FILE REFERENCE: 1129-R-02  
; CURRENT APPLICATION NUMBER: US/10/322,142  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 60/341,349  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/374,754  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-322-142-9

Query Match 74.1%; Score 43; DB 15; Length 12;  
Best Local Similarity 77.8%; Pred. No. 0.7;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 4 QHHYGNPT 12

## RESULT 7

US-10-322-142-32  
; Sequence 32, Application US/10322142  
; Publication No. US20030113322A1  
; GENERAL INFORMATION:  
; APPLICANT: BES, CEDRIC  
; APPLICANT: BRIANT-LONGUET, LAURENCE  
; APPLICANT: CERUTTI, MARTINE  
; APPLICANT: CHARDES, THIERRY  
; APPLICANT: DEVAUCHELLE, GERARD  
; APPLICANT: DEVAUX, CHRISTIAN  
; APPLICANT: GRANIER, CLAUDE  
; APPLICANT: MAWAS, CLAUDE  
; APPLICANT: OLIVE, DANIEL  
; APPLICANT: PAU, BERNARD  
; TITLE OF INVENTION: CDR-H1-DERIVED PETIDE CB11, PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: MADE THEREFROM AND METHODS OF TREATING DISORDERS IN  
; FILE REFERENCE: 1129-R-02  
; CURRENT APPLICATION NUMBER: US/10/322,142  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 60/341,349  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/374,754  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 32

## ; LENGTH: 107

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VL  
; OTHER INFORMATION: domain of the anti-CD4 mAb 13B82  
US-10-322-142-32

Query Match 74.1%; Score 43; DB 15; Length 107;  
Best Local Similarity 77.8%; Pred. No. 5.6;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 89 QHHYGNPT 97

## RESULT 8

US-09-423-800-61  
; Sequence 61, Application US/09423800  
; Patent No. US20020165363A1  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUNENARI, TOSHIKAKI  
; APPLICANT: ISHII, KIMIE  
; TITLE OF INVENTION: CACHEXIA REMEDY  
; FILE REFERENCE: 04853-0036  
; CURRENT APPLICATION NUMBER: US/09/423,800  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: PCT/JP98/02116  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 125505/1997  
; PRIOR FILING DATE: 1997-05-15  
; PRIOR APPLICATION NUMBER: JP 194445/1997  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-423-800-61

Query Match 69.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 66.7%; Pred. No. 4e+05;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
Db 1 QOHYSTPT 9

## RESULT 9

US-09-269-921-5  
; Sequence 5, Application US/09269921  
; Publication No. US20030045691A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshihiko  
; APPLICANT: Teuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koishihara, Yasuo  
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
; FILE REFERENCE: 35029-20007.00  
; CURRENT APPLICATION NUMBER: US/09/269,921  
; CURRENT FILING DATE: 1999-04-01  
; EARLIER APPLICATION NUMBER: PCT/JP97/03553  
; EARLIER FILING DATE: 1997-10-03  
; EARLIER APPLICATION NUMBER: JP 8-264756  
; EARLIER FILING DATE: 1996-10-04  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: murine
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of CDR(3) of L chain V region of
; OTHER INFORMATION: mouse anti-HM 1.24 antibody
US-09-269-921-5

Query Match          69.0%; Score 40; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 4e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 1 QHHYSTPFT 9

RESULT 10
US-09-509-098-7
; Sequence 7, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR (3) of L
; OTHER INFORMATION: chain V region of anti-HM1.24 antibody
US-09-509-098-7

Query Match          69.0%; Score 40; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 4e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 1 QHHYSTPFT 9

RESULT 11
US-10-218-253-5
; Sequence 5, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: murine
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of CDR(3) of L chain V region of
; OTHER INFORMATION: mouse anti-HM 1.24 antibody
US-10-218-253-5

Query Match          69.0%; Score 40; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 4e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 1 QHHYSTPFT 9

RESULT 12
US-10-182-018-61
; Sequence 61, Application US/10182018
; Publication No. US20030049211A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
; FILE REFERENCE: PH-1092-PCT
; CURRENT APPLICATION NUMBER: US/10/182,018
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: JP 2000-83034
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-182-018-61

Query Match          69.0%; Score 40; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 4e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 1 QHHYSTPFT 9

RESULT 13
US-10-169-003-61
; Sequence 61, Application US/10169003
; Publication No. US20030124119A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation for
; TITLE OF INVENTION: Injection
; FILE REFERENCE: PH-1093-PCT
; CURRENT APPLICATION NUMBER: US/10/169,003
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 11-375203
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-169-003-61

Query Match          69.0%; Score 40; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 4e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
```

Db 1 QHYSTPFT 9

## RESULT 14

US-09-509-098-133  
; Sequence 133, Application US/09509098  
; Publication No. US20030103970A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0274  
; CURRENT APPLICATION NUMBER: US/09/509,098  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: JP 9-271726  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 133  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence of the L chain V region of RVLa  
US-09-509-098-133

Query Match 69.0%; Score 40; DB 12; Length 106;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHYGTPT 9  
Db 89 QHYSTPFT 97

## RESULT 15

US-09-509-098-130  
; Sequence 130, Application US/09509098  
; Publication No. US20030103970A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0274  
; CURRENT APPLICATION NUMBER: US/09/509,098  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: JP 9-271726  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 130  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence of the L chain V region of AHM  
US-09-509-098-130

Query Match 69.0%; Score 40; DB 12; Length 107;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHYGTPT 9  
Db 89 QHYSTPFT 97

## RESULT 16

US-09-509-098-134  
; Sequence 134, Application US/09509098  
; Publication No. US20030103970A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0274  
; CURRENT APPLICATION NUMBER: US/09/509,098  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: JP 9-271726  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 134  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence of the L chain V region of RVLb  
US-09-509-098-134

Query Match 69.0%; Score 40; DB 12; Length 107;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHYGTPT 9  
Db 89 QHYSTPFT 97

## RESULT 17

US-09-800-908-11  
; Sequence 11, Application US/09800908  
; Patent No. US20020111462A1  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; BIGDA, Jacek  
; BELETSKY, Igor  
; METT, Igor  
; TITLE OF INVENTION: TNF LIGANDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEWMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/800,908  
; FILING DATE: 08-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,347  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: IL 106271  
; FILING DATE: 08-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, G. Kevin  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: WALLACH=10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633

```

; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 119 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-800-908-11
Query Match          69.0%; Score 40; DB 11; Length 119;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
Db 87 QHHYSTPT 95

RESULT 18
US-09-760-723-6
; Sequence 6, Application US/09760723
; Patent No. US20020034507A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
; FILE REFERENCE: 053466/0295
; CURRENT APPLICATION NUMBER: US/09/760,723
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/367,833
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: PCT/JP98/00831
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of L chain V region version a of humanized anti-HM1.24
US-09-760-723-6
Query Match          69.0%; Score 40; DB 10; Length 126;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
Db 108 QHHYSTPT 116

RESULT 19
US-09-355-925-6
; Sequence 6, Application US/09355925
; Patent No. US20020037288A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of L chain V region version a of humanized anti-HM1.24
US-09-760-723-6
Query Match          69.0%; Score 40; DB 10; Length 126;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
Db 108 QHHYSTPT 116

RESULT 20
US-09-269-921-106
; Sequence 106, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V region
US-09-269-921-106
Query Match          69.0%; Score 40; DB 12; Length 126;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
Db 108 QHHYSTPT 116

RESULT 21
US-09-269-921-107
; Sequence 107, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
US-09-269-921-107
Query Match          69.0%; Score 40; DB 12; Length 126;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QHHYGTPT 9
Db 108 QHHYSTPT 116
```

; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V region  
; OTHER INFORMATION: version b  
US-09-269-921-107

Query Match 69.0%; Score 40; DB 12; Length 126;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 108 QHYSPTPT 116

RESULT 22  
US-09-509-098-12  
; Sequence 12, Application US/09509098  
; Publication No. US20030103970A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0274  
; CURRENT APPLICATION NUMBER: US/09/509,098  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: JP 9-271726  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanized L chain V  
; OTHER INFORMATION: region of anti-HM1.24 antibody  
US-09-509-098-12

Query Match 69.0%; Score 40; DB 12; Length 126;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 108 QHYSPTPT 116

RESULT 23  
US-09-509-098-14  
; Sequence 14, Application US/09509098  
; Publication No. US20030103970A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0274  
; CURRENT APPLICATION NUMBER: US/09/509,098  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: JP 9-271726  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 126

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanized L chain V  
; OTHER INFORMATION: region of anti-HM1.24 antibody  
US-09-509-098-14

Query Match 69.0%; Score 40; DB 12; Length 126;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 108 QHYSPTPT 116

RESULT 24  
US-10-218-253-106  
; Sequence 106, Application US/10218253  
; Publication No. US20030129185A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshihiko  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koishihara, Yasuo  
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
; FILE REFERENCE: 35029-20007.00  
; CURRENT APPLICATION NUMBER: US/10/218,253  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/269,921  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: PCT/JP97/03553  
; PRIOR FILING DATE: 1997-10-03  
; PRIOR APPLICATION NUMBER: JP 8-264756  
; PRIOR FILING DATE: 1996-10-04  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 106  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V region  
; OTHER INFORMATION: version a  
US-10-218-253-106

Query Match 69.0%; Score 40; DB 14; Length 126;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 108 QHYSPTPT 116

RESULT 25  
US-10-218-253-107  
; Sequence 107, Application US/10218253  
; Publication No. US20030129185A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshihiko  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koishihara, Yasuo  
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
; FILE REFERENCE: 35029-20007.00  
; CURRENT APPLICATION NUMBER: US/10/218,253  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/269,921  
; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: PCT/JP97/03553  
; PRIOR FILING DATE: 1997-10-03  
; PRIOR APPLICATION NUMBER: JP 8-264756  
; PRIOR FILING DATE: 1996-10-04  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody L chain V region  
; OTHER INFORMATION: version b  
US-10-218-253-107

Query Match 69.0%; Score 40; DB 14; Length 126;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 108 QHHYSTPT 116

## RESULT 26

US-10-315-125-6  
; Sequence 6, Application US/10315125  
; Publication No. US20030113334A1  
; GENERAL INFORMATION:  
; APPLICANT: KOISHIHARA, YASUO  
; APPLICANT: YOSHIMURA, YASUSHI  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS  
; FILE REFERENCE: 053466/0255  
; CURRENT APPLICATION NUMBER: US/10/315,125  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US/09/355,925  
; PRIOR FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/00568  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: JP 9-41410  
; PRIOR FILING DATE: 1997-02-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence of L chain V region version a of  
; OTHER INFORMATION: humanized anti-HM1.24 antibody  
US-10-315-125-6

Query Match 69.0%; Score 40; DB 15; Length 126;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 108 QHHYSTPT 116

## RESULT 27

US-09-269-921-104  
; Sequence 104, Application US/09269921  
; Publication No. US20030045691A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshihiko  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koishihara, Yasuo

; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
; FILE REFERENCE: 35029-20007.00  
; CURRENT APPLICATION NUMBER: US/09/269,921  
; CURRENT FILING DATE: 1999-04-01  
; EARLIER APPLICATION NUMBER: PCT/JP97/03553  
; EARLIER FILING DATE: 1997-10-03  
; EARLIER APPLICATION NUMBER: JP 8-264756  
; EARLIER FILING DATE: 1996-10-04  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 104  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: murine  
; FEATURE:  
; LOCATION:  
; OTHER INFORMATION: Amino acid sequence of anti-HM 1.24 antibody L chain V region  
US-09-269-921-104

Query Match 69.0%; Score 40; DB 12; Length 131;  
Best Local Similarity 66.7%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 113 QHHYSTPT 121

## RESULT 28

US-09-509-098-2  
; Sequence 2, Application US/09509098  
; Publication No. US20030103970A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0274  
; CURRENT APPLICATION NUMBER: US/09/509,098  
; CURRENT FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: JP 9-271726  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence of L chain V region of mouse anti-HM1.24  
; OTHER INFORMATION: antibody  
US-09-509-098-2

Query Match 69.0%; Score 40; DB 12; Length 131;  
Best Local Similarity 66.7%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
| | | | |  
Db 113 QHHYSTPT 121

## RESULT 29

US-10-218-253-104  
; Sequence 104, Application US/10218253  
; Publication No. US20030129185A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshihiko  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koishihara, Yasuo

```

; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 104
; LENGTH: 131
; TYPE: PRT
; ORGANISM: murine
; FEATURE:
; LOCATION:
; OTHER INFORMATION: Amino acid sequence of anti-HM 1.24 antibody L chain V region
US-10-218-253-104

Query Match          69.0%; Score 40; DB 14; Length 131;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
DB      113 QHHYSTPFT 121

RESULT 30
US-10-221-558-2
; Sequence 2, Application US/10221558
; Publication No. US20030105316A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; APPLICANT: Bull, Christof
; TITLE OF INVENTION: Regulation of human Opsin-related GPCR
; FILE REFERENCE: L10039 foreign countries
; CURRENT APPLICATION NUMBER: US/10/221,558
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/191,717
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ( )..( )
; OTHER INFORMATION: Xaa = any amino acid
US-10-221-558-2

Query Match          67.2%; Score 39; DB 15; Length 175;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
DB      150 QHHYGHYSYS 158

RESULT 31
US-09-816-248-17
; Sequence 17, Application US/09816248
; Patent No. US20020137703A1
; GENERAL INFORMATION:
; APPLICANT: BAUMANN, PETER
; APPLICANT: CSCH, THOMAS R.
; TITLE OF INVENTION: PROTECTION-OF-TELOMERE-1 (POT-1) PROTEIN AND ENCODING
; TITLE OF INVENTION: POLYNUCLEOTIDES

```

```

; FILE REFERENCE: 089491/0201
; CURRENT APPLICATION NUMBER: US/09/816,248
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-816-248-17

Query Match          67.2%; Score 39; DB 11; Length 518;
Best Local Similarity 85.7%; Pred. No. 1.le+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 HHYGTPT 8
DB      499 HHYGTGY 505

RESULT 32
US-10-096-246-16
; Sequence 16, Application US/10096246
; Publication No. US2003010060A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
; FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; CURRENT APPLICATION NUMBER: US/10/096,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-16

Query Match          66.4%; Score 38.5; DB 15; Length 110;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1 QHHYGTPT 9
DB      89 QHHYG-PFT 96

RESULT 33
US-09-730-857-83
; Sequence 83, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; APPLICANT: Interleukin-8
; TITLE OF INVENTION: Reshaped Human Antibody to
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730.857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-730-857-83
;
; Query Match 65.5%; Score 38; DB 10; Length 9;
; Best Local Similarity 66.7%; Pred. No. 4e+05;
; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 QHHYGTPT 9
; DB 1 QHHFGFPT 9
;
; RESULT 34
; US-09-730-857-73
; Sequence 73, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; Matsumoto, Yoshihiro
; Yamada, Yoshiki
; Sato, Koh
; Tsuchiya, Masayuki
; Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730.857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
;
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-730-857-73
;
; Query Match 65.5%; Score 38; DB 10; Length 126;
; Best Local Similarity 66.7%; Pred. No. 42;
; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 QHHYGTPT 9
; DB 108 QHHFGFPT 116
;
; RESULT 35
; US-09-730-857-77
; Sequence 77, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; Matsumoto, Yoshihiro
; Yamada, Yoshiki
; Sato, Koh
; Tsuchiya, Masayuki
; Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730.857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids

```

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-730-857-77

Query Match      65.5%; Score 38; DB 10; Length 126;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
Db      108 QHFGFPRT 116

RESULT 36
US-09-730-857-27
; Sequence 27, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
;              Matsumoto, Yoshihiro
;              Yamada, Yoshiki
;              Sato, Koh
;              Tsuchiya, Masayuki
;              Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
;                   Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...20
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;
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-730-857-27

Query Match      65.5%; Score 38; DB 10; Length 127;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
Db      109 QHFGFPRT 117

RESULT 37
US-09-887-853-2
; Sequence 2, Application US/09887853
; Patent No. US20020168375A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
;              Oppermann, Hermann
;              Houston, L. L.
;              Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
;                   Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/887,853
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-887-853-2

Query Match      63.8%; Score 37; DB 11; Length 250;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 QHHYGTPT 9
Db      224 QQHYRVPYT 232

RESULT 38
US-09-899-896-8
; Sequence 8, Application US/09899896
; Patent No. US20020072588A1
```

```

; GENERAL INFORMATION:
; APPLICANT: von Bingen, Hans-Christian
; APPLICANT: Genain, Claude P.
; APPLICANT: Hauser, Stephen L.
; TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
; TITLE OF INVENTION: Antagonists
; FILE REFERENCE: SF01-025-2
; CURRENT APPLICATION NUMBER: US/09/899,896
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/691,654
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 100
; TYPE: PRT
; ORGANISM: human
US-09-899-896-8

Query Match          62.1%; Score 36; DB 10; Length 100;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 89 QHYSPLT 97

RESULT 39
US-09-880-748-2110
; Sequence 2110, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2110
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2110

Query Match          62.1%; Score 36; DB 12; Length 237;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9
Db 218 QQSYGTPT 226

RESULT 40
US-09-987-482-2
; Sequence 2, Application US/09987482
; Publication No. US20020184656A1
; GENERAL INFORMATION:
; APPLICANT: BHANDARI, POONAM
; APPLICANT: SHASHIDHARA, L.S.
; TITLE OF INVENTION: IN VIVO ASSAY SYSTEM FOR SCREENING AND VALIDATION OF
```

```

; TITLE OF INVENTION: DRUGS AND OTHER SUBSTANCES
; FILE REFERENCE: 056859-0134
; CURRENT APPLICATION NUMBER: US/09/987,482
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-482-2

Query Match          62.1%; Score 36; DB 11; Length 912;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 2 HHY----GTPY 8
Db 886 HHYPTIEGTPY 896

Search completed: July 18, 2003, 15:35:58
Job time : 24.22 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:05 ; Search time 11.7 Seconds  
(without alignments)  
73.950 Million cell updates/sec

Title: US-10-007-790-10.

Perfect score: 58

Sequence: 1 QHHYGTPT 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 73.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	93.1	106	2 B47329	Ig kappa chain V r
2	54	93.1	128	2 S31488	Ig kappa chain pre
3	50	86.2	107	2 S24290	Ig kappa chain V r
4	48	82.8	98	2 PH1069	Ig light chain V r
5	48	82.8	108	1 KVM349	Ig kappa chain V r
6	47	81.0	101	2 S20810	Ig kappa chain V r
7	45	77.6	62	2 PLO266	Ig kappa chain V r
8	44	75.9	104	2 PH1053	Ig light chain V r
9	44	75.9	106	2 PLO088	Ig kappa chain V r
10	44	75.9	107	2 S32191	Ig kappa chain V r
11	44	75.9	107	2 S32192	Ig kappa chain V r
12	44	75.9	214	2 S68212	Ig kappa chain (Ma
13	42	72.4	107	2 PLO080	Ig kappa chain V r
14	42	72.4	332	2 T26992	hypothetical prote
15	42	72.4	474	2 T26990	hypothetical prote
16	40	69.0	237	2 B81245	hydrolase, probabl
17	40	69.0	808	1 QPKEX	glucose dehydrogen
18	40	69.0	1246	2 T00826	hypothetical prote
19	40	69.0	1816	2 A84845	probable ABC trans
20	39	67.2	79	2 A28840	Ig kappa chain V r
21	39	67.2	81	2 S22024	Ig kappa chain - m
22	38.5	66.4	134	2 S11245	Ig kappa chain pre
23	38	65.5	106	2 A49138	IgA kappa rheumato
24	38	65.5	287	2 D69536	hypothetical prote
25	38	65.5	393	2 D64391	flavoprotein - Met
26	38	65.5	849	2 T04242	abdominal segment
27	37	63.8	129	2 S52792	Ig kappa chain V r
28	37	63.8	199	2 B86659	hypothetical prote
29	37	63.8	288	2 S73455	fructose-bisphosph

30	37	63.8	450	2 D71101	hypothetical prote
31	37	63.8	451	2 D75139	hypothetical prote
32	37	63.8	568	2 T28876	hypothetical prote
33	36	62.1	152	2 S30751	Ig kappa chain pre
34	36	62.1	173	2 I38617	zinc finger protei
35	36	62.1	223	2 E69747	two-component resp
36	36	62.1	299	2 AB0440	hypothetical prote
37	36	62.1	309	2 C81954	probable transcrip
38	36	62.1	309	2 H81011	transcription regu
39	36	62.1	416	2 A43561	homeotic protein m
40	36	62.1	439	2 D86440	unknown protein li
41	36	62.1	589	2 B70915	probable membrane
42	36	62.1	731	2 S46115	hypothetical prote
43	36	62.1	2843	1 RBHUAP	adenomatous polyo
44	36	62.1	2845	2 I49505	adenomatous polyo
45	35	60.3	113	2 JC2270	PL7-6 antibody lig

ALIGNMENTS

RESULT 1

B47329

Ig kappa chain V region (PRL) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence\_revision 17-Jul-1994 #text\_change 21-Jan-2000

C;Accession: B47329

R;Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.

A;Title: A recombinant immunotoxin that is active on prostate cancer cells and that is c

A;Reference number: A47329; MUID:93133825; PMID:8421689

A;Accession: B47329

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-106 <BRI>

A;Experimental source: Balb/c

A;Note: sequence modified after extraction from NCBI backbone

A;Note: sequence extracted from NCBI backbone (NCBI:122874)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 54; DB 2; Length 106;  
Best Local Similarity 88.9%; Pred. No. 0.011;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9

DB 89 QHHYGTPT 97

RESULT 2

S31488

Ig kappa chain precursor V region (F11) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C;Accession: S31488

R;Respalov, I.A.; Shiyonov, P.A.; Lukashovich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova

submitted to the EMBL Data Library, December 1992

A;Reference number: S31488

A;Accession: S31488

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-128 <BES>

A;Cross-references: EMBL:X69859; NID:G50929; PIDN:CAA49493.1; PID:G50930

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 54; DB 2; Length 128;  
Best Local Similarity 88.9%; Pred. No. 0.013;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
|||||:|  
Db 109 QHHYGTPT 117

RESULT 3  
S24290  
Ig kappa chain V region (J534/32) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Jun-2000  
C:Accession: S24290  
R:Monchamont, B.  
A:Submitted to the EMBL Data Library, September 1991  
A:Description: Cloning and sequencing of the cDNA coding for the variable regions of the  
A:Reference number: S24287  
A:Accession: S24290  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <MON>  
A:Cross-references: EMBL:X62704; NID:g51693; PIDN:CAA44580.1; PID:g1333967  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 50; DB 2; Length 107;  
Best Local Similarity 88.9%; Pred. No. 0.058;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
|||||:|  
Db 89 QHHYGTPT 97

RESULT 4  
PH1069  
Ig light chain V region (clone 185-cl) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1069  
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1069  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-98 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 48; DB 2; Length 98;  
Best Local Similarity 88.9%; Pred. No. 0.12;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
|||||:|  
Db 89 QHHYGTPT 97

RESULT 5  
KVM849  
Ig kappa chain V region (M149) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 16-Aug-1986  
C:Accession: A01919  
R:Appella, E.; Alvarez, V.L.  
Mol. Immunol. 17, 1507-1513, 1980  
A:Title: Amino acid sequence of the variable region of M149 mouse myeloma light chain: c  
A:Reference number: A01919; MUID:82057806; PMID:6795447  
A:Accession: A01919  
A:Molecule type: protein

A:Residues: 1-108 <APP>

A:Experimental source: strain BALB/c  
A>Note: this chain was isolated from a myeloma protein  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la;  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer

F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 82.8%; Score 48; DB 1; Length 108;  
Best Local Similarity 77.8%; Pred. No. 0.13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
|||||:|  
Db 89 QHHYGTPT 97

RESULT 6  
S20810  
Ig kappa chain V region (hybridoma C8) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S20810  
R:Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.  
submitted to the EMBL Data Library, September 1990  
A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine antib  
A:Reference number: S20809  
A:Accession: S20810  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-101 <HOO>

A:Cross-references: EMBL:X54693; NID:g50251; PIDN:CAA38509.1; PID:g50252  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 47; DB 2; Length 101;  
Best Local Similarity 88.9%; Pred. No. 0.19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
|||||:|  
Db 82 QHHYGTPT 90

RESULT 7  
PL0266  
Ig kappa chain V region (anti-DNA, 6PVK) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-May-1997  
C:Accession: PL0266  
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n  
A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A:Accession: PL0266  
A:Molecule type: mRNA  
A:Residues: 1-62 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-5/Region: framework 2  
F:6-12/Region: complementarity-determining 2  
F:13-44/Region: framework 3  
F:45-53/Region: complementarity-determining 3  
F:54-62/Region: framework 4

Query Match 77.6%; Score 45; DB 2; Length 62;  
Best Local Similarity 77.8%; Pred. No. 0.25;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9

Db 45 QNHYGTPYT 53  
|||||

## RESULT 8

PH1053  
Ig kappa chain V region (clone 163.100) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1053  
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell gene rearrangement  
A:Reference number: PH0971; PMID:92381444; PMID:1512540  
A:Accession: PH1053  
A:Molecule type: mRNA  
A:Residues: 1-104 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 104;  
Best Local Similarity 77.8%; Pred. No. 0.67;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QNHYGTPYT 9  
|||||  
Db 95 QQHYSPTPT 103

## RESULT 9

PL0088  
Ig kappa chain V regions (12S18-1, 12S28-16) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PL0088  
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1999  
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A:Reference number: PL0080; PMID:89094248; PMID:2492056  
A:Accession: PL0088  
A:Molecule type: mRNA  
A:Residues: 1-106 <MEE>  
A:Cross-references: GB:X58581; GB:Y00794; NID:951592; PIDN:CAA41457.1; PID:g930151  
A:Note: the sequence shown here is from the V kappa regions an antiidiotypic monoclonal  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 106;  
Best Local Similarity 77.8%; Pred. No. 0.68;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QNHYGTPYT 9  
|||||  
Db 88 QQHYSPTPT 96

## RESULT 10

S32191  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S32191  
R:Izui, S.  
submitted to the EMBL Data Library, February 1993

A:Reference number: S32185  
A:Accession: S32191  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <IZU>

A:Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 107;  
Best Local Similarity 77.8%; Pred. No. 0.69;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QNHYGTPYT 9  
|||||  
Db 89 QQHYSPTPT 97

## RESULT 11

S32192  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S32192  
R:Izui, S.  
submitted to the EMBL Data Library, February 1993

A:Reference number: S32185  
A:Accession: S32192  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <IZU>  
A:Cross-references: EMBL:X70097; NID:g288262; PIDN:CAA49701.1; PID:g288263  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 107;  
Best Local Similarity 77.8%; Pred. No. 0.69;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QNHYGTPYT 9  
|||||  
Db 89 QQHYSPTPT 97

## RESULT 12

S68212  
Ig kappa chain (Mab03-1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jan-2000  
C:Accession: S68212  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A:Reference number: S68211; PMID:96085223; PMID:7498516  
A:Accession: S68212  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-214 <TAK>  
A:Cross-references: EMBL:D29668  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 75.9%; Score 44; DB 2; Length 214;  
Best Local Similarity 77.8%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QNHYGTPYT 9  
|||||  
Db 95 QQHYSPTPT 103

## RESULT 13

PL0080  
Ig kappa chain V region (E4) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PL0080

R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1999  
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A;Reference number: PL0080; MUID:89094248; PMID:2492056  
A;Accession: PL0080  
A;Molecule type: mRNA  
A;Residues: 1-107 <MEE>  
A;Cross-references: GB:X58596; GB:Y00794; NID:951574; PIDN:CAA41471.1; PID:938255  
A;Experimental source: strain BALB/c  
A;Note: 106-Leu is translated from the codon CUN  
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclonal  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 42; DB 2; Length 107;  
Best Local Similarity 85.7%; Pred. No. 1.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OHHYGTP 7  
||| |||  
Db 89 OHHYGSP 95

RESULT 14  
T26992  
hypothetical protein Y48A6C.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T26992  
R;Gardner, A.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z20296  
A;Accession: T26992  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-332 <WIL>  
A;Cross-references: EMBL:AL032642; PIDN:CAA21653.1; GSPDB:GN00021; CESP:Y48A6C.3  
A;Experimental source: clone Y48A6C  
C;Genetics:  
A;Gene: CESP:Y48A6C.3  
A;Map position: 3  
A;Introns: 20/2; 70/2; 109/3; 132/3

Query Match 72.4%; Score 42; DB 2; Length 332;  
Best Local Similarity 85.7%; Pred. No. 5.3;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPT 8  
||| |||  
Db 256 HHYATPT 262

RESULT 15  
T26990  
hypothetical protein Y48A6C.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T26990  
R;Gardner, A.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z20296  
A;Accession: T26990  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-474 <WIL>  
A;Cross-references: EMBL:AL032642; PIDN:CAA21651.1; GSPDB:GN00021; CESP:Y48A6C.1  
A;Experimental source: clone Y48A6C  
C;Genetics:  
A;Gene: CESP:Y48A6C.1  
A;Map position: 3  
A;Introns: 27/3; 37/2; 87/2; 126/3; 149/3; 349/3; 385/3; 426/1; 465/3

R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1999  
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A;Reference number: PL0080; MUID:89094248; PMID:2492056  
A;Accession: PL0080  
A;Molecule type: mRNA  
A;Residues: 1-107 <MEE>  
A;Cross-references: GB:X58596; GB:Y00794; NID:951574; PIDN:CAA41471.1; PID:938255  
A;Experimental source: strain BALB/c  
A;Note: 106-Leu is translated from the codon CUN  
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclonal  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 42; DB 2; Length 474;  
Best Local Similarity 85.7%; Pred. No. 7.8;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPT 8  
||| |||  
Db 273 HHYATPT 279

RESULT 16  
B81245  
hydrolyase, probable NMB0040 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C;Accession: B81245  
R;Petcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: AB1000; MUID:20175755; PMID:10710307  
A;Accession: B81245  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-237 <TET>  
A;Cross-references: GB:AE002364; GB:AE002098; NID:97225269; PIDN:AAF40511.1; PID:9722526  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB0040

Query Match 69.0%; Score 40; DB 2; Length 237;  
Best Local Similarity 75.0%; Pred. No. 8.5;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OHHYGTPT 8  
||| |||  
Db 220 QNHNTPT 227

RESULT 17  
QPKEK  
glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17) - Gluconobacter oxydans  
C;Species: Gluconobacter oxydans  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 22-May-1998  
C;Accession: S17716; S19265  
R;Clecon-Jansen, A.M.; Dekker, S.; van de Putte, P.; Goosen, N.  
Mol. Gen. Genet. 229, 206-212, 1991  
A;Title: A single amino acid substitution changes the substrate specificity of quinoprote  
A;Reference number: S17716; MUID:92017653; PMID:1833618  
A;Accession: S17716  
A;Molecule type: DNA  
A;Residues: 1-808 <CLE>  
A;Cross-references: EMBL:X62710  
R;Goosen, N.  
submitted to the EMBL Data Library, February 1992  
A;Reference number: S19265  
A;Accession: S19265  
A;Molecule type: DNA  
A;Residues: 1-212, 'A', 214-808 <GOO>  
A;Cross-references: EMBL:X62710; NID:g58416; PID:g58417  
C;Genetics:  
A;Gene: gdh  
C;Function:  
A;Description: catalyzes the oxidation of D-glucose to D-gluconic acid by ubiquinone  
A;Pathway: respiratory chain  
C;Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)  
C;Keywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane p  
F;9-28/Domain: transmembrane #status predicted <TM1>  
F;35-54/Domain: transmembrane #status predicted <TM2>  
F;60-76/Domain: transmembrane #status predicted <TM3>  
F;94-110/Domain: transmembrane #status predicted <TM4>  
F;122-138/Domain: transmembrane #status predicted <TM5>

F:91,93/Binding site: ubiquinone (Arg, Asp) #status predicted  
F:470/Active site: Asp #status predicted

Query Match 69.0%; Score 40; DB 1; Length 808;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8  
|||  
Db 647 QHNYGIPY 654

## RESULT 18

T00826

hypothetical protein T32G6.22 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 23-Mar-2001

C:Accession: T00826

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul  
submitted to the EMBL Data Library, November 1997

A:Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.

A:Reference number: Z14163

A:Accession: T00826

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1246 <ROU>

A:Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618705

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 2

A:Introns: 33/3; 95/2; 113/3; 137/3; 168/3; 361/3; 421/2; 432/3; 493/3; 521/3; 535/3; 56  
A:Note: T32G6.22

## Query Match

Best Local Similarity 69.0%; Score 40; DB 2; Length 1246;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9

|||  
Db 100 KHHYGVGYT 108

## RESULT 19

A84845

probable ABC transporter [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: A84845

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84845

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1816 <STO>

A:Cross-references: GB:AE002093; NID:g6598351; PIDN:AA02761.2; GSPDB:GN00139

C:Genetics:

A:Gene: At2g41700

A:Map position: 2

## Query Match

Best Local Similarity 69.0%; Score 40; DB 2; Length 1816;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9

|||  
Db 670 KHHYGVGYT 678

## RESULT 20

A84845

probable ABC transporter [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: A84845

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999

## A28840

IG kappa chain V region (HP21) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Jul-1999

C:Accession: A28840; M25114

R:Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Fougereau, M.

EMBO J. 4, 3681-3688, 1985

A:Title: The idiotypic network and the internal image: possible regulation of a germ-line  
A:Reference number: A91028; MUID:86136012; PMID:3937730

A:Accession: A28840

A:Molecule type: mRNA

A:Residues: 1-79 <OLL>

A:Cross-references: GB:X03387; NID:g52168; PIDN:CAA27118.1; PID:g52169

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 67.2%; Score 39; DB 2; Length 79;

Best Local Similarity 66.7%; Pred. No. 4;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9

|||  
Db 61 QHFGAPWT 69

## RESULT 21

S22024

IG kappa chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Jun-2000

C:Accession: S22024

R:Caulfield, M.J.

submitted to the EMBL Data Library, September 1991

A:Description: Nucleotide sequences of the mRNA/cDNA encoding a pathogenic anti-erythrocy

A:Reference number: S22023

A:Accession: S22024

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-81 <CAU>

A:Cross-references: EMBL:X60425; NID:g51028; PIDN:CAA42956.1; PID:g1333923

C:Genetics:

A:Introns: 65/3; 72/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 67.2%; Score 39; DB 2; Length 81;

Best Local Similarity 66.7%; Pred. No. 4.1;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9

|||  
Db 73 QHFGAPWT 81

## RESULT 22

S11245

IG kappa chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C:Accession: S11245

R:Wellman, A.A.; Meares, C.F.

Nucleic Acids Res. 18, 5281, 1990

A:Title: Sequences of the Lym-1 antibody heavy and light chain variable regions.

A:Reference number: S11244; MUID:90384832; PMID:2119497

A:Accession: S11245

A:Molecule type: mRNA

A:Residues: 1-134 <WEL>

A:Cross-references: EMBL:X53484

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 66.4%; Score 38.5; DB 2; Length 134;

Best Local Similarity 77.8%; Pred. No. 8.6;  
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QHHYGTPT 9  
| | | | |  
Db 110 QHHYG-PFT 117

## RESULT 23

A49138  
Iga kappa rheumatoid factor variable - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: A49138  
R;Gause, A.; Kupperts, R.; Mierau, R.  
Clin. Exp. Immunol. 88, 430-434, 1992  
A;Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light  
A;Reference number: A49138; MUID:92298590; PMID:1606727  
A;Accession: A49138  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-106 <GAU>  
A;Cross-references: GB:G37926; NID:G298207; PIDN:AAB22366.1; PID:G298208  
A;Note: sequence inconsistent with the nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:106633, NCBIP:106637)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;20-99/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 38; DB 2; Length 106;  
Best Local Similarity 66.7%; Pred. No. 8.2;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 9  
| : | | | |  
Db 98 QQYVSTPT 106

## RESULT 24

D69536  
Hypothetical protein AF2292 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 04-Mar-2000  
C;Accession: D69536  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: D69536  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-287 <KLE>  
A;Cross-references: GB:AE000946; GB:AE000782; NID:G2689269; PIDN:AAB88967.1; PID:G264823  
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF2292

Query Match 65.5%; Score 38; DB 2; Length 287;  
Best Local Similarity 62.5%; Pred. No. 24;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 8  
| : | | | |  
Db 212 QHYVGAPF 219

## RESULT 25

D64391  
Flavoprotein - Methanococcus jannaschii  
C;Species: Methanococcus jannaschii  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: D64391

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;  
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
rison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A;Title: Complete genome sequence of the methanogenic archaeson, Methanococcus jannaschii  
A;Reference number: A64300; MUID:96337999; PMID:8688087  
A;Accession: D64391

A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-393 <BUL>

A;Cross-references: GB:U67519; GB:L77117; NID:G1591436; PIDN:AAB98728.1; PID:G1591446; T;  
C;Genetics:  
A;Map position: REV665441-664260

A;Start codon: GTG  
C;Superfamily: Methanobacterium flavoprotein A  
C;Keywords: flavoprotein

Query Match 65.5%; Score 38; DB 2; Length 393;  
Best Local Similarity 85.7%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHYGTPT 8  
| | | | |  
Db 26 HGYGTPT 32

## RESULT 26

T04242  
abdominal segment formation protein pumilio homolog F14M19.160 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 30-Apr-1999  
C;Accession: T04242  
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkee, W.; Stiekema, W.; Hohéisel, J.; Mew  
submitted to the Protein Sequence Database, March 1999  
A;Reference number: Z15262  
A;Accession: T04242  
A;Molecule type: DNA  
A;Residues: 1-849 <BEV>  
A;Cross-references: EMBL:AL049480  
A;Experimental source: cultivar Columbia; BAC clone F14M19  
C;Genetics:  
A;Map position: 4  
A;Introns: 100/1; 145/3; 505/1; 576/3; 612/3; 683/3; 720/3; 785/3; 843/1  
A;Note: F14M19.160

Query Match 65.5%; Score 38; DB 2; Length 849;  
Best Local Similarity 75.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QHHYGTPT 8  
| | | | |  
Db 267 QPHYGQPY 274

## RESULT 27

S52792  
Ig kappa chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C;Accession: S52792  
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995  
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A;Reference number: S52789  
A;Accession: S52792  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-129 <ROC>

A;Cross-references: EMBL:X85996; NID:G758598; PIDN:CAA59988.1; PID:G758599  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 63.8%; Score 37; DB 2; Length 129;  
 Best Local Similarity 66.7%; Pred. No. 15;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 9  
 | |||||  
 Db 111 QQSYGTPT 119

RESULT 28  
 B86659  
 hypothetical protein nrdG [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
 C:Species: Lactococcus lactis subsp. lactis  
 C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: B86659  
 R:Boletini, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: B86659  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-199 <SPO>  
 A:Cross-references: GB:AE005176; PID:gl2723135; PIDN:AAK04372.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: nrdG

Query Match 63.8%; Score 37; DB 2; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9  
 | |||||  
 Db 59 YGTPYT 64

RESULT 29  
 S73455  
 fructose-bisphosphate aldolase (EC 4.1.2.13) tar - Mycoplasma pneumoniae (strain ATCC 29  
 N;Alternate names: hypothetical protein B01\_orf288  
 C:Species: Mycoplasma pneumoniae  
 A:Variety: ATCC 29342  
 C>Date: 26-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
 C:Accession: S73455  
 R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk1, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
 A:Reference number: S73327; MUID:97105885; PMID:8948633  
 A:Accession: S73455  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-288 <HTM>  
 A:Cross-references: EMBL:AB000015; GB:U00089; NID:gl673779; PIDN:AAB95777.1; PID:gl67378  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 C:Genetics:  
 A:Gene: tsr  
 A:Genetic code: SGC3  
 A:Superfamily: fructose-bisphosphate aldolase II  
 C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 63.8%; Score 37; DB 2; Length 288;  
 Best Local Similarity 62.5%; Pred. No. 36;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHHYGTPT 8  
 | |||||  
 Db 14 QHHYAVPH 21

RESULT 30  
 D71101

hypothetical protein PH1071 - Pyrococcus horikoshii  
 C:Species: Pyrococcus horikoshii  
 C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 05-Nov-1999  
 C:Accession: D71101  
 R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
 DNA Res. 5, 55-76, 1998  
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic al  
 A:Reference number: A71000; MUID:98344137; PMID:9679194  
 A:Accession: D71101  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-450 <RAW>  
 A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30170.1; PID:di031113; PID:g325748  
 A:Experimental source: strain OT3  
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C:Genetics:  
 A:Gene: PH1071

Query Match 63.8%; Score 37; DB 2; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9  
 | |||||  
 Db 110 YGTPYT 115

RESULT 31  
 D75139  
 hypothetical protein PAB1751 - Pyrococcus abyssi (strain Orsay)  
 C:Species: Pyrococcus abyssi  
 C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C:Accession: D75139  
 R:anonymous, Genoscope  
 submitted to the EMBL Data Library, July 1999  
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
 A:Reference number: A75001  
 A:Accession: D75139  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-451 <RAW>  
 A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49829.1; PID:e151572;  
 A:Experimental source: strain Orsay  
 C:Genetics:  
 A:Gene: PAB1751

Query Match 63.8%; Score 37; DB 2; Length 451;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGTPYT 9  
 | |||||  
 Db 106 YGTPYT 111

RESULT 32  
 T28876  
 hypothetical protein R04E5.10 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T28876  
 R:Miller, N.  
 submitted to the EMBL Data Library, December 1995  
 A:Description: The sequence of C. elegans cosmid R04E5.  
 A:Reference number: Z20535  
 A:Accession: T28876  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-568 <MIL>  
 A:Cross-references: EMBL:U41538; PIDN:AAC48176.1; GSPDB:GN00028; CESP:R04E5.10  
 A:Experimental source: strain Bristol N2; clone R04E5  
 C:Genetics:

A;Gene: CESP:R04B5.10  
A;Map position: X  
A;Introns: 70/3; 108/3; 141/2; 308/3; 331/3; 386/3; 441/1; 474/3; 526/3  
C;Superfamily: Intermediate filament protein Av71

Query Match 63.8%; Score 37; DB 2; Length 568;  
Best Local Similarity 62.5%; Pred. No. 75;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHYGTPTT 9  
Db 427 HHYGSYS 434  
|||||:

RESULT 33  
S30751  
Ig kappa chain precursor V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000  
C;Accession: S30751  
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.  
Nucleic Acids Res. 15, 5496, 1987  
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.  
A;Reference number: S30751; MUID: 87260030; PMID: 3601683  
A;Accession: S30751  
A;Molecule type: mRNA  
A;Residues: 1-152 <GRA>  
A;Cross-references: EMBL:X05877; NID:G52195; PIDN:CAA29301.1; PID:G52196  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;45-119/Domain: immunoglobulin homology <IMM>  
F;138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>

Query Match 62.1%; Score 36; DB 2; Length 152;  
Best Local Similarity 66.7%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QHHYGTPTT 9  
Db 118 QHHYSTPLT 126  
|||||

RESULT 34  
I38617  
zinc finger protein ZNF142 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 05-Nov-1999  
C;Accession: I38617  
R;Tommerup, N.; Vissing, H.  
Genomics 27, 259-264, 1995  
A;Title: Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identified  
A;Reference number: A57785; MUID: 96044430; PMID: 7557990  
A;Accession: I38617  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-173 <RES>  
A;Cross-references: EMBL:U09849; NID:G495569; PIDN:AAC50265.1; PID:G495570  
C;Genetics:  
A;Gene: GDB: ZNF142  
A;Cross-references: GDB: I37047  
A;Map position: 2q34-2q35

Query Match 62.1%; Score 36; DB 2; Length 173;  
Best Local Similarity 85.7%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHHYGTPTT 7  
Db 75 QHHPGTP 81  
|||||

RESULT 35  
E69747

two-component response regulator [YbdK] homolog ybdJ - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C;Accession: E69747  
R;Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallucci, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelie, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Authors: Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID: 98044033; PMID: 9384377  
A;Accession: E69747  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-223 <KUN>  
A;Cross-references: GB:Z99105; GB:AL009126; NID:G2632457; PIDN:CAB11994.1; PID:G2632486  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: ybdJ  
C;Superfamily: ompR protein; response regulator homology  
C;Keywords: phosphoprotein  
F;6-112/Domain: response regulator homology <RRH>  
F;52/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 62.1%; Score 36; DB 2; Length 223;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QHHYGT 6  
Db 117 EHHYGT 122  
|||||

RESULT 36  
AB0440  
hypothetical protein YPO3617 [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C;Accession: AB0440  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F. il. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I. Nature 413, 523-527, 2001  
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A;Reference number: AB0001; MUID: 21470413; PMID: 11586360  
A;Accession: AB0440  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-299 <KUR>  
A;Cross-references: GB:AL590842; PIDN:CAC93086.1; PID:G15981538; GSPDB:GN00175  
C;Genetics:  
A;Gene: YPO3617

Query Match 62.1%; Score 36; DB 2; Length 299;  
Best Local Similarity 83.3%; Pred. No. 57;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHYGTPTT 8  
Db 98 HHCTPTT 103  
|||||

RESULT 37  
C81954

probable transcription activator protein MTR NMA0381 [imported] - Neisseria meningitidis  
C/Species: Neisseria meningitidis  
C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C/Accession: C81954  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jags, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A/Reference number: A81775; MUID:20222556; PMID:10761919  
A/Accession: C81954  
A/Molecule type: DNA  
A/Status: preliminary  
A/Residues: 1-309 <PAR>  
A/Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83682.1; PID:g737913  
A/Experimental source: serogroup A, strain Z2491  
C/Genetics:  
A/Gene: metR; NMA0381  
C/Superfamily: regulatory protein lysR

Query Match 62.1%; Score 36; DB 2; Length 309;  
Best Local Similarity 71.4%; Pred. No. 59;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QHHYGTTP 7  
Db 44 ENHYGTP 50

RESULT 38  
H81011  
transcription regulator, LysR family NMB2055 [imported] - Neisseria meningitidis (strain  
C/Species: Neisseria meningitidis  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C/Accession: H81011  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A/Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A/Reference number: A81000; MUID:20175755; PMID:10710307  
A/Accession: H81011  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-309 <TET>  
A/Cross-references: GB:AE002555; GB:AE002098; NID:g7272310; PIDN:AAF42375.1; PID:g727231  
A/Experimental source: serogroup B, strain MC58  
C/Genetics:  
A/Gene: NMB2055  
C/Superfamily: regulatory protein lysR

Query Match 62.1%; Score 36; DB 2; Length 309;  
Best Local Similarity 71.4%; Pred. No. 59;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QHHYGTTP 7  
Db 44 ENHYGTP 50

RESULT 39  
A43561  
homeotic protein msh-2 - fruit fly (Drosophila melanogaster)  
N/Alternate names: homeotic protein NK-4  
C/Species: Drosophila melanogaster  
C/Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 24-Sep-1999  
C/Accession: A43561; D33976  
R;Bodmer, R.; Jan, L.Y.; Jan, Y.N.  
Development 110, 661-669, 1990  
A/Title: A new homeobox-containing gene, msh-2, is transiently expressed early during me  
A/Reference number: A43561; MUID:91209226; PMID:1982429  
A/Accession: A43561  
A/Status: preliminary

A/Molecule type: mRNA  
A/Residues: 1-416 <BOD>  
A/Cross-references: GB:X55192; NID:g10345; PIDN:CAA38978.1; PID:g10346  
R;Kim, Y.; Nirenberg, M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7716-7720, 1989  
A/Title: Drosophila NK-homeobox genes.  
A/Reference number: A33976; MUID:90046666; PMID:2573058  
A/Accession: D33976  
A/Molecule type: DNA  
A/Residues: 267-416 <KIM>  
A/Cross-references: GB:M27292; NID:g157639; PIDN:AAA28619.1; PID:g552094  
C/Genetics:  
A/Gene: FlyBase:tin  
A/Cross-references: FlyBase:FBgn0004110  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;302-358/Domain: homeobox homology <HOK>

Query Match 62.1%; Score 36; DB 2; Length 416;  
Best Local Similarity 62.5%; Pred. No. 81;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QHHYGTTP 8  
Db 140 QHHGHHPH 147

RESULT 40  
D86440  
unknown protein [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C/Accession: D86440  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: D86440  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-439 <STO>  
A/Cross-references: GB:AE005172; NID:g11054668; PIDN:AAG27888.1; GSPDB:GN00141  
C/Genetics:  
A/Map position: 1

Query Match 62.1%; Score 36; DB 2; Length 439;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 HHVGTTP 8  
Db 108 HHFGTSY 114

Search completed: July 18, 2003, 15:10:47  
Job time : 12.7 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:05 ; Search time 6.5 Seconds  
(without alignments)  
73.950 Million cell updates/sec

Title: US-10-007-790-6  
Perfect score: 30  
Sequence: 1 SCYNA 5  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	215	2 S19431	hypothetical prote
2	30	100.0	463	2 A81337	glutamate-tRNA lig
3	30	100.0	514	2 C64154	hypothetical prote
4	30	100.0	522	2 T28323	ORF MSV162 probabl
5	27	90.0	88	2 B72809	gp86 protein - Myc
6	27	90.0	88	2 S31031	gene 86 protein -
7	27	90.0	108	2 T14799	hypothetical prote
8	27	90.0	137	2 S22515	thionin precursor.
9	27	90.0	195	2 T11982	anthranilate synth
10	27	90.0	246	2 T51829	IB1C3-1 protein [I
11	27	90.0	267	2 B83109	probable transcrip
12	27	90.0	281	1 B47629	cell surface glyco
13	27	90.0	284	2 T25314	hypothetical prote
14	27	90.0	287	2 T23637	hypothetical prote
15	27	90.0	288	2 H81309	hypothetical prote
16	27	90.0	282	2 A10422	conserved hypothet
17	27	90.0	292	2 AG0900	conserved hypothet
18	27	90.0	298	2 C65106	hypothetical 33.2K
19	27	90.0	298	2 H91133	hypothetical prote
20	27	90.0	298	2 C85979	hypothetical prote
21	27	90.0	325	2 T33297	hypothetical prote
22	27	90.0	325	2 F82350	lipid A biosynthes
23	27	90.0	340	1 B55973	transcription fact
24	27	90.0	349	1 I51739	transcription fact
25	27	90.0	358	1 A55973	transcription fact
26	27	90.0	358	1 I51735	transcription fact
27	27	90.0	359	1 I51734	transcription fact
28	27	90.0	359	1 T46160	caffeic acid O-met
29	27	90.0	363	1 C55973	transcription fact

30	27	90.0	388	2 T49253	purple acid phosph
31	27	90.0	396	2 B71414	hypothetical prote
32	27	90.0	422	2 C91296	hypothetical prote
33	27	90.0	446	2 A84940	pmbA protein [impo
34	27	90.0	460	2 A96555	unknown protein [i
35	27	90.0	484	2 S36339	pherophorin II - v
36	27	90.0	499	2 S74224	aldehyde dehydroge
37	27	90.0	512	1 A55684	aldehyde dehydroge
38	27	90.0	516	2 S56604	hypothetical 58.0K
39	27	90.0	516	2 E86137	hypothetical prote
40	27	90.0	516	2 AB1073	conserved hypothet
41	27	90.0	552	2 JC7666	serine-type carbox
42	27	90.0	650	2 T44660	nitrous-oxide redu
43	27	90.0	663	2 AE3290	propionate-CoA lig
44	27	90.0	665	2 T25228	hypothetical prote
45	27	90.0	714	2 F86345	F16F4.8 protein -

ALIGNMENTS

RESULT 1

S19431 hypothetical protein YCR020c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 29-Oct-1999

C:Accession: S19431; S07692

R:Feldmann, H.; Mannhaupt, G.; Vetter, I.

submitted to the Protein Sequence Database, March 1992

A:Reference number: S19429

A:Accession: S19431

A:Molecule type: DNA

A:Residues: 1-215 <PEL>

A:Cross-references: EMBL:X59720; NID:G1907116; PIDN:CAA42311.1; PID:e264484; PID:G190716;

R:Toh-e, A.; Sahashi, Y.

Yeast 1, 159-171, 1985

A:Title: The PET18 locus of Saccharomyces cerevisiae: a complex locus containing multiple

A:Reference number: S07692; MUID:89131254; PMID:3916862

A:Accession: S07692

A:Molecule type: DNA

A:Residues: 1-39, 'M', 41-103, 'G', 105-121, 'S', 123-215 <TOH>

C:Genetics:

A:Gene: SGD:PET18

A:Cross-references: SGD:S0000613; MIPS:YCR020C

A:Map position: 3R

Query Match 100.0%; Score 30; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

DB 211 SCYNA 215

RESULT 2

A81337

glutamate-tRNA ligase (EC 6.1.1.17) Cj1288c [imported] - Campylobacter jejuni (strain NC7

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002

C:Accession: A81337

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: A81337

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-463 <PAR>

A:Cross-references: GB:AL139077; GB:AL111168; NID:G96968444; PIDN:CAB73541.1; PID:G9696872C

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A;Gene: gltX2; Cj1288c  
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology  
C;Keywords: ligase

Query Match 100.0%; Score 30; DB 2; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
|||||  
Db 299 SCYNA 303

## RESULT 3

C64154  
hypothetical protein HI0521 - Haemophilus influenzae (strain Rd KW20)  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999  
C;Accession: C64154  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;  
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.;  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: C64154  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-514 <TIGR>  
A;Cross-references: GB:U32734; GB:U42023; NID:G1573498; PIDN:AAC22179.1; PID:G1573504; T  
A;Note: best homolog was a hypothetical protein from Escherichia coli

Query Match 100.0%; Score 30; DB 2; Length 514;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
|||||  
Db 230 SCYNA 234

## RESULT 4

T28323  
ORF MSV162 probable NAD+ dependent DNA ligase - Melanoplus sanguinipes entomopoxvirus  
C;Species: Melanoplus sanguinipes entomopoxvirus  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T28323  
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.  
J. Virol. 73, 533-552, 1999  
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.  
A;Reference number: Z20484; MUID:99102612; PMID:9847359  
A;Accession: T28323  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-522 <AFO>  
A;Cross-references: EMBL:AF063866; NID:G4049647; PIDN:AAC97679.1; PID:G4049719  
C;Genetics:  
A;Note: MSV162

Query Match 100.0%; Score 30; DB 2; Length 522;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
|||||  
Db 321 SCYNA 325

## RESULT 5

B72809  
gp86 protein - Mycobacterium phage D29  
C;Species: Mycobacterium phage D29

C;Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 20-Apr-2001  
C;Accession: B72809  
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.  
J. Mol. Biol. 279, 143-164, 1998  
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.  
A;Reference number: A72800; MUID:98300335; PMID:9636706  
A;Accession: B72809  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-88 <FOR>  
A;Cross-references: GB:AF022214; NID:G3172250; PIDN:AAC18516.1; PID:G3172223  
C;Genetics:  
A;Gene: 86

Query Match 90.0%; Score 27; DB 2; Length 88;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
|||||  
Db 51 ACYNA 55

## RESULT 6

S31031  
gene 86 protein - Mycobacterium phage L5  
C;Species: Mycobacterium phage L5  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Oct-1999  
C;Accession: S31031  
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.  
Mol. Microbiol. 7, 407-417, 1993  
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic transfer  
A;Reference number: S30949; MUID:93211283; PMID:8459767  
A;Accession: S31031  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-88 <DON>  
A;Cross-references: EMBL:Z18946; NID:G15859; PIDN:CAA79462.1; PID:G15942  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
C;Genetics:  
A;Gene: 86

Query Match 90.0%; Score 27; DB 2; Length 88;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
|||||  
Db 51 ACYNA 55

## RESULT 7

T14799  
hypothetical protein DKFPz434N221.1 - human.  
C;Species: Homo sapiens (man)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 02-Jun-2000  
C;Accession: T14799  
R;Foustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999  
A;Reference number: Z18183  
A;Accession: T14799  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-108 <FOU>  
A;Cross-references: EMBL:AL110299  
A;Experimental source: adult testis; clone DKFPz434N221  
C;Genetics:  
A;Note: DKFPz434N221.1  
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 90.0%; Score 27; DB 2; Length 108;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 SCYNA 5
      :||||
Db      62 NCYNA 66

RESULT 8
S22515
thionin precursor, leaf - barley
N;Alternate names: jasmonate-induced protein 2
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-feb-1994 #text_change 17-Mar-1999
C;Accession: S22515
R;Andersen, I.; Becker, W.; Schlueter, K.; Burges, J.; Parthier, B.; Apel, K.
Plant Mol. Biol. 19, 193-204, 1992
A;Title: The identification of leaf thionin as one of the main jasmonate-induced protein
A;Reference number: S22514; MUID:92322947; PMID:1377959
A;Accession: S22515
A;Molecule type: mRNA
A;Residues: 1-137 <AND>
A;Cross-references: EMBL:S39760
C;Superfamily: viscotoxin

      Query Match          90.0%; Score 27; DB 2; Length 137;
      Best Local Similarity 80.0%; Pred. No. 1.7e+02;
      Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      :||||
Db      39 NCYNA 43

RESULT 9
Tl1982
antranilate synthase component II - red alga (Cyanidium caldarium) chloroplast
C;Species: chloroplast Cyanidium caldarium
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C;Accession: Tl1982
R;Gloeckner, G.; Rosenthal, A.; Valentin, K.
submitted to the EMBL Data Library, September 1997
A;Description: Organisation of 46 kb of the Cyanidium caldarium RK1 plastid genome.
A;Reference number: Z17374
A;Accession: Tl1982
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-195 <GLO>
A;Cross-references: EMBL:AF022186; NID:G2465730; PIDN:AAB82675.1; PID:G2465746
A;Experimental source: strain RK1
C;Genetics:

A;Genome: chloroplast
A;Note: trpG
C;Superfamily: glutamine amidotransferase; trpG homology
C;Keywords: chloroplast
F;2-190/Domain: trpG homology <TRG>

      Query Match          90.0%; Score 27; DB 2; Length 195;
      Best Local Similarity 80.0%; Pred. No. 2.2e+02;
      Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      :||||
Db      87 TCYNA 91

RESULT 10
T51829
IBIC3-1 protein [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C;Accession: T51829
R;Aubourg, S.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z25476

```

```

A;Accession: T51829
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-246 <AUB>
A;Cross-references: EMBL:AJ011845; PIDN:CAA09808.1
C;Genetics:

A;Gene: IBIC3-1
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F16G20.50

      Query Match          90.0%; Score 27; DB 2; Length 246;
      Best Local Similarity 80.0%; Pred. No. 2.6e+02;
      Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      :||||
Db      186 SCYNS 190

RESULT 11
B83109
probable transcription regulator PA4288 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83109
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: B83109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Cross-references: GB:AE004845; GB:AE004091; NID:99950507; PIDN:AG07676.1; GSPDB:GN001;
A;Experimental source: strain PA01
C;Genetics:

A;Gene: PA4288

      Query Match          90.0%; Score 27; DB 2; Length 267;
      Best Local Similarity 80.0%; Pred. No. 2.8e+02;
      Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYNA 5
      :||||
Db      76 SCYNS 80

RESULT 12
B47629
cell surface glycoprotein CD37 - rat
N;Alternate names: leukocyte antigen CD37
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: B47629; JCI501
R;Classon, B.J.; Williams, A.F.; Willis, A.C.; Seed, B.; Stamenkovic, I.
J. Exp. Med. 172, 1007, 1990
A;Reference number: A47629; MUID:90354767; PMID:2388030
A;Accession: B47629
A;Molecule type: mRNA
A;Residues: 1-281 <CLA>
A;Cross-references: EMBL:X53517; NID:955911; PIDN:CAA37596.1; PID:955912
C;Comment: This antigen is expressed abundantly on B lymphocytes and is also seen at low
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lymphocyte; transmembrane protein
F;2-12/Domain: intracellular #status predicted <CY1>
F;13-38/Domain: transmembrane #status predicted <TM1>
F;39-59/Domain: extracellular #status predicted <EX1>
F;60-80/Domain: transmembrane #status predicted <TM2>
F;81-85/Domain: intracellular #status predicted <CY2>
F;86-110/Domain: transmembrane #status predicted <TM3>
F;111-241/Domain: extracellular #status predicted <EX2>

```

F;242-267/Domain: transmembrane #status predicted <TM4>  
 F;268-278/Domain: intracellular #status predicted <CY3>  
 F;170,183,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.0%; Score 27; DB 1; Length 281;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
 Db 180 SCYNS 184

RESULT 13  
 T25314  
 hypothetical protein T26E4.13 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 26-May-2000  
 C;Accession: T25314  
 R;McMurray, A.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: Z20013  
 A;Accession: T25314  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-284 <WIL>  
 A;Cross-references: EMBL:Z81132; PIDN:CAB03439.1; GSPDB:GN00023; CESP:T26E4.13  
 A;Experimental source: clone T26E4  
 C;Genetics:  
 A;Gene: CESP:T26E4.13  
 A;Map position: 5  
 A;Introns: 206/2  
 C;Superfamily: Caenorhabditis elegans hypothetical protein B0250.6

Query Match 90.0%; Score 27; DB 2; Length 284;  
 Best Local Similarity 80.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
 Db 164 SCYNS 168

RESULT 14  
 T23637  
 hypothetical protein M01B2.4 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 26-May-2000  
 C;Accession: T23637  
 R;Lloyd, C.  
 submitted to the EMBL Data Library, November 1996  
 A;Reference number: Z19776  
 A;Accession: T23637  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-287 <WIL>  
 A;Cross-references: EMBL:Z83116; PIDN:CAB05562.1; GSPDB:GN00023; CESP:M01B2.4  
 C;Genetics:  
 A;Gene: CESP:M01B2.4  
 A;Map position: 5  
 A;Introns: 211/3  
 C;Superfamily: Caenorhabditis elegans hypothetical protein B0250.6

Query Match 90.0%; Score 27; DB 2; Length 287;  
 Best Local Similarity 80.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
 Db 166 SCYNS 170

## RESULT 15

H81309  
 hypothetical protein Cj1069 [imported] - Campylobacter jejuni (strain NCTC 11168)  
 C;Species: Campylobacter jejuni  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C;Accession: H81309  
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
 Nature 403, 665-668, 2000  
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
 A;Reference number: A81250; MUID:20150912; PMID:10688204  
 A;Accession: H81309  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-288 <PAR>  
 A;Cross-references: GB:AL139077; GB:AL111168; NID:G6968444; PIDN:CAB73324.1; PID:G696850  
 A;Experimental source: serotype O2, strain NCTC 11168  
 C;Genetics:  
 A;Gene: Cj1069  
 C;Superfamily: conserved hypothetical protein HI0461

Query Match 90.0%; Score 27; DB 2; Length 288;  
 Best Local Similarity 80.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
 Db 63 ACYNA 67

## RESULT 16

AI0422  
 conserved hypothetical protein YPO3480 [imported] - Yersinia pestis (strain CO92)  
 C;Species: Yersinia pestis  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
 C;Accession: AI0422  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
 deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F  
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I  
 Nature 413, 523-527, 2001  
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: AI0422  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-292 <KOR>  
 A;Cross-references: GB:AL590842; PIDN:CAC92709.1; PID:G15981404; GSPDB:GN00175  
 C;Genetics:  
 A;Gene: YPO3480  
 C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 292;  
 Best Local Similarity 80.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5  
 Db 117 NCYNA 121

## RESULT 17

AG0900  
 conserved hypothetical protein STY3458 [imported] - Salmonella enterica subsp. enterica  
 C;Species: Salmonella enterica subsp. enterica serovar Typhi  
 A;Note: this species has also been called Salmonella typhi  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
 C;Accession: AG0900  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar

A;Reference number: AB0502; PMID:11677608  
A;Accession: AG0900  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-292 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD07797.1; PID:G16504345; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY3458  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 292;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 117 NCYNA 121

RESULT 18  
C65106  
hypothetical 33.2K protein b3159 - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C;Accession: C65106  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: C65106  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-298 <BLAT>  
A;Cross-references: GB:AE000396; GB:U00096; NID:G1789536; PIDN:AACT6153.1; PID:G1789549;  
A;Experimental source: strain K-12, substrain MG1655  
C;Genetics:  
A;Gene: ynbV  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 123 NCYNA 127

RESULT 19  
H91133  
hypothetical protein ECs4040 [imported] - Escherichia coli (strain O157:H7, substrain R1)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C;Accession: H91133  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome analysis.  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H91133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-298 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA837463.1; PID:G13363513; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: ECs4040  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 123 NCYNA 127

RESULT 19  
H91133  
hypothetical protein ECs4040 [imported] - Escherichia coli (strain O157:H7, substrain R1)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C;Accession: H91133  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome analysis.  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H91133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-298 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA837463.1; PID:G13363513; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: ECs4040  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 123 NCYNA 127

RESULT 19  
H91133  
hypothetical protein ECs4040 [imported] - Escherichia coli (strain O157:H7, substrain R1)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C;Accession: H91133  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome analysis.  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H91133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-298 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA837463.1; PID:G13363513; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: ECs4040  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 123 NCYNA 127

RESULT 19  
H91133  
hypothetical protein ECs4040 [imported] - Escherichia coli (strain O157:H7, substrain R1)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C;Accession: H91133  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome analysis.  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H91133  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-298 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA837463.1; PID:G13363513; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: ECs4040  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 123 NCYNA 127

RESULT 20  
C85979  
hypothetical protein yhbV [imported] - Escherichia coli (strain O157:H7, substrain EDL93;  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C;Accession: C85979  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: C85979  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-298 <STO>  
A;Cross-references: GB:AE005174; NID:G12517767; PIDN:AAG58295.1; GSPDB:GN00145; UWGP:Z45;  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: yhbV  
C;Superfamily: Escherichia coli hypothetical 33.2K protein b3159

Query Match 90.0%; Score 27; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 123 NCYNA 127

RESULT 21  
T33297  
hypothetical protein H05B21.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jan-2000  
C;Accession: T33297  
R;Miller, N.  
submitted to the EMBL Data Library, May 1998  
A;Description: The sequence of C. elegans cosmid H05B21.  
A;Reference number: Z21317  
A;Accession: T33297  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-325 <MIL>  
A;Cross-references: EMBL:AF068717; PIDN:AAC17763.1; GSPDB:GN00023; CESP:H05B21.2  
A;Experimental source: strain Bristol N2; clone H05B21  
C;Genetics:  
A;Gene: CESP:H05B21.2  
A;Map position: 5  
A;Introns: 104/1  
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 90.0%; Score 27; DB 2; Length 325;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 2 NCYNA 6

RESULT 22  
F82350  
lipid A biosynthesis (kdo)2-(lauroyl)-lipid IVA acyltransferase VC0212 [imported] - Vibrio  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C;Accession: F82350

R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermlaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82350

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <HEI>

A;Cross-references: GB:AE004111; GB:AE003852; NID:99654614; PIDN:AAF93388.1; GSPDB:GN001

A;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc

C;Genetics:

A;Gene: VC0212

A;Map position: 1

Query Match 90.0%; Score 27; DB 2; Length 325;

Best Local Similarity 80.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 252 SCYNS 256

|||||

#### RESULT 23

B55973

N;transcription factor isl-2b - chinook salmon (fragment)

N;Alternate names: insulin enhancer-binding protein isl-2b; islet-2b protein

C;Species: Oncorhynchus tshawytscha (chinook salmon)

C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text\_change 16-Jul-1999

C;Accession: B55973; S52091; S19956

R;Gong, Z.; Hui, C.; Hew, C.L.

J. Biol. Chem. 270, 3335-3345, 1995

A;Title: Presence of isl-1-related LIM domain homeobox genes in teleost and their similar

A;Reference number: A55973; MUID:95155429; PMID:7852419

A;Accession: B55973

A;Molecule type: mRNA

A;Residues: 1-340 <GON>

A;Cross-references: EMBL:X64884; NID:964208; PIDN:CAA46102.1; PID:964209

A;Note: authors translated the codon CTG for residue 251 as Met, and ATG for residue 256

R;Gong, Z.; Hew, C.L.

Biochim. Biophys. Acta 1260, 349-354, 1995

A;Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynch

A;Reference number: S52089; MUID:95178560; PMID:7873614

A;Accession: S52091

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-340 <G02>

A;Cross-references: EMBL:X64884; NID:964208; PIDN:CAA46102.1; PID:964209

A;Note: the authors translated the codon CAG for residue 105 as His, GTG for residue 107

C;Genetics:

A;Gene: isl-2b

C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h

C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc

F;9-62/Domain: LIM metal-binding repeat homology <LIM1>

F;71-124/Domain: LIM metal-binding repeat homology <LIM2>

F;173-229/Domain: homeobox homology <HOX>

Query Match 90.0%; Score 27; DB 1; Length 340;

Best Local Similarity 80.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 189 TCYNA 193

|||||

#### RESULT 24

B51739

N;transcription factor isl-1 - zebra fish

N;Alternate names: insulin enhancer-binding protein isl-1; islet-1 protein

C;Species: Brachydanio rerio (zebra fish)

C;Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999

C;Accession: I51739

R;Inoue, A.; Takahashi, M.; Hotta, K.; Hotta, Y.; Okamoto, H.

Dev. Dyn. 199, 1-11, 1994

A;Title: Developmental regulation of islet-1 mRNA expression during neuronal differentiation

A;Reference number: I51739; MUID:94220748; PMID:8167375

A;Accession: I51739

A;Status: preliminary; translated from GB/EMBL/DD8J

A;Molecule type: mRNA

A;Residues: 1-349 <INO>

A;Cross-references: GB:D21135; NID:9497897; PIDN:BAA04670.1; PID:9497898

C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h

C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc

F;17-70/Domain: LIM metal-binding repeat homology <LIM1>

F;79-132/Domain: LIM metal-binding repeat homology <LIM2>

F;182-238/Domain: homeobox homology <HOX>

Query Match 90.0%; Score 27; DB 1; Length 349;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 198 TCYNA 202

|||||

#### RESULT 25

A55973

N;transcription factor isl-2a, long form - chinook salmon

N;Alternate names: insulin enhancer-binding protein isl-2a; islet-2a protein

C;Species: Oncorhynchus tshawytscha (chinook salmon)

C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text\_change 07-May-1999

C;Accession: A55973; S52092; S19957

R;Gong, Z.; Hui, C.; Hew, C.L.

J. Biol. Chem. 270, 3335-3345, 1995

A;Title: Presence of isl-1-related LIM domain homeobox genes in teleost and their similar

A;Reference number: A55973; MUID:95155429; PMID:7852419

A;Accession: A55973

A;Molecule type: mRNA

A;Residues: 1-358 <GON>

A;Cross-references: EMBL:X64885

R;Gong, Z.; Hew, C.L.

Biochim. Biophys. Acta 1260, 349-354, 1995

A;Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynch

A;Reference number: S52089; MUID:95178560; PMID:7873614

A;Accession: S52092

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-358 <GO2>

A;Cross-references: EMBL:X64885

A;Note: the authors translated the codon GAG for residue 135 as Asp

C;Genetics:

A;Gene: isl-2a

A;Introns: 83/2

C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h

C;Keywords: alternative splicing; DNA binding; duplication; homeobox; nucleus; transcript

F;27-80/Domain: LIM metal-binding repeat homology <LIM1>

F;89-142/Domain: LIM metal-binding repeat homology <LIM2>

F;191-247/Domain: homeobox homology <HOX>

Query Match 90.0%; Score 27; DB 1; Length 358;

Best Local Similarity 80.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 207 TCYNA 211

|||||

#### RESULT 26

I51735

N;transcription factor isl-3 - zebra fish

N;Alternate names: insulin enhancer-binding protein isl-3; islet-3 protein

C;Species: Brachydanio rerio (zebra fish)  
C;Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999  
C;Accession: I51735  
R;Tokumoto, M.; Gong, Z.; Tsubokawa, T.; Hew, C.L.; Uyemura, K.; Hotta, Y.; Okamoto, H.  
Dev. Biol. 171, 578-589, 1995  
A;Title: Molecular heterogeneity among primary motoneurons and within myotomes revealed  
A;Reference number: I51734; MUID:96005022; PMID:7556938  
A;Accession: I51735  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-358 <TK>  
A;Cross-references: GB:D38454; NID:g1037167; PIDN:BAA07485.1; PID:g1037168  
C;Genetics:  
A;Gene: isl-3  
C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat  
C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc  
F;27-80/Domain: LIM metal-binding repeat homology <LIM1>  
F;89-142/Domain: LIM metal-binding repeat homology <LIM2>  
F;192-248/Domain: homeobox homology <HOX>

Query Match 90.0%; Score 27; DB 1; Length 358;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 208 TCYNA 212

RESULT 27  
I51734  
transcription factor isl-2 - zebra fish  
N;Alternate names: insulin enhancer-binding protein isl-2; islet-2 protein  
C;Species: Brachydanio rerio (zebra fish)  
C;Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999  
C;Accession: I51734; S57407  
R;Tokumoto, M.; Gong, Z.; Tsubokawa, T.; Hew, C.L.; Uyemura, K.; Hotta, Y.; Okamoto, H.  
Dev. Biol. 171, 578-589, 1995  
A;Title: Molecular heterogeneity among primary motoneurons and within myotomes revealed  
A;Reference number: I51734; MUID:96005022; PMID:7556938  
A;Accession: I51734  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-359 <TK>  
A;Cross-references: GB:D38453; NID:g1037165; PIDN:BAA07484.1; PID:g1037166  
R;Appel, B.; Korzh, V.; Glasgow, E.; Thor, S.; Edlund, T.; Dawid, L.; Eisen, J.  
submitted to the EMBL Data Library, June 1995  
A;Description: Motoneuron fate specification and patterned LIM homeobox gene expression  
A;Reference number: S57407  
A;Accession: S57407  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-359 <APP>  
A;Cross-references: EMBL:X88805; NID:g871000; PIDN:CAA61283.1; PID:g871001  
C;Genetics:  
A;Gene: isl-2  
C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat  
C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc  
F;27-80/Domain: LIM metal-binding repeat homology <LIM1>  
F;89-142/Domain: LIM metal-binding repeat homology <LIM2>  
F;192-248/Domain: homeobox homology <HOX>

Query Match 90.0%; Score 27; DB 1; Length 359;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 208 TCYNA 212

RESULT 28  
T46160

cafeic acid O-methyltransferase-like protein - Arabidopsis thaliana  
N;Alternate names: protein T4D2.70  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 18-Feb-2000  
C;Accession: T46160  
R;Yakutara, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, December 1999  
A;Reference number: Z23025  
A;Accession: T46160  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-359 <NYA>  
A;Cross-references: EMBL:AL132958  
A;Experimental source: cultivar Columbia; BAC clone T4D2  
C;Genetics:  
A;Map position: 3  
A;Introns: 126/3; 239/1; 260/3  
A;Note: T4D2.70  
C;Superfamily: O-methyltransferase

Query Match 90.0%; Score 27; DB 2; Length 359;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 277 NCYNA 281

RESULT 29  
C55973  
transcription factor isl-3 - chinook salmon  
N;Alternate names: insulin enhancer-binding protein isl-3; islet-3 protein  
C;Species: Oncorhynchus tshawytscha (chinook salmon)  
C;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 07-May-1999  
C;Accession: C55973; S52090  
R;Gong, Z.; Hui, C.; Hew, C.L.  
J. Biol. Chem. 270, 3335-3345, 1995  
A;Title: Presence of isl-3-related LIM domain homeobox genes in teleost and their similar  
A;Reference number: A55973; MUID:95155429; PMID:7852419  
A;Accession: C55973  
A;Molecule type: mRNA  
A;Residues: 1-363 <GON>  
A;Cross-references: GB:X64883  
R;Gong, Z.; Hew, C.L.  
Biochim. Biophys. Acta 1260, 349-354, 1995  
A;Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus  
A;Reference number: S52089; MUID:95178560; PMID:7873614  
A;Accession: S52090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-82, 'IWNKMKMOPGIQQQ' <GO2>  
A;Cross-references: EMBL:X64883  
A;Note: alternative splice form  
C;Genetics:  
A;Gene: isl-3  
C;Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat  
C;Keywords: alternative splicing; DNA binding; duplication; homeobox; nucleus; transcript  
F;27-80/Domain: LIM metal-binding repeat homology <LIM1>  
F;89-142/Domain: LIM metal-binding repeat homology <LIM2>  
F;192-248/Domain: homeobox homology <HOX>

Query Match 90.0%; Score 27; DB 1; Length 363;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 208 TCYNA 212

RESULT 30  
T49253

purple acid phosphatase-related protein F12M12.90 [similarity] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 14-Dec-2001  
 C;Accession: T49253  
 R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;  
 submitted to the Protein Sequence Database, May 2000  
 A;Reference number: 225020  
 A;Accession: T49253  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-388 <OR>  
 A;Cross-references: EMBL:AL355775; GSPDB:GN00061; ATSP:F12M12.90  
 A;Experimental source: cultivar Columbia; BAC clone F12M12  
 C;Genetics:  
 A;Gene: ATSP:F12M12.90  
 A;Map position: 3  
 A;Introns: 56/3; 126/3; 191/3; 219/3; 323/2  
 C;Superfamily: kidney bean purple acid phosphatase; phosphoesterase core homology

Query Match 90.0%; Score 27; DB 2; Length 388;  
 Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 DB 49 ACYNA 53

RESULT 31  
 B71414  
 Hypothetical protein - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 A;Variety: Columbia  
 C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 20-Jun-2000  
 C;Accession: B71414  
 R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel  
 vanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
 Nature 391, 485-488, 1998  
 A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech  
 erhoft, A.; Moors, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And  
 C.; Chalmatzis, N.  
 A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
 A;Reference number: A71400; MUID:98121113; PMID:9461215  
 A;Accession: B71414  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-396 <BEV>  
 A;Cross-references: GB:297337; NID:g2244829; PID:g2244862  
 C;Genetics:  
 A;Map position: 4COP9-4G3845  
 C;Superfamily: Arabidopsis thaliana hypothetical protein F16G20.50

Query Match 90.0%; Score 27; DB 2; Length 396;  
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 DB 232 SCYNS 236

RESULT 32  
 C91296  
 Hypothetical protein EC5339 [imported] - Escherichia coli (strain O157:H7, substrain R1  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
 C;Accession: C91296  
 R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend  
 A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C91296  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-422 <HAY>  
 A;Cross-references: GB:BA000007; PIDN:BA38762.1; PID:g13364817; GSPDB:GN00154  
 A;Experimental source: strain O157:H7, substrain R1MD 0509952  
 C;Genetics:  
 A;Gene: EC5339

Query Match 90.0%; Score 27; DB 2; Length 422;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 DB 235 SCYNS 239

RESULT 33  
 A84940  
 pmbA protein [imported] - Buchnera sp. (strain APS)  
 C;Species: Buchnera sp.  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
 C;Accession: A84940  
 R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
 Nature 407, 81-86, 2000  
 A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
 A;Reference number: A84930; MUID:20445173; PMID:10993077  
 A;Accession: A84940  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-446 <STO>  
 A;Cross-references: GB:AP000398; GSPDB:GN00144  
 A;Experimental source: strain APS  
 C;Genetics:  
 A;Gene: pmbA; BU089  
 C;Superfamily: Escherichia coli pmbA protein

Query Match 90.0%; Score 27; DB 2; Length 446;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 DB 326 NCYNA 330

RESULT 34  
 A96555  
 unknown protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C;Accession: A96555  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huiziar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: A96555  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-460 <STO>  
 A;Cross-references: GB:AE005173; NID:g11094774; PIDN:AAG29707.1; GSPDB:GN00141  
 C;Genetics:  
 A;Gene: F19C24.14  
 A;Map position: 1

Query Match 90.0%; Score 27; DB 2; Length 460;  
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :||||  
 Db 296 TCYNA 300

RESULT 35  
 S36339  
 C;Species: Volvox carteri (fragment)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
 C;Accession: S36339; S37760; S28268  
 R;Sumpster, M.; Berg, E.; Wenzl, S.; Godl, K.  
 EMBO J. 12, 831-836, 1993  
 A;Title: How a sex pheromone might act at a concentration below 10<sup>-16</sup> M.  
 A;Reference number: S36338; MUID:93209229; PMID:8458341  
 A;Accession: S36339  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-484 <SUM>  
 A;Cross-references: EMBL:X69802; NID:g311360; PIDN:CAB56809.1; PID:g6006628  
 A;Accession: S37760  
 A;Molecule type: protein  
 A;Residues: 1-13;182-215,413-441 <SU2>  
 C;Keywords: pheromone

Query Match 90.0%; Score 27; DB 2; Length 484;  
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :||||  
 Db 376 TCYNA 380

RESULT 36  
 S74224  
 A;Title: aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 2 - mouse  
 N;Alternate names: retinaldehyde-specific dehydrogenase  
 C;Species: Mus musculus (house mouse)  
 C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002  
 C;Accession: S74224  
 R;Zhao, D.; McCaffery, P.; Ivins, K.J.; Neve, R.L.; Hogan, P.; Chin, W.W.; Draeger, U.C.  
 Eur. J. Biochem. 240, 15-22, 1996  
 A;Title: Molecular identification of a major retinoic-acid-synthesizing enzyme, a retinaldehyde dehydrogenase, in mouse brain  
 A;Reference number: S74224; MUID:96390857; PMID:8797830  
 A;Accession: S74224  
 A;Molecule type: mRNA  
 A;Residues: 1-499 <ZHA>  
 A;Cross-references: EMBL:X99273; NID:g1430868; PIDN:CAA67666.1; PID:g1430869  
 A;Experimental source: strain C3H/He; cell type embryonal carcinoma; cell line P19 teratocarcinoma  
 C;Genetics: RALDH-2  
 A;Gene: RALDH-2  
 C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology  
 C;Keywords: NAD; oxidoreductase  
 F;57-321/Domain: aldehyde dehydrogenase homology <ALDH>  
 F;193-273/Domain: NAD binding #status predicted <NAD>  
 F;257,301/Active site: Glu, Cys #status predicted  
 F;454/Binding site: NAD (Cys) #status predicted

Query Match 90.0%; Score 27; DB 2; Length 499;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :||||  
 Db 453 NCYNA 457

RESULT 37

A55684  
 A;Title: aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 6 precursor, salivary - human  
 C;Species: Homo sapiens (man)  
 C;Date: 03-Mar-1995 #sequence\_revision 31-Jan-1997 #text\_change 03-Jun-2002  
 C;Accession: A55684  
 R;Hsu, L.C.; Chang, W.C.; Hiraoka, L.; Hsieh, C.L.  
 Genomics 24, 333-341, 1994  
 A;Title: Molecular cloning, genomic organization, and chromosomal localization of an aldehyde dehydrogenase gene  
 A;Reference number: A55684; MUID:95213025; PMID:7698756  
 A;Accession: A55684  
 A;Molecule type: mRNA; DNA  
 A;Residues: 1-512 <HSU>  
 A;Cross-references: GB:U07919; NID:9958997; PIDN:AAA79036.1; PID:g544482  
 C;Comment: This isozyme is found at highest levels in saliva, stomach, and kidney and at lower levels in heart, liver, and muscle  
 C;Genetics:  
 A;Gene: GDB:ALDH6  
 A;Cross-references: GDB:364103; OMIM:600463  
 A;Map position: 15q26-15q26  
 A;Introns: 33/3; 68/3; 115/3; 159/1; 179/3; 222/3; 260/3; 295/1; 356/3; 411/3; 464/2; 481/3  
 C;Function:  
 A;Description: catalyzes oxidation of an aldehyde to an acid using NAD+ and water  
 A;Note: enzymes with this activity are involved in diverse metabolic pathways in various tissues  
 C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology  
 C;Keywords: NAD; oxidoreductase; saliva  
 F;70-334/Domain: aldehyde dehydrogenase homology <ALDH>  
 F;280,314/Active site: Glu, Cys #status predicted  
 F;467/Binding site: NAD (Cys) #status predicted

Query Match 90.0%; Score 27; DB 1; Length 512;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :||||  
 Db 466 NCYNA 470

RESULT 38  
 S56604  
 A;Title: hypothetical 58.0K protein (osmy-deoc intergenic region) - Escherichia coli (strain K-12)  
 N;Alternate names: hypothetical protein f516  
 C;Species: Escherichia coli  
 C;Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 01-Mar-2002  
 C;Accession: S56604; C65253  
 R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.  
 Nucleic Acids Res. 23, 2105-2119, 1995  
 A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 to 93.2 Mb  
 A;Reference number: S56314; MUID:95334362; PMID:7610040  
 A;Accession: S56604  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-516 <BUR>  
 A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97276.1; PID:g537220  
 A;Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1994  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collier, A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of Escherichia coli K-12.  
 A;Reference number: A6720; MUID:97426617; PMID:9278503  
 A;Accession: C65253  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-516 <BLAT>  
 A;Cross-references: GB:AE000508; GB:U00096; NID:G2367382; PIDN:AAC77333.1; PID:g1790840;  
 A;Experimental source: strain K-12, substrain MG1655  
 C;Genetics:  
 A;Gene: Y1J1

Query Match 90.0%; Score 27; DB 2; Length 516;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5

```
Db      235 SCYNS 239
|||||
RESULT 39
E86137
hypothetical protein yjji [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E86137
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: E86137
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: GB:AE005174; NID:gl2519407; PIDN:AG59561.1; GSPDB:GN00145; UWGP:Z59
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yjji

Query Match      90.0%; Score 27; DB 2; Length 516;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SCYNA 5
|||||
Db      235 SCYNS 239

RESULT 40
AB1073
conserved hypothetical protein STY4917 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB1073
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
. S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
C:Accession: AB1073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03401.1; PID:gl5050670; GSPDB:GN00176
C:Genetics:
A:Gene: STY4917

Query Match      90.0%; Score 27; DB 2; Length 516;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SCYNA 5
|||||
Db      235 SCYNS 239

Search completed: July 18, 2003, 15:10:43
Job time : 7.5 secs
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:20 ; Search time 3.1 seconds  
(without alignments)  
66.897 Million cell updates/sec

Title: US-10-007-790-6  
Perfect score: 30  
Sequence: 1 SCYNA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	30	100.0	215	1	PT18_YEAST	P25362 saccharomyc
2	30	100.0	463	1	SYE2_CAMJE	O52914 campylobact
3	30	100.0	514	1	YJJI_HABIN	P44744 haemophilus
4	27	90.0	88	1	VG86_BPM2	O64267 mycobacteri
5	27	90.0	88	1	VG86_BPM5	O05303 mycobacteri
6	27	90.0	137	1	THN5_HORVU	P09617 hordeum vul
7	27	90.0	185	1	TRPG_CYACA	O19914 cyanidium c
8	27	90.0	281	1	CD37_MOUSE	O61470 mus musculu
9	27	90.0	281	1	CD37_RAT	P31053 rattus norv
10	27	90.0	298	1	YHBV_ECOLI	P45475 escherichia
11	27	90.0	340	1	IS2B_ONCTS	P50212 oncorhynch
12	27	90.0	349	1	ISL1_BRARE	P53405 brachydanio
13	27	90.0	358	1	IS2A_ONCTS	P53408 oncorhynch
14	27	90.0	358	1	ISL3_BRARE	P53407 brachydanio
15	27	90.0	359	1	ISL2_BRARE	P53406 brachydanio
16	27	90.0	363	1	ISL3_ONCTS	P53409 oncorhynch
17	27	90.0	398	1	TAP_DROME	O16867 drosophila
18	27	90.0	405	1	TMLH_RAT	O91246 rattus norv
19	27	90.0	421	1	TMLH_HUMAN	Q9NVH6 homo sapien
20	27	90.0	421	1	TMLH_MOUSE	P57190 mus musculu
21	27	90.0	446	1	PMBA_BUCAI	P57191 buchnera ap
22	27	90.0	484	1	PER2_VOLCA	P81132 volvox cart
23	27	90.0	499	1	DHA2_HUMAN	O94788 homo sapien
24	27	90.0	499	1	DHA2_MOUSE	O62148 mus musculu
25	27	90.0	499	1	DHA2_RAT	O63639 rattus norv
26	27	90.0	499	1	DHAS_CHICK	O93344 gallus gall
27	27	90.0	512	1	DHA6_HUMAN	P47895 homo sapien
28	27	90.0	516	1	YJJI_ECOLI	P37342 escherichia
29	27	90.0	675	1	ACSA_CANAL	O94049 candida alb
30	27	90.0	958	1	YA7B_SCHPO	O09764 schizosacch
31	27	90.0	1381	1	CTAI_RAT	P97846 rattus norv
32	27	90.0	1384	1	CTAI_HUMAN	P78357 homo sapien
33	27	90.0	1385	1	CTAI_MOUSE	O54991 mus musculu

34	27	90.0	1959	1	AGRI_RAT	P25304 rattus norv
35	26	86.7	43	1	TX3C_AGEAP	P81745 agelenopsis
36	26	86.7	62	1	NX52_LATCO	P10457 laticauda c
37	26	86.7	62	1	NX5A_LATCR	P25495 laticauda c
38	26	86.7	62	1	NX5B_LATCR	P25496 laticauda c
39	26	86.7	62	1	NX5B_LATLA	P10459 laticauda l
40	26	86.7	62	1	NX5D_LATCO	P10455 laticauda c
41	26	86.7	62	1	NX5D_LATCO	P10455 laticauda c
42	26	86.7	76	1	TX3B_AGEAP	P81744 agelenopsis
43	26	86.7	83	1	NX31_LATSE	P01435 laticauda s
44	26	86.7	99	1	Y150_NPVAC	P41707 autographa
45	26	86.7	100	1	KRF4_COLLI	Q9psv3 columba liv

ALIGNMENTS

RESULT 1  
PT18\_YEAST STANDARD; PRT; 215 AA.  
AC P25362;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE PT18 protein.  
GN PT18 OR HIT2 OR YCR020C OR YCR20C.  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Feldmann H., Mannhaupt G., Vetter I.;  
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89131254; PubMed=3916862;  
RA Toh-E A., Sahashi Y.;  
RT "The PT18 locus of Saccharomyces cerevisiae: a complex locus  
containing multiple genes";  
RL Yeast 1:159-171(1985).  
CC -----  
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CC -----  
CC EMBL; X59720; CAA42311.1; -.  
DR PIR; S07692; S07692.  
DR PIR; S19431; S19431.  
DR SGD; S0000613; PT18.  
DR InterPro; IPR004305; TENA\_THI-4.  
DR Pfam; PF03070; TENA\_THI-4; 1.  
FT CONFLICT 40 40 I -> M (IN REF. 2).  
FT CONFLICT 104 104 D -> G (IN REF. 2).  
FT CONFLICT 122 122 D -> S (IN REF. 2).  
SQ SEQUENCE 215 AA; 25223 MW; 71A2D7C5695CEA13 CRC64;  
Query Match 100.0%; Score 30; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SCYNA 5  
|||  
Db 211 SCYNA 215  
RESULT 2  
SYE2\_CAMJE STANDARD; PRT; 463 AA.  
ID SYE2\_CAMJE

```
AC OS2914; Q9PN11;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase 2 (EC 6.1.1.17) (Glutamate--tRNA ligase 2)
DE (GluRS 2)
GN GLTX2 OR CJ1288C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168; PubMed=10688204;
RX Parkhill J., Wren B.W., Mungall K., Kelsey J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Kariyasev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrall B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
RN [2]
RP SEQUENCE OF 1-82 FROM N.A.
RC STRAIN=129108;
RA Wosten M.W.M., Boeve M., Koot M.G.A., Nuenen A.C.,
RA van der Zeijst B.A.M.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; AL139077; CAB73541.1; -
DR EMBL; AJ002027; CAA03150.1; -
DR HSP; P27000; IGLN.
DR InterPro; IPR004527; Gltx bact.
DR InterPro; IPR000924; Glu tRNA-synt 1c.
DR InterPro; IPR001412; tRNA-synt 1.
DR Pfam; PF00749; tRNA-synt 1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR TIGRFAMs; TIGR00464; gltx_bact; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
FT Complete proteome.
FT SITE 11 21 "HIGH" REGION.
FT SITE 240 244 "KMSKS" REGION.
FT BINDING 243 243 ATP (BY SIMILARITY).
SQ SEQUENCE 463 AA; 53058 MW; D60A0032963E6BED CRC64;
Query Match 100.0%; Score 30; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYNA 5
Db 299 SCYNA 303
|||||
RESULT 3
YJJI HAEIN STANDARD; PRT; 514 AA.
ID YJJI HAEIN
AC P44744;
```

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein HI0521.
GN HI0521.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -1- SIMILARITY: STRONG, TO E.COLI YJJI.
CC -----
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CC -----
DR EMBL; U32734; AAC22179.1; -
DR TIGR; HI0521; -
KW Complete proteome.
SQ SEQUENCE 514 AA; 58159 MW; 69472E231F9FB746 CRC64;
Query Match 100.0%; Score 30; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYNA 5
Db 230 SCYNA 234
|||||
RESULT 4
VG86_BPM2 STANDARD; PRT; 88 AA.
ID VG86_BPM2
AC O64267;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 86 protein (GP86).
DE 86.
GN 86.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC unclassified Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
```

RT "Genome structure of mycobacteriophage D29: implications for phage  
 RL evolution.";  
 J. Mol. Biol. 279:143-164 (1998).  
 CC -----  
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 CC -----  
 DR ENBL; AF022214; AAC18516.1; 232E50427FEBAF02 CRC64;  
 SQ SEQUENCE 88 AA; 10064 MW; 232E50427FEBAF02 CRC64;  
 Query Match 90.0%; Score 27; DB 1; Length 88;  
 Best Local Similarity 80.0%; Pred. No. 34;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCVNA 5  
 Db :|||||  
 51 ACYNA 55  
 RESULT 5  
 VG86\_BPML5 STANDARD; PRT; 88 AA.  
 AC Q05303;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Gene 86 protein (GP86).  
 GS 86.  
 OS Mycobacteriophage L5.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC L5-like viruses.  
 OX NCBI\_TaxID=31757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93211282; PubMed=8459766;  
 RA Hatfull G.F., Sarkis G.J.;  
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
 RT a phage system for mycobacterial genetics.";  
 RL Mol. Microbiol. 7:395-405 (1993).  
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 CC -----  
 DR ENBL; Z18946; CAA79462.1; -;  
 DR PIR; S31031;  
 SQ SEQUENCE 88 AA; 9955 MW; 686EDDB3FF4E6534 CRC64;  
 Query Match 90.0%; Score 27; DB 1; Length 88;  
 Best Local Similarity 80.0%; Pred. No. 34;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCVNA 5  
 Db :|||||  
 51 ACYNA 55  
 RESULT 6  
 THN5\_HORVU STANDARD; PRT; 137 AA.  
 ID THN5\_HORVU  
 AC P09617;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Leaf-specific thionin precursor (Clones PKG1348, PKG1940, PKG2872 and  
 DE DG3).  
 GN TH11.5.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gausing K.;  
 RA "Thionin genes specifically expressed in barley leaves.";  
 RL Planta 171:241-246 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Carina;  
 RX MEDLINE=92322947; PubMed=1377959;  
 RA Andresen I., Becker W., Schluter K., Burges J., Parthier B.,  
 RA Apel K.;  
 RA "The identification of leaf thionin as one of the main  
 RT jasmonate-induced proteins of barley (Hordeum vulgare).";  
 RL Plant Mol. Biol. 19:193-204 (1992).  
 RN [3]  
 RP SEQUENCE OF 29-74 FROM N.A. (CLONE DG3).  
 RC STRAIN=cv. Carina;  
 RA Bohlmann H., Clausen S., Behnke S., Giese H., Hiller C.,  
 RA Reimann-Phillip U., Schrader G., Barkholt V., Apel K.;  
 RT "Leaf-specific thionins of barley - a novel class of cell wall  
 RT proteins toxic to plant-pathogenic fungi and possibly involved in the  
 RT defence mechanism of plants.";  
 RL EMBO J. 7:1559-1565 (1988).  
 CC -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC  
 CC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE  
 CC LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,  
 CC OF THESE PROTEINS IS NOT KNOWN.  
 CC -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.  
 CC -----  
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 CC -----  
 DR ENBL; M19046; AAA32976.1; -;  
 DR ENBL; M19047; AAA32977.1; -;  
 DR ENBL; M19048; AAA32978.1; -;  
 DR HSSP; P01543; 1BHP.  
 DR InterPro; IPR001010; Thionin.  
 DR Pfam; PF00321; plant thionins, 1.  
 DR PROSITE; PS00271; THIONIN, 1.  
 KW Plant defense; Thionin; Plant toxin; Signal; Multigene family.  
 FT SIGNAL 1 28  
 FT CHAIN 29 74 LEAF-SPECIFIC THIONIN.  
 FT CHAIN 75 137 ACIDIC PROTEIN.  
 FT DISULFID 31 68 BY SIMILARITY.  
 FT DISULFID 32 60 BY SIMILARITY.  
 FT DISULFID 40 58 BY SIMILARITY.  
 FT DISULFID 44 54 BY SIMILARITY.  
 FT VARIANT 28 28 A -> G (IN REF. 2).  
 FT VARIANT 135 135 V -> L (IN REF. 2).  
 SQ SEQUENCE 137 AA; 14662 MW; FD00C2DBF6632797 CRC64;  
 Query Match 90.0%; Score 27; DB 1; Length 137;  
 Best Local Similarity 80.0%; Pred. No. 50;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCVNA 5  
 Db :|||||  
 39 NCYNA 43

```
RESULT 7
TRPG_CVAC STANDARD; PRT; 195 AA.
ID TRPG_CVAC
AC Q19914;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Anthranilate synthase component II (EC 4.1.3.27) (Glutamine amido-
transferase).
GN TRPG.
OS Cyanidium caldarium.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RC STRAIN=FROM N.A.
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "the structure and gene repertoire of an ancient red algal plastid
genome.";
RL J. Mol. Evol. 51:382-390(2000).
CC -1- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
pyruvate + L-glutamate.
CC -1- PATHWAY: Tryptophan biosynthesis; first step.
CC -1- SUBUNIT: Tetramer of two components I and two components II.
CC -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
CC
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CC
DR EMBL; AF022186; AAB82675.1; -
DR HSP; Q06129; IQDL.
DR InterPro; IPR002385; Anth synthII.
DR Pfam; PF00117; GATase_1.
DR PRINTS; PR00097; ANTSINHA5II.
DR TIGRFAMs; TIGR00566; trpG_papA; 1.
DR PROSITE; PS00442; GATASE TYPE I; 1.
KW Tryptophan biosynthesis; Lyase; Glutamine amidotransferase;
KW Chloroplast.
FT ACT_SITE 79 79 BY SIMILARITY.
FT ACT_SITE 173 173 BY SIMILARITY.
FT ACT_SITE 175 175 BY SIMILARITY.
SQ SEQUENCE 195 AA; 21984 MW; 51C53AE010352AD0 CRC64;
Query Match 90.0%; Score 27; DB 1; Length 195;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYNA 5
DB 87 TCYNA 91
RESULT 8
ID CD37_MOUSE STANDARD; PRT; 281 AA.
AC Q61470;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte antigen CD37.
GN CD37_MOUSE
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=129/Sv; TISSUE=Liver;
RX MEDLINE=97002026; PubMed=8845018;
RA Tomlinson M.G., Wright M.D.;
RT "Characterisation of mouse CD37: cDNA and genomic cloning.";
RL Mol. Immunol. 33:867-872(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
CC
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CC
DR EMBL; U18372; AAB39500.1; -
DR EMBL; U18367; AAB39500.1; JOINED.
DR EMBL; U18368; AAB39500.1; JOINED.
DR EMBL; U18369; AAB39500.1; JOINED.
DR EMBL; U18370; AAB39500.1; JOINED.
DR EMBL; U18371; AAB39500.1; JOINED.
DR MGI; MGI:88330; CD37.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Antigen; Transmembrane.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 POTENTIAL.
FT DOMAIN 39 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 74 POTENTIAL.
FT DOMAIN 75 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 111 POTENTIAL.
FT DOMAIN 112 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 266 POTENTIAL.
FT DOMAIN 267 281 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 281 AA; 31852 MW; 5B0E11B39CCA22D CRC64;
Query Match 90.0%; Score 27; DB 1; Length 281;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYNA 5
DB 180 SCVNS 184
RESULT 9
ID CD37_RAT STANDARD; PRT; 281 AA.
AC P31053;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte antigen CD37.
GN CD37_RAT
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC STRAIN=FROM N.A.
RX MEDLINE=97002026; PubMed=8845018;
RA Tomlinson M.G., Wright M.D.;
RT "Characterisation of mouse CD37: cDNA and genomic cloning.";
RL Mol. Immunol. 33:867-872(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
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CC
DR EMBL; U18372; AAB39500.1; -
DR EMBL; U18367; AAB39500.1; JOINED.
DR EMBL; U18368; AAB39500.1; JOINED.
DR EMBL; U18369; AAB39500.1; JOINED.
DR EMBL; U18370; AAB39500.1; JOINED.
DR EMBL; U18371; AAB39500.1; JOINED.
DR MGI; MGI:88330; CD37.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Antigen; Transmembrane.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 POTENTIAL.
FT DOMAIN 39 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 74 POTENTIAL.
FT DOMAIN 75 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 111 POTENTIAL.
FT DOMAIN 112 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 266 POTENTIAL.
FT DOMAIN 267 281 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 281 AA; 31852 MW; 5B0E11B39CCA22D CRC64;
Query Match 90.0%; Score 27; DB 1; Length 281;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYNA 5
DB 180 SCVNS 184
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RC STRAIN-PVG X DR;  
RX MEDLINE=90354767; PubMed=2388030;  
RA Classon B.J., Williams A.F., Willis A.C., Seed B., Stamenkovic I.;  
RT "The primary structure of the human leukocyte antigen CD37, a species  
RL J. Exp. Med. 172:1007-1007(1990).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: B LYMPHOCYTES.  
CC -!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.  
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CC  
CC EMBL; X53517; CAA37596.1; -.  
DR F01; B47629; B47629.  
DR F02; JCI501; JCI501.  
DR InterPro: IPR000301; Transmem\_4.  
DR Pfam: PF00335; transmembrane4; 1.  
DR PRINTS: PR00259; TMFOUR.  
DR PROSITE: PS00421; TM4\_1; 1.  
KW Glycoprotein; Antigen; Transmembrane.  
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 18 38 POTENTIAL.  
FT DOMAIN 39 59 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 60 74 POTENTIAL.  
FT DOMAIN 75 85 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 86 111 POTENTIAL.  
FT DOMAIN 112 241 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 242 266 POTENTIAL.  
FT DOMAIN 267 281 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 281 AA; A3462D23E824AA1C CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 281;  
Best Local Similarity 80.0%; Pred. No. 95;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYNA 5  
Db 180 SCVNS 184  
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RESULT 10  
YHVB\_ECOLI  
ID YHVB\_ECOLI STANDARD; PRT; 298 AA.  
AC P45475;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein yhbv.  
GN YHVB OR B3159.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474(1997).  
CC

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CC  
CC EMBL; U18997; AAA57962.1; -.  
DR EMBL; AE000396; AAC76193.1; -.  
DR EcoGene; EG12791; yhbv.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 298 AA; 33192 MW; 671EF53407233EA8 CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 298;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYNA 5  
Db 123 NCYNA 127  
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RESULT 11  
IS2B\_ONCTS  
ID IS2B\_ONCTS STANDARD; PRT; 340 AA.  
AC P50212;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Insulin gene enhancer protein ISL-2B (Islet-2B) (Fragment).  
GN ISL2B.  
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=74940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary;  
RX MEDLINE=95155429; PubMed=7852419;  
RA Gong Z., Hui C.-C., Hew C.L.;  
RT "Presence of isl-1-related LIM domain homeobox genes in teleost and  
RL J. Biol. Chem. 270:3335-3345(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary;  
RX MEDLINE=95178560; PubMed=7873614;  
RA Gong Z., Hew C.L.;  
RT "Several splicing variants of isl-1 like genes in the chinook salmon  
RT (Oncorhynchus tshawytscha) encode truncated transcription factors  
RL Biochim. Biophys. Acta 1260:349-354(1995).  
CC -!- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN  
CC GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF  
CC PRIMARY MOTONEURONS.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
CC IONS.  
CC  
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CC  
CC EMBL; X64884; CAA46102.1; -.  
DR HSSP; F32965; ICTL.  
DR InterPro; IPR001356; Homeobox.  
DR

```
DR InterPro; IPR001781; LIM.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.  
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
Repeat; LIM domain; Metal-binding; Zinc; Multigene family.  
FT NON_TER 1 1  
FT DOMAIN 9 62 LIM 1.  
FT DOMAIN 71 125 LIM 2.  
FT DNA_BIND 172 231 HOMEBOX.  
FT DOMAIN 236 340 GLN-RICH.  
SQ SEQUENCE 340 AA; 38262 MW; BBE58D1FE75B9BF9 CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 340;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYNA 5  
Db 189 TCYNA 193  
  
RESULT 12  
ISL1_BRARE STANDARD; PRT; 349 AA.  
AC P53405;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Inulin gene enhancer protein ISL-1 (Islet-1).  
GN ISL1 OR ISL-1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL EXPRESSION.  
RX MEDLINE=94220748; PubMed=8167375;  
RA Inoue A., Takahashi M., Hotta K., Hotta Y., Okamoto H.;  
RT "Developmental regulation of islet-1 mRNA expression during neuronal  
differentiation in embryonic zebrafish.";  
RL Dev. Dyn. 199; 1-11(1994).  
CC -1- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN  
CC GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF  
CC PRIMARY MOTONEURONS.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IMMEDIATELY AFTER GASTRULATION IN  
CC THE POLSTER, CRANIAL GANGLIA, ROHAN-BEARD NEURONS AND IN  
CC VENTROMEDIAL CELLS OF THE SPINAL CORD. AFTER 16 H, EXPRESSION  
CC IS RESTRICTED TO CELLS SLIGHTLY ANTERIOR TO THE SEGMENT BORDER.  
CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
CC IONS.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; D21135; BAA04670.1; -  
CC ZFIN; ZDB-GENE-980526-112; isl1.  
DR InterPro; IPR001356; Homeobox.  
  
DR InterPro; IPR001781; LIM.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.  
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
Repeat; LIM domain; Metal-binding; Zinc; Multigene family.  
FT NON_TER 1 1  
FT DOMAIN 9 62 LIM 1.  
FT DOMAIN 71 125 LIM 2.  
FT DNA_BIND 172 231 HOMEBOX.  
FT DOMAIN 236 340 GLN-RICH.  
SQ SEQUENCE 340 AA; 38262 MW; BBE58D1FE75B9BF9 CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 340;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCYNA 5  
Db 189 TCYNA 193  
  
RESULT 13  
IS2A_ONCTS STANDARD; PRT; 358 AA.  
AC P53408;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Insulin gene enhancer protein ISL-2A (Islet-2A).  
GN ISL2A.  
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI_TaxID=74940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary;  
RX MEDLINE=95155429; PubMed=7852419;  
RA Gong Z., Hui C.-C., Hew C.L.;  
RT "Presence of isl-1-related LIM domain homeobox genes in teleost and  
RT their similar patterns of expression in brain and spinal cord.";  
RL J. Biol. Chem. 270; 3335-3345(1995).  
RN [2]  
RP SEQUENCE FROM N.A. (ALTERNATIVE SPLICING).  
RC TISSUE=Pituitary;  
RX MEDLINE=95178560; PubMed=7873614;  
RA Gong Z., Hew C.L.;  
RT "Several splicing variants of isl-1 like genes in the chinook salmon  
RT (Oncorhynchus tshawytscha) encode truncated transcription factors  
RT containing a complete LIM domain.";  
RL Blochim. Biophys. Acta 1260; 349-354(1995).  
CC -1- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN  
CC GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF  
CC PRIMARY MOTONEURONS.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THIS PROTEIN ARE PRODUCED BY  
CC ALTERNATIVE SPLICING OF THE SAME GENE. THE SHORTER FORM LACKS  
CC THE HOMODOMAIN.  
CC -1- MISCELLANEOUS: THE N-TERMINAL OF THE SHORT FORM IS INCOMPLETE  
CC (MISSING AA 1-24).  
CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
CC IONS.  
CC  
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 CC -----

DR EMBL; X64885; CAA46103.1; ALT TERM.  
 DR EMBL; X64882; -, NOT\_ANNOTATED\_CDS.  
 DR HSP; P32965; 1CTL.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR001781; LIM.  
 DR Pfam; PF00046; homeobox; 1.  
 DR Pfam; PF00412; LIM; 2.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR ProDom; PD000094; LIM; 2.  
 DR SMART; SM00389; HOX; 1.  
 DR SMART; SM00132; LIM; 2.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00478; LIM\_DOMAIN 1; 2.  
 DR PROSITE; PS50023; LIM\_DOMAIN 2; 2.  
 DR PROSITE; PS50071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Repeat; LIM domain; Metal-binding; Zinc; Multigene family;  
 KW Alternative splicing.  
 FT DOMAIN 27 80 LIM 1.  
 FT DOMAIN 89 143 LIM 2.  
 FT DNA\_BIND 190 249 HOMEBOX.  
 FT DOMAIN 254 358 GLN-RICH.  
 FT VARSPLIC 83 115 RLGIKCANCNIGFCSDDLVMARDNVHNECF -> SVLG  
 FT ARCAAGISCRGMSLCCGTRSCCVLLIMVY (IN SHORT  
 FT ISOFORM).  
 FT VARSPLIC 116 358 MISSING (IN SHORT ISOFORM).  
 FT SEQUENCE 358 AA; 40072 MW; FB726FESACFF25F3 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 358;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 DB 207 TCYNA 211

RESULT 14  
 ISL3 BRARE STANDARD; PRT; 358 AA.  
 AC P53407;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Insulin gene enhancer protein ISL-3 (Islet-3).  
 GN ISL3 OR ISL-3.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND DIFFERENTIAL EXPRESSION.  
 RX MEDLINE=96005022; PubMed=7556938;  
 RA Tokumoto M., Gong Z., Tsubokawa T., Hew C., Uyemura K., Hotta Y.,  
 RA Okamoto H.;  
 RT "Molecular heterogeneity among primary motoneurons and within  
 RT myotomes revealed by the differential mRNA expression of novel  
 RT islet-1 homologs in embryonic zebrafish.";  
 RL Dev. Biol. 171:578-589 (1995).  
 CC -1- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN  
 CC GENE ENHANCER. MAY BE INVOLVED IN THE REGIONAL SPECIFICATION OF  
 CC THE MYOTOME AND ALSO IN TARGET RECOGNITION BY THE CAUDAL PRIMARY  
 CC NEURON.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED 17 H AFTER GASTRULATION MAINLY IN

CC THE VENTRAL MYOTOMES. IN THE HEAD REGION, AFTER 18 H, EXPRESSION  
 CC IS RESTRICTED TO THE ENTIRE REGION OF THE EYES, THE TECTAL REGION  
 CC OF THE MIDBRAIN, TRIGEMINAL GANGLIA AND THE GANGLIA ANTERIOR TO  
 CC THE OTIC VESICLES.  
 CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
 CC IONS.  
 CC -----

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DR EMBL; D38454; BAA07485.1; -  
 DR ZFIN; ZDB-GENE-990415-133; isl3.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR001781; LIM.  
 DR Pfam; PF00046; homeobox; 1.  
 DR Pfam; PF00412; LIM; 2.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR ProDom; PD000094; LIM; 2.  
 DR SMART; SM00389; HOX; 1.  
 DR SMART; SM00132; LIM; 2.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00478; LIM\_DOMAIN 1; 2.  
 DR PROSITE; PS50023; LIM\_DOMAIN 2; 2.  
 DR PROSITE; PS50071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Repeat; LIM domain; Metal-binding; Zinc; Multigene family.  
 FT DOMAIN 27 80 LIM 1.  
 FT DOMAIN 89 143 LIM 2.  
 FT DNA\_BIND 191 250 HOMEBOX.  
 FT DOMAIN 255 358 GLN-RICH.  
 FT SEQUENCE 358 AA; 39848 MW; 3D72568172411D67 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 358;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 DB 208 TCYNA 212

RESULT 15  
 ISL2 BRARE STANDARD; PRT; 359 AA.  
 AC P53406;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Insulin gene enhancer protein ISL-2 (Islet-2).  
 GN ISL2 OR ISL-2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=96005022; PubMed=7556938;  
 RA Tokumoto M., Gong Z., Tsubokawa T., Hew C.L., Uyemura K., Hotta Y.,  
 RA Okamoto H.;  
 RT "Molecular heterogeneity among primary motoneurons and within  
 RT myotomes revealed by the differential mRNA expression of novel  
 RT islet-1 homologs in embryonic zebrafish.";  
 RL Dev. Biol. 171:578-589 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.



GN TAP OR BPS OR CG7659.  
OS Drosophila melanogaster (fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=97115720; PubMed=8954743;  
RX Bush A.B., Hiroimi Y.H., Cole M.D.;  
RA "Biparous: a novel bHLH gene expressed in neuronal and glial  
RT precursors in Drosophila";  
RL Dev. Biol. 180:759-772(1996).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Oregon-R;  
RX MEDLINE=97354289; PubMed=9210583;  
RA Gautier P., Ledent V., Massaer M., Dambly-Chaudiere C., Ghysen A.;  
RT "tap, a Drosophila bHLH gene expressed in chemosensory organs";  
RL Gene 191:15-21(1997).  
[3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Berkely;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
AN Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Mortan J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
[4]  
RN CHARACTERIZATION.  
RP STRAIN=Oregon-R;  
RX MEDLINE=98211586; PubMed=9551861;  
RA Ledent V., Gaillard F., Gautier P., Ghysen A., Dambly-Chaudiere C.;  
RT "Expression and function of tap in the gustatory and olfactory organs  
RT of Drosophila";  
RL Int. J. Dev. Biol. 42:163-170(1998).  
CC -!- FUNCTION: MAY PLAY A ROLE IN THE SPECIFICATION OF THE SUGAR-  
CC SENSITIVE ADULT GUSTATORY NEURON AND AFFECT THE RESPONSE TO SUGAR  
CC AND SALT. REGULATED BY FOXN.

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL; AF022883; AAC80572.1; -;  
DR EMBL; X95845; CAA65103.1; -;  
DR EMBL; AE003524; AAF49352.1; -;  
DR FlyBase; FBgn0015550; tap.  
DR InterPro; IPR001092; HLH\_baseic.  
DR Pfam; PF00010; HLH; 1.  
DR SMART; SM00353; HLH; 1.  
DR PROSITE; PS00038; HLH\_1; FALSE\_NEG.  
DR PROSITE; PS50888; HLH\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription regulation; Neurogenesis;  
KW Developmental protein; Differentiation.  
FT DNA\_BIND 155 166 BASIC DOMAIN (BY SIMILARITY).  
FT DOMAIN 167 207 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
FT DOMAIN 18 23 POLY-ASP.  
FT DOMAIN 308 312 POLY-GLN.  
SQ SEQUENCE 398 AA; 44850 MW; 54FF558483B18258 CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 398;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCVNA 5  
Db :|||  
3 ACTNA 7  
  
RESULT 18  
TMDLH RAT STANDARD; PRT; 405 AA.  
AC Q91ZW6;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Trimethyllysine dioxygenase, mitochondrial precursor (EC 1.14.11.8)  
DE (Epsilon-trimethyllysine 2-oxoglutarate dioxygenase) (TML-alpha-  
DE ketoglutarate dioxygenase) (TML hydroxylase) (TML dioxygenase) (TMLD).  
GN TMLH OR TMLH.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=Wistar;  
RX MEDLINE=21423953; PubMed=11431483;  
RA Vaz F.M., Ofman R., Westinga K., Back J.W., Wanders R.J.A.;  
RT "Molecular and biochemical characterization of rat epsilon-N-  
RT trimethyllysine hydroxylase, the first enzyme of carnitine  
RT biosynthesis";  
RL J. Biol. Chem. 276:33512-33517(2001).  
CC -!- FUNCTION: Converts trimethyllysine (TML) into  
CC hydroxytrimethyllysine (HTML).  
CC -!- CATALYTIC ACTIVITY: N(6),N(6),N(6)-trimethyl-L-lysine + 2-  
CC oxoglutarate + O(2) = 3-hydroxy-N(6),N(6),N(6)-trimethyl-L-lysine  
CC + succinate + CO(2).  
CC -!- COFACTOR: Iron and ascorbate.  
CC -!- PATHWAY: Carnitine biosynthesis; first step.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -!- SIMILARITY: BELONGS TO THE GAMMA-BBH/TMLD FAMILY.  
CC -----

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DR EMBL; AF374406; AAL01252.1; -;  
 DR InterPro; IPR004994; Gamma-BBH.  
 DR Pfam; PF03322; Gamma-BBH; 1.  
 KW Carnitine biosynthesis; Oxidoreductase; Dioxxygenase; Itron;  
 KW Mitochondrion; Transit peptide.  
 FT TRANSIT 1 405 MITOCHONDRION (POTENTIAL).  
 FT CHAIN ? 405 TRIMETHYLlysine DIOXYGENASE.  
 SQ SEQUENCE 405 AA; 47490 MW; DC4A904309B8DA81 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 405;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 Db 68 SCYNS 72

RESULT 19  
 TMLH HUMAN STANDARD; PRT; 421 AA.  
 AC Q9NVH6;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Trimethyllysine dioxxygenase, mitochondrial precursor (EC 1.14.11.8)  
 DE (Epsilon-trimethyllysine 2-oxoglutarate dioxxygenase) (TML-alpha-  
 DE ketoglutarate dioxxygenase) (TML hydroxylase) (TML dioxxygenase) (TMLD).  
 GN TMLHE OR TMLH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21423953; PubMed=11431483;  
 RA Vaz F.M., Oman R., Westinga K., Back J.W., Wanders R.J.A.;  
 RT "Molecular and biochemical characterization of rat epsilon-N-  
 RT trimethyllysine hydroxylase, the first enzyme of carnitine  
 RT biosynthesis.";  
 RL J. Biol. Chem. 276:33512-33517 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Iehida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Iehi S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Negahari K., Masuho Y.,  
 RA Ninomiya K., Iwayanagi T.;  
 RT "NEDO human cDNA sequencing project.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Converts trimethyllysine (TML) into  
 CC hydroxytrimethyllysine (HTML).  
 CC -!- CATALYTIC ACTIVITY: N(6),N(6),N(6)-trimethyl-L-lysine + 2-  
 CC oxoglutarate + O(2) = 3-hydroxy-N(6),N(6),N(6)-trimethyl-L-lysine  
 CC + succinate + CO(2).  
 CC -!- COFACTOR: Iron and ascorbate.  
 CC -!- PATHWAY: Carnitine biosynthesis; first step.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE GAMMA-BBH/TMLD FAMILY.

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DR EMBL; AF373407; AAL01871.1; -;  
 DR EMBL; AK001589; BAA01775.1; -;  
 DR Genew; HGNC:18308; TMLHE.  
 DR InterPro; IPR004994; Gamma-BBH.  
 DR Pfam; PF03322; Gamma-BBH; 1.  
 KW Carnitine biosynthesis; Oxidoreductase; Dioxxygenase; Itron;  
 KW Mitochondrion; Transit peptide.  
 FT TRANSIT 1 421 MITOCHONDRION (POTENTIAL).  
 FT CHAIN ? 421 TRIMETHYLlysine DIOXYGENASE.  
 SQ SEQUENCE 421 AA; 49517 MW; 4E55DF349B866B43 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 421;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 Db 84 SCYNS 88

RESULT 20  
 TMLH MOUSE STANDARD; PRT; 421 AA.  
 AC Q91ZE0; Q91XHL;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Trimethyllysine dioxxygenase, mitochondrial precursor (EC 1.14.11.8)  
 DE (Epsilon-trimethyllysine 2-oxoglutarate dioxxygenase) (TML-alpha-  
 DE ketoglutarate dioxxygenase) (TML hydroxylase) (TML dioxxygenase) (TMLD).  
 GN TMLHE OR TMLH.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 13-421 FROM N.A.  
 RX STRAIN=FVB/N;  
 RX MEDLINE=21423953; PubMed=11431483;  
 RA Vaz F.M., Oman R., Westinga K., Back J.W., Wanders R.J.A.;  
 RT "Molecular and biochemical characterization of rat epsilon-N-  
 RT trimethyllysine hydroxylase, the first enzyme of carnitine  
 RT biosynthesis.";  
 RL J. Biol. Chem. 276:33512-33517 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tissue=Liver;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Converts trimethyllysine (TML) into  
 CC hydroxytrimethyllysine (HTML).  
 CC -!- CATALYTIC ACTIVITY: N(6),N(6),N(6)-trimethyl-L-lysine + 2-  
 CC oxoglutarate + O(2) = 3-hydroxy-N(6),N(6),N(6)-trimethyl-L-lysine  
 CC + succinate + CO(2).  
 CC -!- COFACTOR: Iron and ascorbate.  
 CC -!- PATHWAY: Carnitine biosynthesis; first step.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE GAMMA-BBH/TMLD FAMILY.

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CC -----
DR EMBL; AY033513; AAK54387.1; ALT_INIT.
DR EMBL; BC010495; AAH10495.1; -.
DR InterPro; IPR004994; Gamma-BBH.
DR Pfam; PF03322; Gamma-BBH; 1.
KW Carnitine biosynthesis; Oxidoreductase; Dioxigenase; Iron;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 421 TRIMETHYLLYSINE DIOXYGENASE.
SQ SEQUENCE 421 AA; 49609 MW; 1474AD5742B88F43 CRC64;

Query Match          90.0%; Score 27; DB 1; Length 421;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 84 SCYNS 88

RESULT 21
PMBA_BUCAI
ID PMBA_BUCAI STANDARD; PRT; 446 AA.
AC P57181;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE PmbA protein homolog.
GN PMBA OR BU089.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT Buchnera sp. APS.;
RL Nature 407:81-86(2000).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
CC -----
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CC -----
DR EMBL; AP001118; BAB12809.1; -.
DR InterPro; IPR002510; PmbA_TlDD.
DR Pfam; PF01523; PmbA_TlDD; 1.
KW Complete proteome.
SQ SEQUENCE 446 AA; 50401 MW; 4E6027D1C45213B2 CRC64;

Query Match          90.0%; Score 27; DB 1; Length 446;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 326 NCYNA 330

RESULT 22
PER2_VOLCA
ID PER2_VOLCA STANDARD; PRT; 484 AA.
AC P81132;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC -----
```

```
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Perphorin II (Fragment).
OS Volvox carteri.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Volvox.
OX NCBI_TaxID=3067;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13; 182-215 AND 413-441.
RX MEDLINE=93209229; PubMed=8458341;
RA Sumper M., Berg E., Wenzl S., Godl K.;
RT "How a sex pheromone might act at a concentration below 10(-16) M.";
RL EMBO J. 12:831-836(1993).
CC -!- FUNCTION: MAY BE INVOLVED IN CONVERSION OF ASEXUAL MALES AND
CC FEMALES TO THE SEXUAL PATHWAY.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- INDUCTION: BY SEXUAL INDUCER GLYCOPROTEIN.
CC -----
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CC -----
DR EMBL; X69802; CAB56809.1; -.
DE Extracellular matrix; Glycoprotein; Multigene family.
FT NON_TER 1 1
FT DOMAIN 173 177 POLY-PRO.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 484 AA; 50860 MW; 0733618764BB2345 CRC64;

Query Match          90.0%; Score 27; DB 1; Length 484;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 376 TCYNA 380

RESULT 23
DHA2_HUMAN
ID DHA2_HUMAN STANDARD; PRT; 499 AA.
AC O94788;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific
 dehydrogenase type 2) (RALDH(II)) (RALDH-2).
GN ALDH1A2 OR RALDH2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99038200; PubMed=9819382;
RA Ono Y., Fukuhara N., Yoshie O.;
RT "TALI and LIM-only proteins synergistically induce retinaldehyde
 dehydrogenase 2 expression in T-cell acute lymphoblastic leukemia by
 acting as cofactors for GATA3.";
RL Mol. Cell. Biol. 18:6939-6950(1998).
CC -!- FUNCTION: RECOGNIZES AS SUBSTRATES FREE RETINAL AND CELLULAR
CC RETINOL-BINDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND
CC DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE, ACETALDEHYDE
```

CC AND PROPANAL EFFICIENTLY (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.  
 CC -1- PATHWAY: RETINOIC ACID BIOGENESIS.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AB015226; BAA34785.1; ALT\_INIT.  
 CC HSP; P51977; 1BX.  
 CC GENE; HGNC:15472; ALDH1A2.  
 CC MIM; 603687; -.  
 CC InterPro: IPR002086; Aldehyde\_dehydr.  
 CC Pfam; PF00171; aldedh; 1.  
 CC PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 CC PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 CC Oxidoreductase; NAD.  
 CC NP BIND 244 249 NAD (ADP PART) (BY SIMILARITY).  
 CC ACT\_SITE 267 267 POTENTIAL.  
 CC ACT\_SITE 301 301 POTENTIAL.  
 CC SEQUENCE 499 AA; 54780 MW; FE0B53A47644246B CRC64;  
 CC -----  
 CC Query Match 90.0%; Score 27; DB 1; Length 499;  
 CC Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 SCYNA 5  
 CC :|||||  
 CC Db 453 NCYNA 457  
 CC  
 CC RESULT 24  
 CC DH2\_MOUSE STANDARD; PRT; 499 AA.  
 CC ID Q62148;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific  
 CC dehydrogenase type 2) (RALDH(III)) (RALDH-2).  
 CC GN ALDH1A2 OR ALDH1A7 OR RALDH2.  
 CC OS Mus musculus (Mouse).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC OX NCBI\_TaxID=10090;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=C3H/He;  
 CC RX MEDLINE=96390857; PubMed=8797830;  
 CC RA Zhao D., McCaffery P., Ivins K.J., Neve R.L., Hogan P., Chin W.W.,  
 CC RA Draeger J.C.;  
 CC RT "Molecular identification of a major retinoic-acid-synthesizing  
 CC enzyme, a retinaldehyde-specific dehydrogenase.";  
 CC RL Eur. J. Biochem. 240:15-22(1996).  
 CC -1- FUNCTION: RECOGNIZES AS SUBSTRATES FREE RETINAL AND CELLULAR  
 CC RETINOL-BINDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND  
 CC DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE, ACETALDEHYDE  
 CC AND PROPANAL EFFICIENTLY.  
 CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.  
 CC -1- PATHWAY: RETINOIC ACID BIOGENESIS.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: FOUND IN TESTIS AND LESS ABUNDANTLY IN LUNG,  
 CC BRAIN, HEART, LIVER AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U60063; AAC2637.1; -.  
 CC HSP; P51977; 1BX.  
 CC InterPro: IPR002086; Aldehyde\_dehydr.

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 CC -----  
 CC EMBL; X99273; CAA67666.1; -.  
 CC HSP; P51977; 1BX.  
 CC GENE; MG1:107928; Aldh1a2.  
 CC InterPro: IPR002086; Aldehyde\_dehydr.  
 CC Pfam; PF00171; aldedh; 1.  
 CC PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 CC PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 CC Oxidoreductase; NAD.  
 CC NP BIND 244 249 NAD (ADP PART) (BY SIMILARITY).  
 CC ACT\_SITE 267 267 POTENTIAL.  
 CC ACT\_SITE 301 301 POTENTIAL.  
 CC SEQUENCE 499 AA; 54725 MW; E000596A90B0B7A CRC64;  
 CC -----  
 CC Query Match 90.0%; Score 27; DB 1; Length 499;  
 CC Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 SCYNA 5  
 CC :|||||  
 CC Db 453 NCYNA 457  
 CC  
 CC RESULT 25  
 CC DH2\_RAT STANDARD; PRT; 499 AA.  
 CC ID Q63639;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific  
 CC dehydrogenase type 2) (RALDH(III)) (RALDH-2).  
 CC GN ALDH1A2 OR RALDH2.  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC OX NCBI\_TaxID=10116;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Testis;  
 CC RX MEDLINE=96279178; PubMed=8663198;  
 CC RA Wang X., Penzes P., Napoli J.L.;  
 CC RT "Cloning of a cDNA encoding an aldehyde dehydrogenase and its  
 CC expression in Escherichia coli. Recognition of retinal as substrate.";  
 CC RL J. Biol. Chem. 271:16288-16293(1996).  
 CC -1- FUNCTION: RECOGNIZES AS SUBSTRATES FREE RETINAL AND CELLULAR  
 CC RETINOL-BINDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND  
 CC DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE, ACETALDEHYDE  
 CC AND PROPANAL EFFICIENTLY.  
 CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.  
 CC -1- PATHWAY: RETINOIC ACID BIOGENESIS.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: FOUND IN TESTIS AND LESS ABUNDANTLY IN LUNG,  
 CC BRAIN, HEART, LIVER AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U60063; AAC2637.1; -.  
 CC HSP; P51977; 1BX.  
 CC InterPro: IPR002086; Aldehyde\_dehydr.

DR Pfam; PF00171; aldedh; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 KW Oxidoreductase; NAD.  
 FT NP\_BIND 244 249 NAD (ADP PART) (BY SIMILARITY).  
 FT ACT\_SITE 267 267 POTENTIAL.  
 FT ACT\_SITE 301 301 POTENTIAL.  
 SQ SEQUENCE 499 AA; 54739 MW; E01EF471342267AA CRC64;

Query Match 90.0%; Score 27; DB 1; Length 499;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :|||||  
 Db 453 NCYNA 457

RESULT 26  
 DHAS\_CHICK STANDARD; PRT; 499 AA.  
 ID DHAS\_CHICK O93344;  
 AC O93344;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2).  
 DE dehydrogenase type 2) (RALDH(II)) (RALDH-2).  
 GN ALDH1A2 OR RALDH2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9839476; PubMed=9727493;  
 RA Sockanathan S., Jessell T.M.;  
 RT "Motor neuron-derived retinoid signaling specifies the subtype identity of spinal motor neurons";  
 RL Cell 94:503-514(1998).  
 CC -!- FUNCTION: RECOGNIZES AS SUBSTRATES FREE RETINAL AND CELLULAR RETINOL-BINDING PROTEIN-BOUND RETINAL. DOES METABOLIZE OCTANAL AND DECANAL BUT DOES NOT METABOLIZE CITRAL, BENZALDEHYDE, ACETALDEHYDE AND PROPANAL EFFICIENTLY (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.  
 CC -!- PATHWAY: RETINOIC ACID BIOGENESIS.  
 CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
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 DR EMBL; AF064253; AAC34299.1; -.  
 DR HSSP; P51977; 1BX5.  
 DR Pfam; PF00171; aldedh; 1.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 KW Oxidoreductase; NAD.  
 FT NP\_BIND 244 249 NAD (ADP PART) (BY SIMILARITY).  
 FT ACT\_SITE 267 267 POTENTIAL.  
 FT ACT\_SITE 301 301 POTENTIAL.  
 SQ SEQUENCE 499 AA; 54774 MW; F471F09F3D5645A7 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 499;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :|||||  
 Db 453 NCYNA 457

RESULT 28  
 YUJI\_ECOLI STANDARD; PRT; 516 AA.  
 ID YUJI\_ECOLI P37341;  
 AC P37342; P37341;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

QY 1 SCYNA 5  
 :|||||  
 Db 453 NCYNA 457

RESULT 27  
 DHAA6\_HUMAN STANDARD; PRT; 512 AA.  
 ID DHAA6\_HUMAN P47895;  
 AC P47895;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Aldehyde dehydrogenase 6 (EC 1.2.1.5).  
 GN ALDH1A3 OR ALDH6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Salivary gland;  
 RX MEDLINE=95213025; PubMed=7698756;  
 RA Hsu L.C., Chang W.-C., Hiraoka L., Hsieh C.-L.;  
 RT "Molecular cloning, genomic organization, and chromosomal localization of an additional human aldehyde dehydrogenase gene, ALDH6";  
 RT ALDH6";  
 RL Genomics 24:333-341(1994).  
 CC -!- CATALYTIC ACTIVITY: An aldehyde + NAD(P)(+) + H(2)O = an acid + NAD(P)H.  
 CC -!- PATHWAY: Ethanol utilization; second step.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN MANY TISSUES AND AT HIGHER LEVELS IN SALIVARY GLAND, STOMACH, AND KIDNEY.  
 CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
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 DR EMBL; U07919; AAA79036.1; -.  
 DR HSSP; P51977; 1BX5.  
 DR Genew; HGNC:409; ALDH1A3.  
 DR MIM; 600463; -.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR Pfam; PF00171; aldedh; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 KW Oxidoreductase; NAD.  
 FT NP\_BIND 257 262 NAD (ADP PART) (BY SIMILARITY).  
 FT ACT\_SITE 280 280 BY SIMILARITY.  
 FT ACT\_SITE 314 314 BY SIMILARITY.  
 SQ SEQUENCE 512 AA; 56009 MW; FBF85EFC5A54230 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 512;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 :|||||  
 Db 466 NCYNA 470

RESULT 28  
 YUJI\_ECOLI STANDARD; PRT; 516 AA.  
 ID YUJI\_ECOLI P37341;  
 AC P37342; P37341;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)



RA Dega R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
RT "The genome sequence of Schizosaccharomyces pombe.",  
RL Nature 415:871-880(2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: TO YEAST YGRI25W.  
CC -!- SIMILARITY: CONTAINS 1 STAS DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Z54142; CAA90855.1; -.  
DR InterPro; IPR002645; STAS.  
DR InterPro; IPR001902; Sulfate transp.  
DR Pfam; PF00027; CNMP binding; 1.  
DR Pfam; PF00916; Sulfate\_transp; 1.  
DR Pfam; PF01740; STAS; 1.  
DR SMART; SM00100; CNMP; 1.  
DR PROSITE; PS50801; STAS; 1.  
KW Hypothetical protein; Transmembrane.  
FT TRANSMEM 153 173 POTENTIAL.  
FT TRANSMEM 199 219 POTENTIAL.  
FT TRANSMEM 258 278 POTENTIAL.  
FT TRANSMEM 291 311 POTENTIAL.  
FT TRANSMEM 327 347 POTENTIAL.  
FT TRANSMEM 358 378 POTENTIAL.  
FT TRANSMEM 426 446 POTENTIAL.  
FT TRANSMEM 499 519 POTENTIAL.  
FT TRANSMEM 521 541 POTENTIAL.  
FT TRANSMEM 543 563 POTENTIAL.  
FT TRANSMEM 564 584 POTENTIAL.  
FT TRANSMEM 627 647 POTENTIAL.  
FT TRANSMEM 659 679 POTENTIAL.  
FT DOMAIN 612 733 STAS.  
SQ SEQUENCE 958 AA; 107124 MW; B1275B99CFB7A4D8 CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 958;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SCNA 5  
Db 895 TCYNA 899  
  
RESULT 31  
CTAL\_RAT  
ID CTAL\_RAT STANDARD; PRT; 1381 AA.  
AC P97846;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Contactin associated protein 1 precursor (Caspr) (Caspr1) (Neurexin 4)  
DE (Neurexin IV) [p190] (Paranodin).  
GN CNTNAP1 OR CASPR OR NFXN4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND INTERACTION WITH CONTACTIN.  
RC TISSUE=Pituitary tumor;  
RX MEDLINE=97224125; PubMed=9118959;  
RA Peles E., Nativ M., Lustig M., Grunet M., Schilling J., Martinez R.,  
RA Plowman G.D., Schlesinger J.;  
RT "Identification of a novel contactin-associated transmembrane receptor

with multiple domains implicated in protein-protein interactions.";  
RL EMBL J. 16:978-988(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=97436749; PubMed=9292722;  
RA Menegoz M., Gaspar P., Le Bert M., Galvez T., Burgaya F., Palfrey C.,  
RA Ezan P., Arnos F., Girault J.-A.;  
RL "Paranodin, a glycoprotein of neuronal paranodal membranes.";  
RT Neuron 19:319-331(1997).  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=98060845; PubMed=9396755;  
RA Einheber S., Zanazzi G., Ching W., Scherer S., Milner T.A., Peles E.,  
RA Salzer J.L.;  
RT "The axonal membrane protein Caspr, a homologue of neuixin IV, is a  
RT component of the septate-like paranodal junctions that assemble  
RT during myelination.";  
RL J. Cell Biol. 139:1495-1506(1997).  
RN [4]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=21403569; PubMed=11512672;  
RA Arroyo E.J., Xu T., Pollak S., Watson M., Peles E., Scherer S.S.;  
RT "Internodal specializations of myelinated axons in the central nervous  
RT system.";  
RL Cell Tissue Res. 305:53-66(2001).  
CC -!- FUNCTION: SEEMS TO PLAY A ROLE IN THE FORMATION OF FUNCTIONAL  
CC DISTINCT DOMAINS CRITICAL FOR SALTATORY CONDUCTION OF NERVE  
CC IMPULSES IN MYELINATED NERVE FIBERS. SEEMS TO DEMARCATHE THE  
CC PARANODAL REGION OF THE AXO-GLIAL JUNCTION. IN ASSOCIATION WITH  
CC CONTACTIN MAY HAVE A ROLE IN THE SIGNALING BETWEEN AXONS AND  
CC MYELINATING GLIAL CELLS.  
CC -!- SUBUNIT: INTERACTS WITH CONTACTIN IN CIS FORM.  
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. IN  
CC MYELINATED NERVE FIBERS OF THE CNS PREDOMINANTLY FOUND IN  
CC PARANODAL AXOGLIAL JUNCTIONS. IN UNMYELINATED NERVE FIBERS OF THE  
CC CNS DIFFUSELY DISTRIBUTED ALONG THE ENTIRE SURFACE. WEAK  
CC EXPRESSION IS DETECTED IN OVARY, PANCREAS, COLON, LUNG, HEART,  
CC INTESTINE AND TESTIS.  
CC -!- DEVELOPMENTAL STAGE: DETECTED ON POSTNATAL DAY 7 IN CEREBELLUM.  
CC FOLLOWS A CAUDOROSTRAL PROGRESSION ACCORDING TO THE MYELINATION  
CC PROCESS. APPEARS TO REDISTRIBUTE FROM THE INTERNODE TO THE  
CC PARANODAL REGION DURING MYELIN COMPACTION AND MATURATION.  
CC EXPRESSION REACHES MAXIMAL LEVELS BETWEEN DAYS 14 AND 18 AND  
CC REMAINS AT THE SAME LEVELS UNTIL ADULTHOOD.  
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -!- SIMILARITY: CONTAINS 4 LAMININ G-LIKE DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; U87224; AAB48482.1; -.  
DR EMBL; AF000114; AAC53342.1; -.  
DR HSP; P12259; 1C2T.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000421; FAS8 C.  
DR InterPro; IPR002181; Fibrinogen C.  
DR InterPro; IPR001791; Laminin G.  
DR InterPro; IPR003585; Neurexin-like.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00054; laminin\_G; 4.  
DR Pfam; PF00147; fibrinogen\_C; 1.  
DR Pfam; PF00754; F5\_F8\_type\_C; 1.  
DR SMART; SM00294; 4.1m; 1.

DR SMART; SM00181; EGF; 1.  
DR SMART; SM00231; FA58C; 1.  
DR SMART; SM00282; LamG; 4.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
DR PROSITE; PS01285; FA58C\_1; 1.  
DR PROSITE; PS01286; FA58C\_2; 1.  
DR PROSITE; PS00534; FIBRIN\_AG\_C DOMAIN; FALSE\_NEG.  
DR PROSITE; PS00025; LAM\_G DOMAIN; 4.  
KW Glycoprotein; Cell adhesion; Signal; Transmembrane; SH3-binding;  
Repeat.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 1381 CONTACTIN ASSOCIATED PROTEIN 1.  
FT DOMAIN 21 1284 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1285 1305 POTENTIAL.  
FT DOMAIN 1306 1381 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 26 169 F5/8 TYPE C.  
FT DOMAIN 204 356 LAMININ G-LIKE 1.  
FT DOMAIN 390 539 LAMININ G-LIKE 2.  
FT DOMAIN 544 576 EGF-LIKE 1.  
FT DOMAIN 581 618 FIBRINOGEN C-TERMINAL.  
FT DOMAIN 814 958 LAMININ G-LIKE 3.  
FT DOMAIN 962 996 EGF-LIKE 2.  
FT DOMAIN 1089 1251 LAMININ G-LIKE 4.  
FT SITE 1329 1366 SH3-BINDING (POTENTIAL).  
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 764 764 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 805 805 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 861 861 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 949 949 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 957 957 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1079 1079 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1148 1148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1381 AA; 155867 MW; BCICE83DB57C1BA4 CRC64;  
Query Match 30.08; Score 27; DB 1; Length 1381;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 SCVNA 5  
Db 677 SCVNS 681  
RESULT 32  
CTAL\_HUMAN STANDARD; PRT; 1384 AA.  
AC P78357;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Contactin associated protein 1 precursor (Caspr) (Neurexin 4)  
DE (Neurexin IV) (p190).  
GN CNTNAP1 OR CASPR OR NRXN4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND INTERACTION WITH CONTACTIN.  
RC TISSUE=Neuroblastoma;  
RX MEDLINE=97224125; PubMed=9118959;  
RA Pelles E., Nativ M., Lustig M., Grumet M., Schilling J., Martinez R.,  
RA Plowman G.D., Schlesinger J.;

RT "Identification of a novel contactin-associated transmembrane receptor  
with multiple domains implicated in protein-protein interactions.";  
RL EMBO J. 16:978-988(1997).  
CC -!- FUNCTION: SEEMS TO PLAY A ROLE IN THE FORMATION OF FUNCTIONAL  
DISTINCT DOMAINS CRITICAL FOR SALTATORY CONDUCTION OF NERVE  
IMPULSES IN MYELINATED NERVE FIBERS. SEEMS TO DEMARCATHE THE  
PARANODAL REGION OF THE AXO-GLIAL JUNCTION. IN ASSOCIATION WITH  
CONTACTIN MAY HAVE A ROLE IN THE SIGNALING BETWEEN AXONS AND  
MYELINATING GLIAL CELLS.  
CC -!- SUBUNIT: INTERACTS WITH CONTACTIN IN CIS FORM.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. WEAK  
EXPRESSION DETECTED IN OVARY, PANCREAS, COLON, LUNG, HEART,  
INTESTINE AND TESTIS.  
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -!- SIMILARITY: CONTAINS 4 LAMININ G-LIKE DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.  
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-----  
CC EMBL; U87223; AAB48481.1; -.  
CC HSSP; P12259; 1C2T.  
CC Genew; HGNC:8011; CNTNAP1.  
CC MIM; 602346; -.  
CC InterPro; IPR000561; EGF-like.  
CC InterPro; IPR000421; FASE\_C.  
CC InterPro; IPR002181; Fibrinogen\_C.  
CC InterPro; IPR001791; Laminin\_G.  
CC InterPro; IPR003585; Neurexin-like.  
CC Pfam; PF00008; EGF; 2.  
CC Pfam; PF00054; laminin\_G; 4.  
CC Pfam; PF00147; fibrinogen\_C; 1.  
CC Pfam; PF00754; F5\_F8\_type\_C; 1.  
CC SMART; SM00294; 4.1m; 1.  
CC SMART; SM00181; EGF; 1.  
CC SMART; SM00231; FA58C; 1.  
CC SMART; SM00186; FBG; 1.  
CC SMART; SM00282; LamG; 4.  
CC PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
CC PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
CC PROSITE; PS01285; FA58C\_1; 1.  
CC PROSITE; PS01286; FA58C\_2; 1.  
CC PROSITE; PS00534; FIBRIN\_AG\_C DOMAIN; FALSE\_NEG.  
CC PROSITE; PS00025; LAM\_G DOMAIN; 4.  
KW Glycoprotein; Cell adhesion; Signal; Transmembrane; SH3-binding;  
Repeat.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 1384 CONTACTIN ASSOCIATED PROTEIN 1.  
FT DOMAIN 20 1283 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1284 1304 POTENTIAL.  
FT DOMAIN 1305 1384 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 168 F5/8 TYPE C.  
FT DOMAIN 203 355 LAMININ G-LIKE 1.  
FT DOMAIN 389 538 LAMININ G-LIKE 2.  
FT DOMAIN 540 577 EGF-LIKE 1.  
FT DOMAIN 580 617 FIBRINOGEN C-TERMINAL.  
FT DOMAIN 813 956 EGF-LIKE 2.  
FT DOMAIN 957 996 LAMININ G-LIKE 3.  
FT DOMAIN 1088 1250 LAMININ G-LIKE 4.  
FT SITE 1328 1369 SH3-BINDING (POTENTIAL).  
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 597 597 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 653 653 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 664 664 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 763 763 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 843 843 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 860 860 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 948 948 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 956 956 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1078 1078 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1147 1147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1384 AA; 156265 MW; 7727A13DF626DDCA CRC64;

Query Match 90.0%; Score 27; DB 1; Length 1384;  
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVNA 5  
 |||||  
 676 SCVNS 680

Db

RESULT 33

CTAL\_MOUSE STANDARD; PRT; 1385 AA.

ID CTAL\_MOUSE  
 AC OS4991;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Contactin associated protein 1 precursor (Caspr) (Caspr1) (Neurexin 4)  
 GN CNTNAP1 OR NRXN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND POSSIBLE FUNCTION.  
 RX MEDLINE=21289247; PubMed=11395000;  
 RA Bhat M.A., Rios J.C., Lu Y., Ching W.,  
 RA St Martin M., Li J., Binheber S., Chesler M., Rosenbluth J.,  
 RA Salzer J.L., Beilen H.J.;  
 RT "Axon-glia interactions and the domain organization of myelinated  
 RT axons requires neurexin IV/Caspr/Paranodin.";  
 RL Neuron 30:369-383(2001).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=21403569; PubMed=11512672;  
 RA Arroyo E.J., Xu T., Poliak S., Watson M., Peles E., Scherer S.S.;  
 RA "Internodal specializations of myelinated axons in the central nervous  
 RT system.";  
 RL Cell Tissue Res. 305:53-66(2001).  
 CC -1- FUNCTION: SEEMS TO PLAY A ROLE IN THE FORMATION OF FUNCTIONAL  
 CC DISTINCT DOMAINS CRITICAL FOR SALTATORY CONDUCTION OF NERVE  
 CC IMPULSES IN MYELINATED NERVE FIBERS. SEEMS TO DEMARCAT THE  
 CC PARANODAL REGION OF THE AXO-GLIAL JUNCTION. IN ASSOCIATION WITH  
 CC CONTACTIN MAY HAVE A ROLE IN THE SIGNALING BETWEEN AXONS AND  
 CC MYELINATING GLIAL CELLS. MICE THAT LACK CNTNAP1 EXHIBIT TREMOR,  
 CC ATAXIA, AND SIGNIFICANT MOTOR PARESIS. NORMAL PARANODAL JUNCTIONS  
 CC FAIL TO FORM, AND THE ORGANIZATION OF THE PARANODAL LOOPS IS  
 CC DISRUPTED. CONTACTIN IS UNDETECTABLE IN THE PARANODES, AND  
 CC POTASSIUM CHANNELS ARE DISPLACED FROM THE JUNCTAPARANODAL INTO THE  
 CC PARANODAL DOMAINS. ALSO RESULTS IN A SEVERE DECREASE IN PERIPHERAL  
 CC NERVE CONDUCTION VELOCITY.  
 CC -1- SUBUNIT: INTERACTS WITH CONTACTIN IN CIS FORM (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN. IN MYELINATED NERVE FIBERS  
 CC PREDOMINANTLY FOUND IN PARANODAL AXOGIAL JUNCTIONS. IN THE  
 CC INTERNODAL REGION OF MYELINATED AXONS IN THE CNS AND THE PNS ALSO  
 CC FOUND AS A THIN LINE APPOSING THE INNER MESAXON OF THE MYELIN  
 CC SHEATH. IN PNS NEURONS THIS LINE FORMS A CIRCUMFERENTIAL RING THAT  
 CC APPoses THE INNERMOST ASPECT OF SCHMIDT-LANTERMAN INCISURES.

CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 4 LAMININ G-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF039833; AAB96760.1; -  
 DR HSSP; P12259; LCZT.  
 DR MGD; MGI:1858201; Cntnap1.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000421; FAS8 C.  
 DR InterPro; IPR002181; Fibrinogen C.  
 DR InterPro; IPR001791; Laminin G.  
 DR InterPro; IPR003585; Neurexin-like.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00554; laminin G; 4.  
 DR Pfam; PF00147; fibrinogen C; 1.  
 DR Pfam; PF00754; F5 F8 type C; 1.  
 DR SMART; SM00294; 4-1m; 1.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00231; FAS8C; 1.  
 DR SMART; SM00282; LamG; 4.  
 DR PROSITE; PS00022; EGF 1; FALSE NEG.  
 DR PROSITE; PS01186; EGF 2; FALSE NEG.  
 DR PROSITE; PS01285; FAS8C 1; 1.  
 DR PROSITE; PS01286; FAS8C 2; 1.  
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50025; LAM G\_DOMAIN; 4.  
 KW Glycoprotein; Cell adhesion; Signal; Transmembrane; SH3-binding;  
 KW Repeat.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 1385 CONTACTIN ASSOCIATED PROTEIN 1.  
 FT DOMAIN 21 1284 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1285 1305 POTENTIAL.  
 FT DOMAIN 1306 1385 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 26 169 F5/8 TYPE C.  
 FT DOMAIN 204 356 LAMININ G-LIKE 1.  
 FT DOMAIN 390 539 LAMININ G-LIKE 2.  
 FT DOMAIN 545 577 EGF-LIKE 1.  
 FT DOMAIN 581 618 FIBRINOGEN C-TERMINAL.  
 FT DOMAIN 814 958 LAMININ G-LIKE 3.  
 FT DOMAIN 962 996 EGF-LIKE 2.  
 FT DOMAIN 1089 1251 LAMININ G-LIKE 4.  
 FT SITE 1334 1370 SH3-BINDING (POTENTIAL).  
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 764 764 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 805 805 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 861 861 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 949 949 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 957 957 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1079 1079 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1148 1148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1385 AA; 156437 MW; 5F4FE33629E25DID CRC64;

Query Match 90.0%; Score 27; DB 1; Length 1385;  
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SCYNA 5
Db 677 SCYNS 681
|||||
RESULT 34
AGRI_RAT STANDARD; PRT; 1959 AA.
AC P25304; Q63034;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agrin precursor.
GN AGRN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
RC TISSUE=Embryonic spinal cord;
RX MEDLINE=91222570; PubMed=1851019;
RA Rupp F., Pavan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
RT "Structure and expression of a rat agrin.";
RN Neuron 6:811-823(1991).
[2]
RP SEQUENCE OF 1777-1801 FROM N.A.
RX MEDLINE=92407628; PubMed=1326608;
RA Rupp F., Oezcelik T., Linial M., Peterson K., Francke U., Scheller R.;
RT "Structure and chromosomal localization of the mammalian agrin gene.";
RN J. Neurosci. 12:3535-3544(1992).
CC -1- FUNCTION: COMPONENT OF THE BASAL LAMINA THAT CAUSES THE
CC AGGREGATION OF ACETYLCHOLINE RECEPTORS AND ACETYLCHOLINE-ESTERASE
CC ON THE SURFACE OF MUSCLE FIBERS OF THE NEUROMUSCULAR JUNCTION.
CC -1- SUBUNIT: BINDS TO LAMININ.
CC -1- SUBCELLULAR LOCATION: SYNAPTIC BASAL LAMINA AT THE NEUROMUSCULAR
CC JUNCTION.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4
CC AND 5; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR
CC ACETYLCHOLINE RECEPTOR CLUSTERING ACTIVITY.
CC -1- TISSUE SPECIFICITY: EMBRYONIC NERVOUS SYSTEM AND MUSCLE.
CC -1- DEVELOPMENTAL STAGE: MORE ABUNDANT EARLY IN DEVELOPMENT.
CC -1- PTM: CONTAINS HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-
CC LINKED OLIGOSACCHARIDES (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 9 KAZAL-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SEA DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-18 OR MET-24 IS THE
CC INITIATOR.
CC -----
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CC -----
DR EMBL; M64780; AAA40703.1; -
DR EMBL; M64780; AAA40702.1; ALT_INIT.
DR EMBL; S44194; AAB23326.1; -
DR PIR; JH0399; AGRT.
DR HSP; P00740; 1EDM.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003884; FcR1_MAC.
DR InterPro; IPR003645; FcR1.
DR InterPro; IPR001239; Kazal_inhib.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000082; SEA domain.
DR InterPro; IPR002350; kazal.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00050; Kazal; 9.
DR Pfam; PF00053; laminin_EGF; 2.
DR Pfam; PF00054; laminin_G; 3.
DR Pfam; PF01390; SEA; 1.
DR PRINTS; PR00290; KAZALINHBTR.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00001; EGF_like; 4.
DR SMART; SM00057; FIMAC; 3.
DR SMART; SM00274; FOLN; 5.
DR SMART; SM00280; KAZAL; 9.
DR SMART; SM00282; LamG; 3.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ TYPE EGF; 1.
DR PROSITE; PS00025; LAM_G DOMAIN; 3.
DR PROSITE; PS00024; SEA; 1.
KW Glycoprotein; EGF-like domain; Repeat; Alternative splicing; Signal;
KW Laminin EGF-like domain; Proteoglycan; Heparan sulfate.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 1959 AGRN.
FT DOMAIN 65 137 KAZAL-LIKE 1.
FT DOMAIN 141 212 KAZAL-LIKE 2.
FT DOMAIN 213 284 KAZAL-LIKE 3.
FT DOMAIN 287 356 KAZAL-LIKE 4.
FT DOMAIN 361 429 KAZAL-LIKE 5.
FT DOMAIN 430 494 KAZAL-LIKE 6.
FT DOMAIN 495 559 KAZAL-LIKE 7.
FT DOMAIN 563 645 KAZAL-LIKE 8.
FT DOMAIN 688 741 LAMININ EGF-LIKE 1.
FT DOMAIN 742 788 LAMININ EGF-LIKE 2.
FT DOMAIN 794 864 KAZAL-LIKE 9.
FT DOMAIN 1023 1145 SEA.
FT DOMAIN 1220 1258 EGF-LIKE 1.
FT DOMAIN 1263 1439 LAMININ G-LIKE 1.
FT DOMAIN 1440 1477 EGF-LIKE 2.
FT DOMAIN 1479 1516 EGF-LIKE 3.
FT DOMAIN 1526 1708 LAMININ G-LIKE 2.
FT DOMAIN 1709 1748 EGF-LIKE 4.
FT DOMAIN 1784 1956 LAMININ G-LIKE 3.
FT DOMAIN 869 992 SER/THR-RICH.
FT DOMAIN 1147 1215 SER/THR-RICH.
FT DISULFID 97 116 POTENTIAL.
FT DISULFID 105 137 POTENTIAL.
FT DISULFID 171 191 POTENTIAL.
FT DISULFID 180 212 POTENTIAL.
FT DISULFID 244 263 POTENTIAL.
FT DISULFID 252 284 POTENTIAL.
FT DISULFID 316 335 POTENTIAL.
FT DISULFID 324 356 POTENTIAL.
FT DISULFID 389 408 POTENTIAL.
FT DISULFID 397 429 POTENTIAL.
FT DISULFID 454 473 POTENTIAL.
FT DISULFID 462 494 POTENTIAL.
FT DISULFID 518 538 POTENTIAL.
FT DISULFID 527 559 POTENTIAL.
FT DISULFID 604 624 POTENTIAL.
FT DISULFID 613 645 POTENTIAL.
FT DISULFID 688 700 BY SIMILARITY.
FT DISULFID 690 707 BY SIMILARITY.
FT DISULFID 709 718 BY SIMILARITY.
FT DISULFID 721 739 BY SIMILARITY.
FT DISULFID 742 754 BY SIMILARITY.
FT DISULFID 744 761 BY SIMILARITY.
FT DISULFID 763 772 BY SIMILARITY.
FT DISULFID 775 786 BY SIMILARITY.
FT DISULFID 823 843 POTENTIAL.
FT DISULFID 832 864 POTENTIAL.
FT DISULFID 1224 1235 BY SIMILARITY.
FT DISULFID 1229 1246 BY SIMILARITY.

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FT DISULFID 1248 1257 BY SIMILARITY.  
 FT DISULFID 1444 1455 POTENTIAL.  
 FT DISULFID 1449 1465 POTENTIAL.  
 FT DISULFID 1467 1476 POTENTIAL.  
 FT DISULFID 1483 1494 BY SIMILARITY.  
 FT DISULFID 1488 1504 BY SIMILARITY.  
 FT DISULFID 1506 1515 BY SIMILARITY.  
 FT DISULFID 1713 1727 BY SIMILARITY.  
 FT DISULFID 1721 1736 BY SIMILARITY.  
 FT DISULFID 1738 1747 BY SIMILARITY.  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 827 827 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 957 957 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1144 1152 MISSING (IN ISOFORM 2).  
 FT VARSPLIC 1780 1798 MISSING (IN ISOFORM 3).  
 FT VARSPLIC 1788 1798 MISSING (IN ISOFORM 4).  
 FT VARSPLIC 1780 1787 MISSING (IN ISOFORM 5).  
 FT VARIANT 314 314 V -> VTCD (IN A VARIANT).  
 SQ SEQUENCE 1959 AA; 208645 MW; 7FEFDFAF89CC31 CRC64;  
 Query Match 90.0%; Score 27; DB 1; Length 1959;  
 Best Local Similarity 80.0%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYNA 5  
 Db 997 SCYNS 1001  
 RESULT 35  
 TX3C\_AGEAP STANDARD; PRT; 43 AA.  
 AC P81745;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Omega-agatoxin IIIC (Omega-Aga-IIIC) (Fragment).  
 OS Agelenopsis aperta (Funnel-web spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.  
 OX NCBI\_TaxID=6908;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=94227039; PubMed=8172884;  
 RA Ertel E.A., Warren V.A., Adams M.E., Griffin P.R., Cohen C.J.,  
 RA Smith M.M.;  
 RT "Type III omega-agatoxins: a family of probes for similar binding  
 sites on L- and N-type calcium channels.";  
 RL Biochemistry 33:5098-5108(1994).  
 CC -!- FUNCTION: OMEGA-AGATOXINS ARE ANTAGONISTS OF VOLTAGE-SENSITIVE  
 CALCIUM CHANNELS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- PTM: DISULFIDE BONDS ARE PRESENT (POTENTIAL).  
 CC -!- SIMILARITY: BELONGS TO THE OMEGA-AGATOXIN FAMILY.  
 KW Calcium channel inhibitor; Neurotoxin; Toxin; Presynaptic neurotoxin.  
 FT NON\_TER 43  
 SQ SEQUENCE 43 AA; 4773 MW; 67DD548E58E0A29C CRC64;  
 Query Match 86.7%; Score 26; DB 1; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYN 4  
 Db 26 SCYN 29  
 RESULT 36  
 NXS2\_LATCO STANDARD; PRT; 62 AA.  
 ID NXS2\_LATCO

AC P10457;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Short neurotoxin II.  
 OS Laticauda colubrina (Yellow-lipped sea krait).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Laticaudinae; Laticauda.  
 OX NCBI\_TaxID=8628;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Japanese, and Philippines; TISSUE=Venom;  
 RA Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,  
 RA Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;  
 RT "Neurotoxins of sea snakes genus Laticauda."  
 RL Toxicon 21 Suppl. 3:445-447(1983)  
 CC -!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR  
 TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC  
 ACETYLCHOLINE RECEPTOR.  
 CC PIR; B25866; B25866.  
 DR HSP; P01435; IQKE.  
 DR InterPro: IPR003571; Snake\_toxin.  
 DR Pfam: PF00087; toxin; 1.  
 DR ProDom: PD000206; Snake\_toxin; 1.  
 DR PROSITE: PS00272; SNAKE\_TOXIN; 1.  
 KW Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene family.  
 FT DISULFID 3 24 BY SIMILARITY.  
 FT DISULFID 17 41 BY SIMILARITY.  
 FT DISULFID 43 54 BY SIMILARITY.  
 FT DISULFID 55 60 BY SIMILARITY.  
 SQ SEQUENCE 62 AA; 7037 MW; BCBF27EED2D71D4E CRC64;  
 Query Match 86.7%; Score 26; DB 1; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYN 4  
 Db 23 SCYN 26  
 RESULT 37  
 NXSA\_LATCR STANDARD; PRT; 62 AA.  
 ID NXSA\_LATCR  
 AC P25495;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Short neurotoxin A.  
 OS Laticauda crockeri (Crocker's sea krait).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Laticaudinae; Laticauda.  
 OX NCBI\_TaxID=8629;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,  
 RA Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;  
 RT "Neurotoxins of sea snakes genus Laticauda."  
 RL Toxicon 21 Suppl. 3:445-447(1983)  
 CC -!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR  
 TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC  
 ACETYLCHOLINE RECEPTOR.  
 CC HSP; P01435; IQKE.  
 DR InterPro: IPR003571; Snake\_toxin.  
 DR Pfam: PF00087; toxin; 1.  
 DR ProDom: PD000206; Snake\_toxin; 1.  
 DR PROSITE: PS00272; SNAKE\_TOXIN; 1.  
 KW Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene family.  
 FT DISULFID 3 24 BY SIMILARITY.  
 FT DISULFID 17 41 BY SIMILARITY.

```

FT DISULFID 43 54 BY SIMILARITY.
FT DISULFID 55 60 BY SIMILARITY.
SQ SEQUENCE 62 AA; 7023 MW; 056C228901737F8F CRC64;

Query Match 86.7%; Score 26; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
DB 23 SCYN 26

RESULT 38
NXSB_LATCR STANDARD; PRT; 62 AA.
AC P25496;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Short neurotoxin B.
OS Laticauda crockeri (Crocker's sea krait).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=9629;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,
RA Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;
RT "Neurotoxins of sea snakes genus Laticauda.";
RL Toxicon 21 Suppl. 3:445-447(1983).
CC -!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
CC TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
CC ACETYLCHOLINE RECEPTOR.
DR HSSP; P01435; 1QKE.
DR InterPro: IPR003571; Snake_toxin.
DR Pfam: PF00087; toxin; 1.
DR ProDom: PD000206; Snake_toxin; 1.
DR PROSITE: PS00272; SNAKE_TOXIN; 1.
KW Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene family.
FT DISULFID 3 24 BY SIMILARITY.
FT DISULFID 17 41 BY SIMILARITY.
FT DISULFID 43 54 BY SIMILARITY.
FT DISULFID 55 60 BY SIMILARITY.
SQ SEQUENCE 62 AA; 7040 MW; 056A943901737C40 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
DB 23 SCYN 26

RESULT 39
NXSB_LATLA STANDARD; PRT; 62 AA.
AC P10459;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Short neurotoxin B.
OS Laticauda laticaudata (Blue-ringed sea krait).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8630;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;

```

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RX MEDLINE=86159724; PubMed=3955004;
RA Tamiya N.;
RL Unpublished results, cited by:
RL Endo T., Nakanishi M., Furukawa S., Joubert F.J., Tamiya N.,
RL Hayashi K.;
RL Biochemistry 25:395-404(1986).
CC -!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
CC TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
CC ACETYLCHOLINE RECEPTOR.
DR PIR; G25866; G25866.
DR HSSP; P01435; 1QKE.
DR InterPro: IPR003571; Snake_toxin.
DR Pfam: PF00087; toxin; 1.
DR ProDom: PD000206; Snake_toxin; 1.
DR PROSITE: PS00272; SNAKE_TOXIN; 1.
KW Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene family.
FT DISULFID 3 24 BY SIMILARITY.
FT DISULFID 17 41 BY SIMILARITY.
FT DISULFID 43 54 BY SIMILARITY.
FT DISULFID 55 60 BY SIMILARITY.
SQ SEQUENCE 62 AA; 6973 MW; 0571DBF401737C40 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
DB 23 SCYN 26

RESULT 40
NXSC_LATCO STANDARD; PRT; 62 AA.
AC P10455;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Short neurotoxin C.
OS Laticauda colubrina (Yellow-lipped sea krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8628;
RN [1]
RP SEQUENCE.
RC STRAIN=Salomon Island, and Fiji; TISSUE=Venom;
RA Tamiya N., Sato A., Kim H.S., Teruuchi T., Takasaki C., Ishikawa Y.,
RA Guinea M.L., McCoy M., Heatwole H., Cogger H.G.;
RT "Neurotoxins of sea snakes genus Laticauda.";
RL Toxicon 21 Suppl. 3:445-447(1983).
CC -!- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
CC TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
CC ACETYLCHOLINE RECEPTOR.
DR PIR; G25866; C25866.
DR HSSP; P01435; 1QKE.
DR InterPro: IPR003571; Snake_toxin.
DR Pfam: PF00087; toxin; 1.
DR ProDom: PD000206; Snake_toxin; 1.
DR PROSITE: PS00272; SNAKE_TOXIN; 1.
KW Venom; Neurotoxin; Postsynaptic neurotoxin; Multigene family.
FT DISULFID 3 24 BY SIMILARITY.
FT DISULFID 17 41 BY SIMILARITY.
FT DISULFID 43 54 BY SIMILARITY.
FT DISULFID 55 60 BY SIMILARITY.
SQ SEQUENCE 62 AA; 7064 MW; BCA94B3ED2D71D4E CRC64;

Query Match 86.7%; Score 26; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYN 4
DB 23 SCYN 26

```

Db 23 SCYN 26

Search completed: July 18, 2003, 15:07:15  
Job time : 3.1 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:02:40 ; Search time 12.9 Seconds  
(without alignments)  
79.863 Million cell updates/sec

Title: US-10-007-790-6  
Perfect score: 30  
Sequence: 1 SCYNA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriapi:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	346	4 Q95274	Q95274 homo sapien
2	30	100.0	346	4 Q9UJ74	Q9UJ74 homo sapien
3	30	100.0	460	10 Q9FG85	Q9FG85 arabidopsis
4	30	100.0	522	12 Q9XVT0	Q9XVT0 melanoplus
5	27	90.0	105	12 Q9WAZ6	Q9WAZ6 tt virus. o
6	27	90.0	108	4 Q9UFY0	Q9UFY0 homo sapien
7	27	90.0	114	10 Q9S9A0	Q9S9A0 viscum albu
8	27	90.0	118	17 Q8ZU2	Q8ZU2 pyrobaculum
9	27	90.0	129	12 Q9JFM1	Q9JFM1 human adeno
10	27	90.0	137	10 Q42838	Q42838 hordeum vul
11	27	90.0	148	10 Q65095	Q65095 picea maria
12	27	90.0	150	10 Q9SPX8	Q9SPX8 picea abies
13	27	90.0	151	10 Q9SPX9	Q9SPX9 picea abies
14	27	90.0	151	10 Q9SPW5	Q9SPW5 picea glauc
15	27	90.0	154	10 Q9SPX7	Q9SPX7 picea abies
16	27	90.0	154	10 Q9SPW4	Q9SPW4 picea glauc

17	27	90.0	156	10	Q65097	Q65097 picea maria
18	27	90.0	156	12	Q9LEX6	Q9LEX6 cydia pomon
19	27	90.0	203	2	Q07298	Q07298 pseudomonas
20	27	90.0	209	5	Q9BI13	Q9BI13 entamoeba h
21	27	90.0	241	2	Q9ZA84	Q9ZA84 proteus mir
22	27	90.0	246	10	Q82652	Q82652 arabidopsis
23	27	90.0	267	16	Q9HWE2	Q9HWE2 pseudomonas
24	27	90.0	278	4	Q9NDU18	Q9NDU18 homo sapien
25	27	90.0	284	5	Q45844	Q45844 caenorhabdi
26	27	90.0	287	5	Q17958	Q17958 caenorhabdi
27	27	90.0	288	16	Q9PNM5	Q9PNM5 campylobact
28	27	90.0	292	16	Q8ZBD6	Q8ZBD6 versinia pe
29	27	90.0	292	16	Q8Z314	Q8Z314 salmonella
30	27	90.0	298	16	Q8ZLF9	Q8ZLF9 salmonella
31	27	90.0	298	16	Q8XA90	Q8XA90 escherichia
32	27	90.0	304	3	Q13628	Q13628 schizosacch
33	27	90.0	325	5	Q61969	Q61969 caenorhabdi
34	27	90.0	325	16	Q9KVD4	Q9KVD4 vibrio chol
35	27	90.0	341	5	Q966W1	Q966W1 halocynthia
36	27	90.0	352	11	Q55162	Q55162 rattus norv
37	27	90.0	359	10	Q9SCP7	Q9SCP7 arabidopsis
38	27	90.0	363	11	Q91YK8	Q91YK8 mus musculu
39	27	90.0	376	2	Q9X500	Q9X500 uncultured
40	27	90.0	376	2	Q9X504	Q9X504 uncultured
41	27	90.0	376	2	Q9X505	Q9X505 uncultured
42	27	90.0	376	2	Q9X506	Q9X506 uncultured
43	27	90.0	376	2	Q9X508	Q9X508 uncultured
44	27	90.0	376	2	Q9X511	Q9X511 uncultured
45	27	90.0	376	2	Q9X516	Q9X516 uncultured

#### ALIGNMENTS

#### RESULT 1

ID Q95274 PRELIMINARY; PRT; 346 AA.

AC Q95274;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE GPI-anchored metastasis-associated protein homolog.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21139111; PubMed=11245483;  
RA Smith B.A., Kennedy W.J., Harnden P., Selby P.J., Trejdosiewicz L.K.,  
RA Southgate J.;  
RT "Identification of genes involved in human urothelial cell-matrix  
RT interactions: implications for the progression pathways of malignant  
RT urothelium.";  
RL Cancer Res. 61:1678-1685(2001).  
DR EMBL; AF082889; AAD13751.1; -.  
DR InterPro; IPR001526; LY6\_UPAR.  
DR SMART; SM00134; LU; 1.  
SQ SEQUENCE 346 AA; 35924 MW; CDFP9948FF493130 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 346;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYNA 5

Db 160 SCYNA 164

#### RESULT 2

Q9UJ74 PRELIMINARY; PRT; 346 AA.  
ID Q9UJ74  
AC Q9UJ74;

```
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 36.0 kDa protein (C4.4A protein).
GN C4.4A.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hassel B., Reimann M., Wuerfel J., Claas A., Savelyeva L., Schwab M.,
RA Roessel M., Matzku S., Zoeller M.;
RT "Cloning of the human homologue of the metastasis-associated rat
RT C4.4A.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
RA Danganan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefficient J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of 19q13.2.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ223603; CAAL1469.2; -
DR EMBL; AC018758; AAG09062.1; -
DR InterPro; IPR001526; LV6_UPAR.
DR SMART; SM00134; LU; 1.
KW Hypothetical protein.
SQ SEQUENCE 346 AA; 35970 MW; 97FF9B4A554934PF CRC64;

Query Match 100.0%; Score 30; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
DB 160 SCYNA 164

RESULT 3
ID Q9FG85 PRELIMINARY; PRT; 460 AA.
AC Q9FG85;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Genomic DNA, chromosome 5, P1 clone:MQB19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026651; BAB11307.1; -
DR InterPro; IPR002885; PPR.
DR Pfam; PF01535; PPR; 7.
DR TIGRFAms; TIGR00756; PPR; 5.
SQ SEQUENCE 460 AA; 51644 MW; B956D35DFE01C3A1 CRC64;

Query Match 100.0%; Score 30; DB 10; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SCYNA 5
DB 283 SCYNA 287

RESULT 4
ID Q9YV70 PRELIMINARY; PRT; 522 AA.
AC Q9YV70;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ORF MSV162 putative NAD+ dependent DNA ligase, similar to Thermus
DE thermophilus SW:P26996.
GN MSV162.
OS Melanoplus sanguinipes entomopoxvirus (MaEPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=83191;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=TUCSON;
RX MEDLINE=99102612; PubMed=9847359;
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
RL J. Virol. 73:533-552(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=TUCSON;
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063866; AAC97679.1; -
DR InterPro; IPR001679; DNALigase.
DR InterPro; IPR001679; DNALigase.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01653; DNA_ligase_N; 1.
DR Pfam; PF03120; DNA_ligase_OB; 1.
DR ProDom; PD003944; DNALigase; 1.
DR SMART; SM00532; LIGANC; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 522 AA; 60235 MW; 1B17E513872C33A2 CRC64;

Query Match 100.0%; Score 30; DB 12; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
DB 321 SCYNA 325

RESULT 5
ID Q9WAZ6 PRELIMINARY; PRT; 105 AA.
AC Q9WAZ6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF2 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=HIJ/2-4-E;
RX MEDLINE=99335592; PubMed=10405352;
RA Hijikata M., Takahashi K., Mishihiro S.;
RT "Complete circular DNA genome of a TT virus variant (isolate name
RT SANBAN) and 44 partial ORF2 sequences implicating a great degree of
RT diversity beyond genotypes.";
RL Virology 260:17-22(1999).
```

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DR EMBL; AB024357; BAA77424.1; -.
DR InterPro; IPR004118; TT_ORF2.
DR Pfam; PF02957; TT_ORF2; 1.
FT NON TER 105_105
SQ SEQUENCE 105 AA; 11792 MW; 4F2949E0F796EA3C CRC64;

Query Match 90.0%; Score 27; DB 12; Length 105;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db :||||
47 ACYNA 51

RESULT 6
Q9UFY0 PRELIMINARY; PRT; 108 AA.
AC Q9UFY0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 12.0 kDa protein.
GN DKFZP434N221.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL110299; CAB53740.1; -.
DR HSSP; P51977; 1BXS.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF00171; aldehyd; 1.
KW Hypothetical protein.
SQ SEQUENCE 108 AA; 11956 MW; 59572E281D3FB01B CRC64;

Query Match 90.0%; Score 27; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db :||||
62 NCYNA 66

RESULT 7
Q9S9A0 PRELIMINARY; PRT; 114 AA.
AC Q9S9A0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE THIONIN.
OS Viscum album (European mistletoe).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=3972;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94122387; PubMed=8292787;
RA Schrader-Fischer G., Apel K.;
RL Plant Mol. Biol. 23:1233-1242(1993).
CC -!- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO
CC ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL
CC OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE
CC PROTEINS IS NOT KNOWN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
DR HSSP; P01544; 2PLH.

DR EMBL; IPR001010; Thionin.
DR Pfam; PF00321; plant thionins; 1.
DR PROSITE; PS00271; THIONIN; 1.
KW Plant toxin; Thionin.
SQ SEQUENCE 114 AA; 11981 MW; D30BFC724907CE7D CRC64;

Query Match 90.0%; Score 27; DB 10; Length 114;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db :||||
37 NCYNA 41

RESULT 8
Q8ZUU2 PRELIMINARY; PRT; 118 AA.
AC Q8ZUU2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Conserved within P. aerophilum.
GN PAE2605.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AF009886; AAL64314.1; -.
KW Complete proteome.
SQ SEQUENCE 118 AA; 13466 MW; BAE5CDAF26BD132 CRC64;

Query Match 90.0%; Score 27; DB 17; Length 118;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db :||||
29 ACYNA 33

RESULT 9
Q9JFM1 PRELIMINARY; PRT; 129 AA.
AC Q9JFM1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Early E3B 14.5 kDa protein.
OS Human adenovirus type 8..
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=31545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PREIBURG 1127;
RX MEDLINE=20475623; PubMed=11022786;
RA Burger H.G., Blusch J.H.;
RT "Immunomodulatory functions encoded by the E3 transcription unit of
RT adenoviruses."
RL Virus Genes 21:13-25(2000).
DR EMBL; AF086570; AAF31748.1; -.
SQ SEQUENCE 129 AA; 14750 MW; B347ES0EPPFA56DEB CRC64;

Query Match 90.0%; Score 27; DB 12; Length 129;
```

Best Local Similarity 80.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1;

QY 1 SCYNA 5  
:||||  
Db 33 NCYNA 37

## RESULT 10

Q42838 Q42838 PRELIMINARY; PRT; 137 AA.  
AC Q42838;  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DE Thionin.  
GN BTH7.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Holtorf S., Schuetz C., Apel K., Bohlmann H.;  
RT "Specific and distinct expression patterns of two members of the  
RT thionin multigene family of barley in transgenic tobacco."  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC TO  
CC ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE LEVEL  
CC OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS, OF THESE  
CC PROTEINS IS NOT KNOWN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.  
DR EMBL; L36883; AAA91048.1; -.  
DR HSP; P01543; IBHP.  
DR InterPro; IPR001010; Thionin.  
DR Pfam; PF00321; plant thionins; 1.  
DR PROSITE; PS00271; THIONIN; 1.  
KW Plant toxin; Thionin.  
SQ SEQUENCE 137 AA; 14676 MW; 78DBAF7082F205BE CRC64;

Query Match 90.0%; Score 27; DB 10; Length 137;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 39 NCYNA 43

## RESULT 11

O65095 O65095 PRELIMINARY; PRT; 148 AA.  
AC O65095;  
DT 01-AUG-1998 (T-EMBLrel. 07, Created)  
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)  
DE Thionin.  
DE ATAFI-like protein (Fragment).  
GN SB29.  
OS Picea mariana (Black spruce).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
OX NCBI\_TaxID=3335;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Perry D.J., Bousquet J.;  
RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development,  
RT characterization and analysis of linkage in black spruce."  
RL Genetics 149:1089-1098(1998).  
DR EMBL; AF051748; AAC32165.1; -.  
FT NON TER 1  
SQ SEQUENCE 148 AA; 16658 MW; 78091616816D081A CRC64;

Query Match 90.0%; Score 27; DB 10; Length 148;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1;

QY 1 SCYNA 5  
:||||  
Db 13 TCYNA 17

## RESULT 12

Q9SPX8 Q9SPX8 PRELIMINARY; PRT; 150 AA.  
AC Q9SPX8;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DE ATAFI-like protein (Fragment).  
GN SB29.  
OS Picea abies (Norway spruce) (Picea excelsa).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
OX NCBI\_TaxID=3329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=99436016; PubMed=10504420;  
RA Perry D.J., Isabel N., Bousquet J.;  
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and  
RT nature of variation revealed in norway spruce."  
RL Hereditas 83:239-248(1999).  
DR EMBL; AF127441; AAF02458.1; -.  
FT NON TER 1  
SQ SEQUENCE 150 AA; 16881 MW; 9041961A0A027040 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 150;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||  
Db 12 TCYNA 16

## RESULT 13

Q9SPX9 Q9SPX9 PRELIMINARY; PRT; 151 AA.  
AC Q9SPX9;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DE ATAFI-like protein (Fragment).  
GN SB29.  
OS Picea abies (Norway spruce) (Picea excelsa).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
OX NCBI\_TaxID=3329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=99436016; PubMed=10504420;  
RA Perry D.J., Isabel N., Bousquet J.;  
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and  
RT nature of variation revealed in norway spruce."  
RL Hereditas 83:239-248(1999).  
DR EMBL; AF127440; AAF02457.1; -.  
FT NON TER 1  
SQ SEQUENCE 151 AA; 17040 MW; F66A2D3F38C8938 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 151;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
:||||

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Db 12 TCYNA 16

RESULT 14
Q9SPW5 ID Q9SPW5 PRELIMINARY; PRT; 151 AA.
AC Q9SPW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ATAF1-like protein (Fragment).
GN SB29.
OS Picea glauca (White spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Heredit 83:239-248(1999)
DR EMBL; AF127599; AAF02475.1; -.
FT NON_TER 1
SQ SEQUENCE 151 AA; 16989 MW; D7CB90183E39E4BC CRC64;

Query Match 90.0%; Score 27; DB 10; Length 151;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 12 TCYNA 16

RESULT 15
Q9SPX7 ID Q9SPX7 PRELIMINARY; PRT; 154 AA.
AC Q9SPX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ATAF1-like protein (Fragment).
GN SB29.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Heredit 83:239-248(1999)
DR EMBL; AF127442; AAF02459.1; -.
FT NON_TER 1
SQ SEQUENCE 154 AA; 17227 MW; AE819A9BF970C85D CRC64;

Query Match 90.0%; Score 27; DB 10; Length 154;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 12 ACYNA 16

RESULT 16
Q9SPW4 ID Q9SPW4 PRELIMINARY; PRT; 154 AA.
AC Q9SPW4;
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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ATAF1-like protein (Fragment).
GN SB29.
OS Picea glauca (White spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436016; PubMed=10504420;
RA Perry D.J., Isabel N., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: the amount and
RT nature of variation revealed in norway spruce.";
RL Heredit 83:239-248(1999)
DR EMBL; AF127600; AAF02476.1; -.
FT NON_TER 1
SQ SEQUENCE 154 AA; 17306 MW; 409443B6ED916940 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 154;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 12 TCYNA 16

RESULT 17
O65097 ID O65097 PRELIMINARY; PRT; 156 AA.
AC O65097;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATAF1-like protein (Fragment).
GN SB29.
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes. Development,
RT characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998)
DR EMBL; AF051750; AAC32167.1; -.
FT NON_TER 1
SQ SEQUENCE 156 AA; 17505 MW; 477DE40D27F1C969 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 156;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 12 TCYNA 16

RESULT 18
Q91EX6 ID Q91EX6 PRELIMINARY; PRT; 156 AA.
AC Q91EX6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ORF79 similar to ACMPV ORF150.
GN ORF79.
OS Cydia pomonella granulosis virus (OpGV) (Cydia pomonella
OS Granulovirus).
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OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=28289;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=93188168; PubMed=8445726;
RX Crook N.E., Clem R.J., Miller L.K.;
RA "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
RT motif.";
RL J. Virol. 67:2168-2174 (1993).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=96207404; PubMed=8615018;
RX Theilmann D.A., Chantler J.K., Stewart S., Flipsen H.T., Vlak J.M.,
RA Crook N.E.;
RA "Characterization of a highly conserved baculovirus structural protein
RT that is specific for occlusion-derived virions.";
RL Virology 218:148-158 (1996).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=97380577; PubMed=9237352;
RX Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;
RA "Complete sequence and transposon mutagenesis of the BamHI J fragment
RT of Cydia pomonella granulosis virus.";
RL Virus Genes 14:131-136 (1997).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=98418511; PubMed=9747739;
RX Kang W., Tristem M., Maeda S., Crook N.E., O'Reilly D.R.;
RA "Identification and characterization of the Cydia pomonella
RT granulovirus cathepsin and chitinase genes.";
RL J. Gen. Virol. 79:2283-2292 (1998).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RA "The complete sequence of the Cydia pomonella granulovirus genome.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53466; AAK70739.1; -.
DR InterPro; IPR002557; Chitin_bind_PerA.
DR Pfam; PF01607; CBM_14.1.
SQ SEQUENCE 156 AA; 17807 MW; E5E0E0107C5554FA CRC64;

Query Match 90.0%; Score 27; DB 12; Length 156;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
DB 127 TCYNA 131

RESULT 19
O07298 PRELIMINARY; PRT; 203 AA.
AC O07298;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dioxigenase.
GN PAHD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OUS82;
RA Takizawa N.;
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=28289;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=93188168; PubMed=8445726;
RX Crook N.E., Clem R.J., Miller L.K.;
RA "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
RT motif.";
RL J. Virol. 67:2168-2174 (1993).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=96207404; PubMed=8615018;
RX Theilmann D.A., Chantler J.K., Stewart S., Flipsen H.T., Vlak J.M.,
RA Crook N.E.;
RA "Characterization of a highly conserved baculovirus structural protein
RT that is specific for occlusion-derived virions.";
RL Virology 218:148-158 (1996).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=97380577; PubMed=9237352;
RX Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;
RA "Complete sequence and transposon mutagenesis of the BamHI J fragment
RT of Cydia pomonella granulosis virus.";
RL Virus Genes 14:131-136 (1997).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC MEDLINE=98418511; PubMed=9747739;
RX Kang W., Tristem M., Maeda S., Crook N.E., O'Reilly D.R.;
RA "Identification and characterization of the Cydia pomonella
RT granulovirus cathepsin and chitinase genes.";
RL J. Gen. Virol. 79:2283-2292 (1998).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=MEXICAN 1;
RC Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RA "The complete sequence of the Cydia pomonella granulovirus genome.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53466; AAK70739.1; -.
DR InterPro; IPR002557; Chitin_bind_PerA.
DR Pfam; PF01607; CBM_14.1.
SQ SEQUENCE 156 AA; 17807 MW; E5E0E0107C5554FA CRC64;

Query Match 90.0%; Score 27; DB 12; Length 156;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
DB 127 TCYNA 131

RESULT 19
O07298 PRELIMINARY; PRT; 203 AA.
AC O07298;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dioxigenase.
GN PAHD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OUS82;
RA Takizawa N.;
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
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[2]
RN SEQUENCE FROM N.A.
RP STRAIN=OUS82;
RC Noboru T., Toshiya I., Takashi S., Kazuhiro Y., Masamichi K.,
RA Yue-Wu W., Masao F., Hozoh K.;
RA "The molecular analysis of NAH7-type cluster located on the
RT chromosomes of Pseudomonas aeruginosa Paki and Pseudomonas putida
RT OUS82.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004059; BAA20398.1; -.
DR InterPro; IPR004287; HCCA isomerase.
DR Pfam; PF03046; HCCA isomerase; 1.
SQ SEQUENCE 203 AA; 23134 MW; 6779C14A8E862CB6 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 203;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
DB 32 TCYNA 36

RESULT 20
O9B113 PRELIMINARY; PRT; 209 AA.
AC O9B113;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 24.0 kDa protein.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1:IMSS;
RX MEDLINE=21428156; PubMed=11545438;
RA Willhoest U., Campos-Congora E., Touzni S., Bruchhaus I., Tannich E.;
RT "Introns of Entamoeba histolytica and Entamoeba dispar.";
RL Protist 152:149-156 (2001).
DR EMBL; AJ311623; CAC34301.1; -.
KW Hypothetical protein.
SQ SEQUENCE 209 AA; 24041 MW; 618A8EC9CD515FCB CRC64;

Query Match 90.0%; Score 27; DB 5; Length 209;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
DB 80 SCYNS 84

RESULT 21
O9ZA84 PRELIMINARY; PRT; 241 AA.
AC O9ZA84;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE STM-proteaseB (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HI4320;
RX MEDLINE=99140151; PubMed=10206698;
RA Zhao H., Li X., Johnson D.E., Mobley H.L.;
RT "Identification of protease and rpoN-associated genes of uropathogenic
RT Proteus mirabilis by negative selection in a mouse model of ascending
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RT urinary tract infection.";
RL Microbiology 145:185-195(1999).
RL EMBL; AF089881; AAC64578.1; -.
FW Protease.
KT NON TER 241 241
SQ SEQUENCE 241 AA; 27628 MW; 074A6CE9731E41FB CRC64;

Query Match
Best Local Similarity 90.0%; Score 27; DB 2; Length 241;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 117 NCYNA 121

RESULT 22
O82652 PRELIMINARY; PRT; 246 AA.
AC O82652;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TB1C3-1 protein (Fragment).
GN TB1C3-1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA 0; TISSUE=SILIQUES;
RA Aubourg S.;
RL Thesis (1998), Universite Paris, FRANCE.
DR EMBL; AJ011845; CAA09808.1; -.
DR InterPro; IPR004314; DUF239.
DR Pfam; PF03080; DUF239; 1.
FT NON TER 1 1
FT NON TER 246 246
SQ SEQUENCE 246 AA; 28017 MW; 23107880586D1980 CRC64;

Query Match
Best Local Similarity 90.0%; Score 27; DB 10; Length 246;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 186 SCYNS 190

RESULT 23
O9HWB2 PRELIMINARY; PRT; 267 AA.
AC O9HWB2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable transcriptional regulator.
GN FA4288.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.B., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AE004845; AAG07676.1; -.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF00165; HTH AtAc; 2.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH ARAC; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 267 AA; 30168 MW; 1F6FEC2B26ECD266 CRC64;

Query Match
Best Local Similarity 90.0%; Score 27; DB 16; Length 267;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 76 SCYNS 80

RESULT 24
Q9NU18 PRELIMINARY; PRT; 278 AA.
AC Q9NU18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DJ298J18.3 (Novel protein similar to putative HIV-1 induced protein
DE HIN-1 and Drosophila ovarian tumor locus protein OTU) (Fragment).
GN DJ298J18.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawlor S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096764; CAB89278.1; -.
DR InterPro; IPR003323; OTU.
DR Pfam; PF02338; OTU; 1.
DR PROSITE; PS50802; OTU; 1.
FT NON TER 1 1
FT NON TER 278 278
SQ SEQUENCE 278 AA; 32183 MW; E2266035B8752505 CRC64;

Query Match
Best Local Similarity 90.0%; Score 27; DB 4; Length 278;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 201 ACYNA 205

RESULT 25
O45844 PRELIMINARY; PRT; 284 AA.
AC O45844;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T2624.13 protein.
GN T2624.13.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Telodermata; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP SEQUENCE FROM N.A.
RA McMurray A.A.; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE 99069613; PubMed=9851916;
RX MEDLINE=99069613;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81132; CAB03439.1; -.
DR InterPro; IPR002892; DUF40.
DR Pfam; PF01838; DUF40; 1.
SQ SEQUENCE 284 AA; 32288 MW; 62C42A32215A5D74 CRC64;

Query Match 90.0%; Score 27; DB 5; Length 284;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 164 SCYNS 168

RESULT 26
O17958 PRELIMINARY; PRT; 287 AA.
AC O17958;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE M01B2.4 protein.
GN M01B2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z83116; CAB05562.1; -.
DR InterPro; IPR002892; DUF40.
DR Pfam; PF01838; DUF40; 1.
SQ SEQUENCE 287 AA; 32892 MW; 0C627F0AF7E0DEFE CRC64;

Query Match 90.0%; Score 27; DB 5; Length 287;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 166 SCYNS 170

RESULT 27
Q9PNM5 PRELIMINARY; PRT; 288 AA.
AC Q9PNM5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein Cj1069.
GN Cj1069.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;

RP SEQUENCE FROM N.A.
RA NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 11168; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
  Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
  Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
  Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
  Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
  reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; ALI39077; CAB73324.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 288 AA; 34645 MW; 21E9C8CF4DC221E CRC64;

Query Match 90.0%; Score 27; DB 16; Length 288;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 63 ACYNA 67

RESULT 28
Q8ZBD6 PRELIMINARY; PRT; 292 AA.
AC Q8ZBD6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein YPO3480.
GN YPO3480.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=CO-92 / BIOVAR ORIENTALIS;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
  Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
  Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
  Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
  Feltwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
  Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
  Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414157; CAC92709.1; -.
DR InterPro; IPR001539; Peptidase U32.
DR ProDom; PD004398; Peptidase U32; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 292 AA; 32714 MW; 3CC6EDD893C7AA9F CRC64;

Query Match 90.0%; Score 27; DB 16; Length 292;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5
Db 117 NCYNA 121

RESULT 29
Q8Z3I4 PRELIMINARY; PRT; 292 AA.
AC Q8Z3I4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
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DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein STY3458.
GN STY3458.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627278; CAD07797.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 292 AA; 32530 MW; B49857895AF2E6A3 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 292;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVNA 5
Db 117 NCYNA 121

RESULT 30
Q8ZLT9 PRELIMINARY; PRT; 298 AA.
AC Q8ZLT9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Putative protease.
GN YHBV OR STM3275.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008850; AAL22147.1; --
KW Protease; Hypothetical protein; Complete proteome.
SQ SEQUENCE 298 AA; 33130 MW; 2F426C1DFF08FABE CRC64;

Query Match 90.0%; Score 27; DB 16; Length 298;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVNA 5
Db 123 NCYNA 127

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RESULT 31
Q8XA90 PRELIMINARY; PRT; 298 AA.
AC Q8XA90;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Orf, hypothetical protein.
GN YHBV OR Z4520 OR ECS4040.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005544; AAG58295.1; --
DR EMBL; AP02564; BAB37463.1; --
KW Complete proteome.
SQ SEQUENCE 298 AA; 33206 MW; F30AD7D492D62A1B CRC64;

Query Match 90.0%; Score 27; DB 16; Length 298;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVNA 5
Db 123 NCYNA 127

RESULT 32
O13628 PRELIMINARY; PRT; 304 AA.
AC O13628;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PAS4 protein.
GN P1036.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972 H-;
RX MEDLINE=20089027; PubMed=10620777;
RA Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K.,
RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA Sakai M., Aoki K., Ogura K., Kikuchi H., Zhang M.Q.,
RA Yanagida M.;

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RT "A 38 kb segment containing the cdc2 gene from the left arm of fission  
 RT yeast chromosome II: sequence analysis and characterization of the  
 RT genomic DNA and cDNAs encoded on the segment.";

RL Yeast 16:71-80(2000).

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; AB004537; BAA21416.1; -

DR InterPro; IPR001841; Znf ring.

DR Pfam; PF000097; zf-C3HC4; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS00518; ZF\_RING\_1; 1.

KW Zinc-finger.

SQ SEQUENCE 304 AA; 34283 MW; C87F5F5A24217F23 CRC64;

Query Match 90.0%; Score 27; DB 3; Length 304;  
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCVNA 5

Db 244 SCVNS 248

RESULT 33

O61969 PRELIMINARY; PRT; 325 AA.

AC O61969;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical 38.0 kDa protein.

GN H05B21.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Pelodirinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode C. elegans: a platform for

RT investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Miller N.;

RT "The sequence of C. elegans cosmid H05B21.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RT "Direct Submission.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF068717; AAC17763.1; -

DR InterPro; IPR003003; 7TM\_chemo2.

DR InterPro; IPR000168; 7TM\_nematode.

DR InterPro; IPR000215; Serpin.

DR Pfam; PF01604; 7tm 5; 1.

DR PROSITE; PS00284; SERPIN; UNKNOWN 1.

KW Hypothetical protein.

SQ SEQUENCE 325 AA; 37998 MW; B0FA2C7390F5619E CRC64;

Query Match 90.0%; Score 27; DB 5; Length 325;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCVNA 5

Db 2 NCVNA 6

RESULT 34

O9KVD4

ID O9KVD4 PRELIMINARY; PRT; 325 AA.

AC O9KVD4;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Lipid A biosynthesis (kdo)2-(lauroyl)-lipid IVA acyltransferase.

GN VC0212.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI\_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N16961 / SEROTYPE O1;

RA MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio

RT cholerae.";

RL Nature 406:477-483(2000).

DR EMBL; AS004111; AAF93388.1; -

DR TIGR; VC0212; -

DR InterPro; IPR004960; LipA\_acyltrns.

DR Pfam; PF03279; Lip\_A\_acyltrns; 1.

KW Complete proteome.

SQ SEQUENCE 325 AA; 37215 MW; 3F949ED94B5C5F92 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 325;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCVNA 5

Db 252 SCVNS 256

RESULT 35

O966W1

ID O966W1 PRELIMINARY; PRT; 341 AA.

AC O966W1;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Ficolin 4.

GN ASFCN4.

OS Halocynthia roretzi (Sea squirt).

OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;

OC Stolidobranchia; Pyuridae; Halocynthia.

OX NCBI\_TaxID=7729;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21282877; PubMed=11259430;

RA Kenjo A., Takahashi M., Matsushita M., Endo Y., Nakata M.,

RA Mizuochi T., Fujita T.;

RT "Cloning and Characterization of Novel Ficolins from the Solitary

RT Ascidian, Halocynthia roretzi.";

RL J. Biol. Chem. 276:19959-19965(2001).

DR EMBL; AB049622; BAB60707.1; -

DR InterPro; IPR002181; Fibrinogen\_C.

DR Pfam; PF00147; fibrinogen\_C; 1.

DR PROSITE; PS00514; FIBRINAG\_C DOMAIN; UNKNOWN 1.

SQ SEQUENCE 341 AA; 38851 MW; CD08EF8D521781578 CRC64;

Query Match 90.0%; Score 27; DB 5; Length 341;

Best Local Similarity 80.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 294 SCYNS 298

RESULT 36

O55162 PRELIMINARY; PRT; 352 AA.

AC O55162;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Metastasis-associated GPI-anchored protein.  
OS Rattus norvegicus (rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BD IX; TISSUE=COLON CARCINOMA;  
RX MEDLINE=99002492; PubMed=9788443;  
RA Roessel M., Claas C., Seiter S., Herlevsen M., Zoeller M.;  
RT "Cloning and functional characterization of a new phosphatidylinositol anchored molecule of a metastasizing rat pancreatic tumor.";  
RL Oncogene 17:1989-2002(1998).  
DR EMBL; AJ001043; CAA04497.1; -.  
DR InterPro; IPR001526; LY6\_UPAR.  
DR SMART; SM00134; LU; 1.  
KW GPI-anchor.  
SQ SEQUENCE 352 AA; 36961 MW; 1894500CF9CAF5 CRC64;

Query Match 90.0%; Score 27; DB 11; Length 352;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 162 NCYNA 166

RESULT 37

O9SCP7 PRELIMINARY; PRT; 359 AA.

AC O9SCP7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Caffeic acid O-methyltransferase-like protein  
DE (AT395140/T4D2\_70).  
GN T4D2\_70.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,  
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quettier F.,  
RA Salanoubat M.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,  
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,  
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,

RA Davis R.W., Theologis A., Ecker J.R.;  
RT "Arabidopsis cDNA clones."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL132958; CAB64217.1; -.  
DR EMBL; AF367289; AAK56277.1; -.  
DR InterPro; IPR001601; Methyltransf.  
DR InterPro; IPR001077; O\_Metransf2.  
DR Pfam; PF00891; Methyltransf\_2; 1.  
KW Methyltransferase; Transrase.  
SQ SEQUENCE 359 AA; 39688 MW; 5847B43BF7563781 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 359;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 277 NCYNA 281

RESULT 38

O91YK8 PRELIMINARY; PRT; 363 AA.

AC O91YK8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Similar to metastasis-associated GPI-anchored protein.  
GN C4.4A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016549; AAH16549.1; -.  
DR MGD; MGI:1919684; C4.4a.  
SQ SEQUENCE 363 AA; 37489 MW; D6CE5139A17CC5FA CRC64;

Query Match 90.0%; Score 27; DB 11; Length 363;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
Db 162 NCYNA 166

RESULT 39

O9X500 PRELIMINARY; PRT; 376 AA.

AC O9X500;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Nitrous oxide reductase (Fragment).  
GN NOSZ.  
OS uncultured bacterium ProQ.  
OC Bacteria; environmental samples.  
OX NCBI\_TaxID=92148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99203128; PubMed=10103268;  
RA Scala D.J., Kerkhof L.J.;  
RT "Diversity of nitrous oxide reductase (nosZ) genes in continental shelf sediments."  
RL Appl. Environ. Microbiol. 65:1681-1687(1999).  
DR EMBL; AF119936; AAD26832.1; -.  
FT NON\_TER 1  
FT NON\_TER 376  
SQ SEQUENCE 376 AA; 42055 MW; 8811C5909084F8EA CRC64;

Query Match 90.0%; Score 27; DB 2; Length 376;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 ||||:  
 Db 161 SCYNS 165

RESULT 40

Q9X504  
 ID Q9X504 PRELIMINARY; PRT; 376 AA.  
 AC Q9X504;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE Nitrous oxide reductase (Fragment).  
 GN NOSZ.  
 OS uncultured bacterium 696T.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=92152;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99203128; PubMed=10103268;  
 RA Scala D.J., Kerkhof L.J.;  
 RT "Diversity of nitrous oxide reductase (nosZ) genes in continental  
 shelf sediments.";  
 RL Appl. Environ. Microbiol. 65:1681-1687(1999).  
 DR EMBL; AF119940; AAD26836.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 376  
 SQ SEQUENCE 376 AA; 41684 MW; D3A9092EFFF56DOE CRC64;

Query Match 90.0%; Score 27; DB 2; Length 376;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYNA 5  
 ||||:  
 Db 161 SCYNS 165

Search completed: July 18, 2003, 15:09:43  
 Job time : 14.9 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:05 ; Search time 14.3 Seconds  
(without alignments)  
73.950 Million cell updates/sec

Title: US-10-007-790-7

Perfect score: 61

Sequence: 1 SGAYRYGVVY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	75.4	306	2 G97132	uncharacterized ph
2	39	63.9	441	2 E72242	Mg-protoporphyrin
3	39	63.9	517	2 T02403	probable beta-gluc
4	39	63.9	1389	2 T41230	hypothetical TPR d
5	38	62.3	740	2 D71602	hypothetical prote
6	38	62.3	1411	2 T18417	hypothetical prote
7	38	62.3	1417	2 T18418	hypothetical prote
8	37	60.7	209	2 H82561	hypothetical prote
9	37	60.7	224	2 B69557	homoserine O-succ
10	37	60.7	285	2 A59141	silaffin sllp pre
11	37	60.7	317	2 S61149	probable membrane
12	37	60.7	384	2 F85439	hypothetical prote
13	37	60.7	558	2 JC5978	plasma hyaluronan
14	37	60.7	560	1 JC4795	plasma hyaluronan
15	37	60.7	574	2 A69196	cell surface glyco
16	37	60.7	695	2 S37439	transketolase (EC
17	37	60.7	705	2 S70029	probable transmemb
18	36	59.0	144	2 A56724	cni protein - fru
19	36	59.0	391	2 T32517	hypothetical prote
20	36	59.0	421	2 E71869	hypothetical prote
21	36	59.0	579	2 AE1855	hypothetical prote
22	36	59.0	597	2 B82140	C4-dicarboxylate t
23	36	59.0	680	1 XJBVTK	transketolase (EC
24	36	59.0	965	2 G96586	hypothetical prote
25	36	59.0	2697	2 T25444	hypothetical prote
26	35	57.4	64	1 Q1B22L	hypothetical prote
27	35	57.4	128	2 AE1330	hypothetical prote
28	35	57.4	130	2 S50638	hypothetical prote
29	35	57.4	147	2 T16672	hypothetical prote

ALIGNMENTS

RESULT 1

G97132

uncharacterized phage related protein [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: G97132  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: G97132  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-306 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK79850.1; PID:gi15024866; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1886

Query Match 75.4%; Score 46; DB 2; Length 306;

Best Local Similarity 87.5%; Pred. No. 0.98;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVRYGVVY 11

Db 117 YVRYGVVY 124

RESULT 2

E72242

Mg-protoporphyrin IX monomethyl ester oxidative cyclase-related protein - Thermotoga maritima  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 01-Mar-2002  
C:Accession: E72242  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.; Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: E72242  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-441 <ARN>  
A:Cross-references: GB:AE001800; GB:AE000512; NID:G4982090; PIDN:AAD36604.1; PID:G4982104  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM1537  
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0865

Query Match 63.9%; Score 39; DB 2; Length 441;

Best Local Similarity 70.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11  
| | | | |  
Db 12 GYYRLGAVY 21

RESULT 3  
T02403  
probable beta-glucosidase At2g44480 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 02-Feb-2001  
C:Accession: T02403; A84879  
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul  
submitted to the EMBL Data Library, May 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.  
A:Reference number: Z14667  
A:Accession: T02403  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-517 <ROU>  
A:Cross-references: EMBL:AC004521; NID:G3128166; PIDN:AAC16094.1; PID:G3128190  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84879  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-517 <STO>  
A:Cross-references: GB:AE002093; NID:G3128190; PIDN:AAC16094.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g44480; F411.29  
A:Map position: 2  
A:Introns: 54/3; 78/1; 97/3; 123/1; 149/1; 178/2; 262/3; 301/2; 374/1; 384/3; 419/1; 455/1  
C:Superfamily: Agrobacterium beta-glucosidase

Query Match 63.9%; Score 39; DB 2; Length 517;  
Best Local Similarity 70.0%; Pred. No. 31;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11  
| | | | |  
Db 477 GYRYGLVY 486

RESULT 4  
T41230  
hypothetical TPR domain-containing protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C:Accession: T41230  
R:Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, January 1999  
A:Reference number: Z21979  
A:Accession: T41230  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1389 <LYN>  
A:Cross-references: EMBL:AL035075; PIDN:CAA22636.1; GSPDB:GN00068; SPDB:SPCC1919.05  
A:Experimental source: strain 972h-; cosmid c1919  
C:Genetics:  
A:Gene: SPDB:SPCC1919.05  
A:Map position: 3  
C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat ho

Query Match 63.9%; Score 39; DB 2; Length 1389;  
Best Local Similarity 85.7%; Pred. No. 86;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AYRYGVV 9  
| | | | |  
Db 540 AYRYGI 546

## RESULT 5

D71602  
hypothetical protein PFB0945w - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743; PMID:9804551  
A:Accession: D71602  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-740 <GAR>  
A:Cross-references: GB:AE001428; GB:AE001362; NID:G3845316; PIDN:AAC71978.1; PID:G3845316;  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0945w

Query Match 62.3%; Score 38; DB 2; Length 740;  
Best Local Similarity 50.0%; Pred. No. 68;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
| | | | |  
Db 188 FYKIGIY 195

## RESULT 6

T18417  
hypothetical protein C0110w - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000  
R:Lawson, D.; Bowman, S.; Barrell, B.  
submitted to the EMBL Data Library, July 1997  
A:Reference number: Z18934  
A:Accession: T18417  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1411 <LAW>  
A:Cross-references: EMBL:Z97348; PIDN:CAB10571.2  
C:Genetics:  
A:Introns: 288/1; 480/1; 498/1; 519/1; 556/1; 613/1; 666/1; 921/3  
A:Note: C0110w  
C:Superfamily: Plasmodium falciparum hypothetical protein C0120w

Query Match 62.3%; Score 38; DB 2; Length 1411;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
| | | | |  
Db 858 FYKIGIY 865

## RESULT 7

T18418  
hypothetical protein C0120w - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T18418  
R:Lawson, D.; Bowman, S.; Barrell, B.  
submitted to the EMBL Data Library, July 1997  
A:Reference number: Z18934  
A:Accession: T18418

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1417 <LAW>

A;Cross-references: EMBL:Z97348; PIDN:CAB10572.2

C;Genetics:

A;Introns: 286/1; 478/1; 496/1; 517/1; 554/1; 616/1; 669/1; 924/3

A;Note: C0120w Plasmodium falciparum hypothetical protein C0120w

C;Superfamily: Plasmodium falciparum hypothetical protein C0120w  
Query Match 62.3%; Score 38; DB 2; Length 1417;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11

Db 861 FYRYGIY 868

#### RESULT 8

H82561

hypothetical protein XF2400 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C;Accession: H82561

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: H82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82561

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-209 <SIM>

A;Cross-references: GB:AE004049; GB:AE003849; NID:g9107579; PIDN:AAF85199.1; GSPDB:GN001

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Miracca, E.C.; Miyaki, C.Y.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF2400

Query Match 60.7%; Score 37; DB 2; Length 209;

Best Local Similarity 50.0%; Pred. No. 28;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11

Db 28 GAFISYGIY 37

#### RESULT 9

B69657

homoserine O-succinyltransferase metB - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000

C;Accession: B69657

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertex

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Kotter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohli, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: B69657

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-224 <KUN>

A;Cross-references: GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB14109.1; PID:G2634611

A;Experimental source: strain 168

C;Genetics:

A;Gene: metB

C;Superfamily: homoserine succinyltransferase

Query Match 60.7%; Score 37; DB 2; Length 224;

Best Local Similarity 66.7%; Pred. No. 30;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVY 9

Db 147 AGLYHYGV 155

#### RESULT 10

A59141

silaffin slipp precursor - diatom (Cylindrotheca fusiformis)

N;Alternate names: polycationic biosilica-associated protein; silica-precipitating polype

C;Species: Cylindrotheca fusiformis

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C;Accession: A59141; B59141; C59141

R;Kroeger, N.; Deutzmann, R.; Sumper, M.

Science 286, 1129-1132, 1999

A;Title: Polycationic peptides from diatom biosilica that direct silica nanosphere format

A;Reference number: A59141; MUID:20018323; PMID:10550045

A;Accession: A59141

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-265 <KRO1>

A;Cross-references: GB:AF191634; NID:G6561486; PIDN:AAF16940.1; PID:G6561487

A;Note: submitted to GenBank, October 1999

A;Accession: B59141

A;Molecule type: protein

A;Residues: 141-150 <KRO2>

A;Accession: C59141

A;Molecule type: protein

A;Residues: 108-120 <KRO3>

C;Genetics:

A;Gene: sll1

C;Keywords: cell wall; methylated amino acid

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-107/Domain: propeptide #status predicted <PRO>

F;108-265/Product: silaffin slipp #status predicted <MAT>

F;110,121/Modified site: N6,N6-dimethyllysine (Lys) #status predicted

F;112/Modified site: N6-methyl-N6-poly(N-methyl-propylamine)lysine (Lys) #status experimental

F;143,165,184,203,222,241/Modified site: N6,N6-dimethyllysine (Lys) #status experimental

F;144,166,185,204,223,242/Modified site: N6-methyl-N6-poly(N-methyl-propylamine)lysine (Lys) #status experimental

Query Match 60.7%; Score 37; DB 2; Length 265;

Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYGVY 8

Db 112 SGSYYSYG 119

```

RESULT 11
S61149
probable membrane protein YDR352w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein D9476.6
C/Species: Saccharomyces cerevisiae
C/Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C/Accession: S61149
R/Du, Z.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of S. cerevisiae cosmid 9476.
A/Reference number: S61148
A/Accession: S61149
A/Molecule type: DNA
A/Residues: 1-317 <DUZ>
A/Cross-references: EMBL:U28372; NID:g849170; PID:g849176; GSPDB:GNO0004; MIPS:YDR352w
C/Genetics:
A/Gene: MIPS:YDR352w
A/Cross-references: SGD:S0002760
A/Map position: 4R
C/Superfamily: Saccharomyces probable membrane protein YBR147w
C/Keywords: transmembrane protein
F:64-80/Domain: transmembrane #status predicted <TMM>

Query Match 60.7%; Score 37; DB 2; Length 317;
Best Local Similarity 60.0%; Pred.No. 43;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11
Db 87 GQYRYGVVH 96
| |||||:
| |||||:

RESULT 12
F85439
hypothetical protein AT4g37210 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C/Accession: F85439
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A/Reference number: A85001; MUID:20083488; PMID:10617198
A/Accession: F85439
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-384 <SFO>
A/Cross-references: GB:NC_001268; NID:g7270704; PIDN:CAB80387.1; GSPDB:GNO0140
C/Genetics:
A/Gene: AT4g37210
A/Map position: 4

Query Match 60.7%; Score 37; DB 2; Length 384;
Best Local Similarity 85.7%; Pred.No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AYRYGV 9
Db 124 AYRYGL 130
| |||||:
| |||||:

RESULT 13
JC5878
plasma hyaluronan-binding protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
C/Accession: JC5878
R/Hashimoto, K.; Tobe, T.; Sumiya, J.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N.
Biol. Pharm. Bull. 20, 1127-1130, 1997
A/Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-bin
A/Reference number: JC5878; MUID:98085239; PMID:9401717
A/Accession: JC5878
A/Molecule type: mRNA
A/Residues: 1-558 <HAS>

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Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.;  
 Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
 A:Reference number: A69000; MUID:98037514; PMID:9371463  
 A:Accession: A69196  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-574 <MTH>  
 A:Cross-references: GB:AE000666; NID:g2621803; PIDN:AA85224.1; PID:g262180  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH719  
 A:Start codon: TTG

Query Match 60.7%; Score 37; DB 2; Length 574;  
 Best Local Similarity 54.5%; Pred. No. 79;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 11  
 |||:||||:  
 Db 504 SGGWRHGRLY 514

RESULT 16  
 S37439  
 transketolase (EC 2.2.1.1) - yeast (Pichia stipitis)  
 C:Species: Pichia stipitis  
 C:Date: 09-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 15-Oct-1999  
 C:Accession: S37439  
 R:Metzger, M.  
 submitted to the EMBL Data Library, September 1993  
 A:Reference number: S37439  
 A:Accession: S37439  
 A:Molecule type: DNA  
 A:Residues: 1-695 <MTH>  
 A:Cross-references: EMBL:Z26486; NID:g403308; PIDN:CA81260.1; PID:g403309  
 C:Superfamily: transketolase; thiamin pyrophosphate-binding domain homology  
 C:Keywords: transferase  
 F:144-194/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 60.7%; Score 37; DB 2; Length 695;  
 Best Local Similarity 77.8%; Pred. No. 96;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 9  
 |||:||||:  
 Db 405 SGRYIRGV 413

RESULT 17  
 S70029  
 probable transmembrane protein TMC - human  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
 C:Accession: S70029  
 R:Lissy, N.A.; Bellacosa, A.; Sonoda, G.; Miller, P.D.; Jhanwar, S.C.; Testa, J.R.  
 Biochim. Biophys. Acta 1306, 137-141, 1996  
 A:Title: Isolation, characterization, and mapping to human chromosome 11q24-25 of a cDNA  
 A:Reference number: S70029; MUID:96221283; PMID:8634329  
 A:Accession: S70029  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-705 <LIS>  
 C:Genetics:  
 A:Map position: 11q24-25

Query Match 60.7%; Score 37; DB 2; Length 705;  
 Best Local Similarity 75.0%; Pred. No. 98;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
 |||:||||:

Db 644 YRFGQVY 651

RESULT 18  
 A56724  
 cni protein - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Jul-2000  
 C:Accession: A56724  
 R:Roth, S.; Neuman-Silberberg, F.S.; Barcelo, G.; Schuepbach, T.  
 Cell 81, 967-978, 1995  
 A:Title: cornichon and the EGF receptor signaling process are necessary for both anterior;  
 A:Reference number: A56724; MUID:95300228; PMID:7540118  
 A:Accession: A56724  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-144 <ROT>  
 A:Cross-references: GB:U28069; NID:g886768; PIDN:AAA86527.1; PID:g886769  
 C:Genetics:  
 A:Gene: FlyBase:cni  
 A:Cross-references: FlyBase:FBgn0000339  
 C:Superfamily: Drosophila cornichon protein

Query Match 59.0%; Score 36; DB 2; Length 144;  
 Best Local Similarity 75.0%; Pred. No. 29;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
 |||:||||:  
 Db 132 YIYGMVY 139

RESULT 19  
 T32517  
 hypothetical protein C49A9.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 20-Apr-2000  
 C:Accession: T32517  
 R:Fulton, B.; Wohldmann, P.  
 submitted to the EMBL Data Library, December 1997  
 A:Description: The sequence of C. elegans cosmid C49A9.  
 A:Reference number: Z21184  
 A:Accession: T32517  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-391 <FUL>  
 A:Cross-references: EMBL:AF036693; PIDN:AA88331.1; CSPDB:GN000022; CESP:C49A9.7  
 A:Experimental source: strain Bristol N2; clone C49A9  
 C:Genetics:  
 A:Gene: CESP:C49A9.7  
 A:Map position: 4  
 A:Introns: 21/3; 84/2; 128/2; 159/2; 199/3; 233/2; 263/3; 347/2  
 C:Superfamily: neurokinin 1 receptor

Query Match 59.0%; Score 36; DB 2; Length 391;  
 Best Local Similarity 77.8%; Pred. No. 80;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 9  
 |||:||||:  
 Db 251 SAAYRYGVV 259

RESULT 20  
 E71869  
 hypothetical protein jhp0937 - Helicobacter pylori (strain J99)  
 C:Species: Helicobacter pylori  
 A:Variety: strain J99  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
 C:Accession: E71869  
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
 Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: E71869  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-421 <ARN>  
A;Cross-references: GB:AE001523; GB:AE001439; MID:g4155513; PIDN:AAD06515.1; PID:g415551  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: jhp0937

Query Match 59.0%; Score 36; DB 2; Length 421;  
Best Local Similarity 44.4%; Pred. No. 87;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 AYRYGVVY 11  
|||  
Db 235 AFNYGIY 243  
|||

RESULT 21  
AE1855  
hypothetical protein all0390 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp.  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C;Accession: AE1855  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AE1855  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-579 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BA072348.1; PID:g17129735; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all0390  
C;Superfamily: Escherichia coli plasmid ColV-K30 aerobactin biosynthesis protein iucC

Query Match 59.0%; Score 36; DB 2; Length 579;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 YRYGVVY 11  
|||  
Db 408 YRYGVV 414  
|||

RESULT 22  
B82140  
C4-dicarboxylate transport sensor protein VC1925 [imported] - Vibrio cholerae (strain N16)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C;Accession: B82140  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: B82140  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-597 <HEI>  
A;Cross-references: GB:AE004268; GB:AE003852; MID:g9656456; PIDN:AAF95073.1; GSPDB:GN001  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1925  
A;Map position: 1

Query Match 59.0%; Score 36; DB 2; Length 597;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAYRYGVVY 11  
|||  
Db 155 GYVYAPVY 164  
|||

RESULT 23  
XJBYTK  
transketolase (EC 2.2.1.1) TKL1 - yeast (Saccharomyces cerevisiae)  
N;Alternate names: glycolaldehydetransferase; protein YP9499.29c; protein YPR074C  
C;Species: Saccharomyces cerevisiae  
C;Date: 31-Mar-1993 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000  
C;Accession: A49510; S54095; S69062; A42084; S21067; S74183; S37409  
R;Sundstroem, M.; Lindqvist, Y.; Schneider, G.; Hellman, U.; Ronne, H.  
J. Biol. Chem. 268, 24346-24352, 1993  
A;Title: Yeast TKL1 gene encodes a transketolase that is required for efficient glycolysis  
A;Reference number: A49510; MUID:94043273; PMID:8226984  
A;Accession: A49510  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-680 <SUN>  
A;Cross-references: EMBL:X73224; NID:g404200; PIDN:CAA51693.1; PID:g404201  
R;Badcock, K.; Churcher, C.M.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: S54059  
A;Accession: S54095  
A;Molecule type: DNA  
A;Residues: 1-680 <BAD>  
A;Cross-references: EMBL:249219; NID:g805025; PIDN:CAA89191.1; PID:g805054; GSPDB:GN001  
A;Experimental source: strain AB972  
R;Couch, J.  
submitted to the EMBL Data Library, March 1996  
A;Description: The sequence of S. cerevisiae cosmid 9513.  
A;Reference number: S69057  
A;Accession: S69062  
A;Molecule type: DNA  
A;Residues: 1-680 <COU>  
A;Cross-references: EMBL:U51033; NID:g1230676; PIDN:AAB69125.1; PID:g1230682; GSPDB:GN001  
R;Fletcher, T.S.; Kwee, I.L.; Nakada, T.; Largman, C.; Martin, B.M.  
Biochemistry 31, 1892-1896, 1992  
A;Title: DNA sequence of the yeast transketolase gene.  
A;Reference number: A42084; MUID:92144611; PMID:1737042  
A;Accession: A42084  
A;Molecule type: DNA  
A;Residues: 1-36, 'RS', 39-44, 'GESNAHEPNQKGTGSTEIDLSCLTVTRSLCCY', 78-135, 'DMPLTTSRA', 144-2;  
SVSPQVILKELRPLHSIRVTS' <FLE>  
A;Cross-references: GB:M63302  
R;Nixon, P.F.; Duggleby, R.G.  
Protein Seq. Data Anal. 4, 325-326, 1991  
A;Title: The N-terminal amino acid sequence of yeast transketolase.  
A;Reference number: S21067; MUID:92253546; PMID:1812485  
A;Accession: S21067  
A;Molecule type: protein  
A;Residues: 2-36 <NIX>  
R;Kovina, M.; Viryasov, M.; Baratova, L.; Kochetov, G.  
FEBS Lett. 392, 293-294, 1996  
A;Title: Localization of reactive tyrosine residues of baker's yeast transketolase.  
A;Reference number: S74183; MUID:96371030; PMID:8774865  
A;Accession: S74183  
A;Molecule type: protein  
A;Residues: 181-187;209-213;368-373;104-105 <KOV>  
C;Comment: The active enzyme catalyzes the transfer of a keto group to an aldehyde acceptor  
optimal activity.  
C;Genetics:  
A;Gene: SGD:TKL1; MIPS:YPR074C  
A;Cross-references: SGD:S0006278; MIPS:YPR074C  
A;Map position: 16R  
C;Complex: homodimer  
C;Function:  
A;Description: transferase

A;Pathway: pentose phosphate pathway  
C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology  
C;Keywords: homodimer; magnesium; pentose phosphate pathway; thiamin pyrophosphate; transketolase; transketolase #status experimental <MAT>  
F;2-680/Product: transketolase #status experimental <MAT>  
F;146-196/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 59.0%; Score 36; DB 1; Length 680;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9  
|||  
Db 408 SGYIRYGI 416  
|||

RESULT 24  
G96586  
hypothetical protein F20D21.30 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: G96586  
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G96586  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-965 <SPO>  
A;Cross-references: GB:AE005173; NID:94585991; PIDN:AAD25627.1; GSPDB:GN00141  
C;Genetics:  
A;Map position: 1

Query Match 59.0%; Score 36; DB 2; Length 965;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVV 11  
|||  
Db 930 GGYRDGVG 939  
|||

RESULT 25  
T25444  
hypothetical protein B0261.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C;Accession: T25444  
R;Scheet, P.; Gattung, S.  
submitted to the EMBL Data Library, April 1997  
A;Description: The sequence of C. elegans cosmid B0261.  
A;Reference number: Z20036  
A;Accession: T25444  
A;Status: preliminary; translated from GB/EMBL/DDEJ  
A;Molecule type: DNA  
A;Residues: 1-2697 <SCH>  
A;Cross-references: EMBL:U97016; PIDN:AA052354.1; GSPDB:GN00019; CBSP:B0261.2  
A;Experimental source: strain Bristol N2; clone B0261  
C;Genetics:  
A;Gene: CBSP:B0261.2  
A;Map position: 1  
A;Introns: 41/3; 75/2; 173/3; 283/3; 354/2; 374/3; 432/2; 470/2; 569/3; 607/3; 667/1; 79  
1/3; 2282/3; 2337/3; 2516/2; 2562/3; 2652/1  
C;Superfamily: yeast TOR2 protein

Query Match 59.0%; Score 36; DB 2; Length 2697;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGV 9  
|||||  
Db 1286 YRYGV 1291  
|||||

RESULT 26  
Q1BP2L  
hypothetical protein B-64 - phage lambda  
C;Species: phage lambda  
C;Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 10-Sep-1999  
C;Accession: H43011; D43017; A04398  
R;Daniels, D.  
submitted to the Nucleic Acid Sequence Database, September 1982  
A;Reference number: A94614  
A;Accession: H43011  
A;Molecule type: DNA  
A;Residues: 1-64 <DAN>  
R;Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.  
J. Mol. Biol. 162, 729-773, 1982  
A;Title: Nucleotide sequence of bacteriophage lambda DNA.  
A;Reference number: A92891; MUID:83189071; PMID:6221115  
A;Accession: D43017  
A;Molecule type: DNA  
A;Residues: 1-64 <SAN>  
A;Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:G215104; I;  
C;Genetics:  
A;Map position: 92.00-92.39  
C;Superfamily: phage lambda hypothetical 7.1K protein (nin region)

Query Match 57.4%; Score 35; DB 1; Length 64;  
Best Local Similarity 66.7%; Pred. No. 19;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAYRYGVV 10  
|||||  
Db 5 GAYRFRV 13  
|||||

RESULT 27  
AE1330  
hypothetical protein lmo2045 [imported] - Listeria monocytogenes (strain EGD-e)  
C;Species: Listeria monocytogenes  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AE1330  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AE1330  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-128 <GLA>  
A;Cross-references: GB:NC\_003210; PIDN:CAD00123.1; PID:G16411515; GSPDB:GN00177  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmo2045

Query Match 57.4%; Score 35; DB 2; Length 128;  
Best Local Similarity 66.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AYRYGVV 11  
|||||  
Db 114 ADLYGIV 122  
|||||

```
RESULT 28
S50638
hypothetical protein YER135c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C:Accession: S50638
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9781, 8198, 9115, 9981, and lambda
A:Reference number: S50437
A:Accession: S50638
A:Molecule type: DNA
A:Residues: 1-130 <DIE>
A:Cross-references: EMBL:U18916; NID:gl384128; PID:g603374; GSPDB:GN000005; MIPS:YER135C
C:Genetics:
A:Gene: MIPS:YER135C
A:Cross-references: SGD:S0000937
A:Map position: 5R
C:Superfamily: Saccharomyces hypothetical protein YER135C

Query Match 57.4%; Score 35; DB 2; Length 130;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVW 10
Db | ||||| :
42 GEYRYSIL 50

RESULT 29
T16672
hypothetical protein R03H10.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T16672
R:Wilcox, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid R03H10.
A:Reference number: Z18557
A:Accession: T16672
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-147 <WIL>
A:Cross-references: EMBL:U29382; NID:g868226; PID:g868230; PIDN:AAA68762.1; CESP:R03H10.
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R03H10.5
A:Introns: 36/1; 82/3
C:Superfamily: Caenorhabditis elegans hypothetical protein T10D4.7

Query Match 57.4%; Score 35; DB 2; Length 147;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9
Db : ||||| :
117 NGVYIEYGL 125

RESULT 30
T08321
hypothetical protein H1243 [imported] - Halobacterium sp. (strain NRC-1) plasmid pNRC100
C:Species: Halobacterium sp.
A:Variety: strain NRC-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000
C:Accession: T08321
R:Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A:Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or
A:Reference number: T16408; MUID:99063795; PMID:9847077
A:Accession: T08321
A>Status: translated from GB/EMBL/DBJ
```

```
A:Molecule type: DNA
A:Residues: 1-204 <DAS>
A:Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822382; HALOSP:H1243;
A:Experimental source: strain NRC-1
C:Genetics:
A:Gene: HALOSP:H1243
A:Genome: plasmid pNRC100
C:Superfamily: Halobacterium plasmid pNRC100 hypothetical protein H1243

Query Match 57.4%; Score 35; DB 2; Length 204;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVV 11
Db ||||| :
78 GAYHAFVY 87

RESULT 31
T19775
hypothetical protein C36B1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19775
R:Lennard, N.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19176
A:Accession: T19775
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-253 <WIL>
A:Cross-references: EMBL:Z80215; PIDN:CAB02269.1; GSPDB:GN000019; CESP:C36B1.4
A:Experimental source: clone C36B1
C:Genetics:
A:Gene: CESP:C36B1.4
A:Map position: 1
A:Introns: 33/3; 117/3; 216/3
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 57.4%; Score 35; DB 2; Length 253;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYV 7
Db ||||| :
151 SGAYYBY 157

RESULT 32
D86693
conserved hypothetical protein yfde [imported] - Lactococcus lactis subsp. lactis (strain
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: D86693
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86693
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <STO>
A:Cross-references: GB:AE005176; PID:gl2723433; PIDN:AAK04646.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yfde

Query Match 57.4%; Score 35; DB 2; Length 255;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AYRYGV 9
Db ||||| :
```

Db 107 AYYEYGV 113

RESULT 33

T27656

hypothetical protein ZK1025.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Jun-2001

C:Accession: T27656

R:Lennard, N.

submitted to the EMBL Data Library, March 1998

A:Reference number: Z20400

A:Accession: T27656

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-338 <WIL>

A:Cross-references: EMBL:AL022288; PIDN:CAAL18370.1; GSPDB:GNO0019; CESP:ZK1025.3

A:Experimental source: clone ZK1025

C:Genetics:

A:Gene: CESP:ZK1025.3

A:Map position: 1

A:Introns: 100/3; 212/1

C:Superfamily: Caenorhabditis elegans hypothetical protein F49C12.2

Query Match 57.4%; Score 35; DB 2; Length 338;

Best Local Similarity 75.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGV 9

Db 191 GKYRYAV 198

RESULT 34

A72780

probable ribosomal protein L3 APE0227 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

C:Accession: A72780

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: A72780

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-344 <KAW>

A:Cross-references: DDBJ:AP000058; NID:G5103388; PIDN:BAA79139.1; PID:G5103618

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0227

C:Superfamily: rat ribosomal protein L3

Query Match 57.4%; Score 35; DB 2; Length 344;

Best Local Similarity 60.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 10

Db 283 AGGFLRYGV 292

RESULT 35

S49464

recombination protein recA - Rhodobacter capsulatus

N:Alternate names: recombinase A

C:Species: Rhodobacter capsulatus

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 02-Feb-2001

C:Accession: S49464

R:Fernandez de Henestrosa, A.R.

submitted to the EMBL Data Library, October 1994

A:Reference number: S49464

A:Accession: S49464

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-355 <PER>

A:Cross-references: EMBL:X82183; NID:G558630; PIDN:CAAS7673.1; PID:G558631

C:Genetics:

A:Gene: recA

C:Superfamily: recombination protein recA

C:Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop;

F:78-85/Region: nucleotide-binding motif A (P-loop)

F:152-157/Region: nucleotide-binding motif B

F:84/Binding site: ATP (Lys) #status predicted

Query Match 57.4%; Score 35; DB 2; Length 355;

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYGV 8

Db 299 SGAWYSYG 306

RESULT 36

H83693

carboxypeptidase G2 BH0352 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C:Accession: H83693

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; HiranNucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H83693

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-374 <STO>

A:Cross-references: GB:AP001508; GB:BA000004; NID:G10172890; PIDN:BAB04071.1; GSPDB:GN0001

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0352

C:Superfamily: folate hydrolase G

Query Match 57.4%; Score 35; DB 2; Length 374;

Best Local Similarity 66.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9

Db 21 SGSYKGV 29

RESULT 37

T25209

hypothetical protein T23H4.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T25209

R:Matthews, L.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z19996

A:Accession: T25209

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-392 <WIL>

A:Cross-references: EMBL:Z93240; PIDN:CA05813.1; GSPDB:GN00019; CESP:T23H4.1

A:Experimental source: clone T23H4

C:Genetics:

A:Gene: CESP:T23H4.1

A:Map position: 1

A:Introns: 26/2; 64/3; 94/1; 115/2; 147/3; 216/3; 275/3; 317/1; 348/1

Query Match 57.4%; Score 35; DB 2; Length 392;

Best Local Similarity 54.5%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 11  
| | | | |  
Db 159 SHRYGYGYFY 169

## RESULT 38

T20439

Hypothetical protein E03H4.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Jun-2001

C;Accession: T20439

R;Dobson, R.

Submitted to the EMBL Data Library, November 1996

A;Reference number: Z19276

A;Accession: T20439

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-399 &lt;WIL&gt;

A;Cross-references: EMBL:Z81492; PIDN:CAB04025.1; GSPDB:GN00019; CESP:E03H4.2

A;Experimental source: clone E03H4

C;Genetics:

A;Gene: CESP:E03H4.2

A;Map position: 1

A;Introns: 165/3; 277/1

C;Superfamily: Caenorhabditis elegans hypothetical protein F49C12.2

Query Match

Best Local Similarity 57.4%; Score 35; DB 2; Length 399;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVV 9

| | | | |

Db 256 GKYRYAV 263

## RESULT 39

I49754

homeobox protein - mouse

N;Alternate names: homeotic protein MAB66

C;Species: Mus musculus (house mouse)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 17-Nov-2000

C;Accession: I49754; F37290; B41606; F38809

R;Benson, G.V.; Nguyen, T.H.; Maas, R.L.

Mol. Cell. Biol. 15, 1591-1601, 1995

A;Title: The expression pattern of the murine Hoxa-10 gene and the sequence recognition

A;Reference number: I49754; MUID:95166244; PMID:7862151

A;Accession: I49754

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-399 &lt;RES&gt;

A;Cross-references: GB:L08757; NID:G825647; PIDN:AAA67125.1; PID:G567213

R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter

Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991

A;Title: Identification of 10 murine homeobox genes.

A;Reference number: A37290; MUID:92073356; PMID:1683707

A;Accession: F37290

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 325-384 &lt;SIN&gt;

R;Murtha, M.T.; Leckman, J.F.; Ruddle, F.H.

Proc. Natl. Acad. Sci. U.S.A. 88, 10711-10715, 1991

A;Title: Detection of homeobox genes in development and evolution.

A;Reference number: A41606; MUID:92073357; PMID:1720547

A;Accession: B41606

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 346-370 &lt;MUR&gt;

A;Cross-references: GB:M81659; NID:G193973; PIDN:AAA63312.1; PID:G193974

C;Genetics:

A;Gene: Hoxa10

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;326-382/Domain: homeobox homology <HOX>

Query Match 57.4%; Score 35; DB 2; Length 399;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11

| | | | |

Db 37 GGYAHGGVY 46

## RESULT 40

H84463

Hypothetical protein At2g04980 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C;Accession: H84463

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84463

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-770 &lt;STO&gt;

A;Cross-references: GB:AE002093; NID:G4585928; PIDN:AAD5588.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g04980

A;Map position: 2

C;Superfamily: Arabidopsis thaliana hypothetical protein T21L8.10

Query Match

Best Local Similarity 70.0%; Score 35; DB 2; Length 770;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAYRYGVVY 11

| | | | |

Db 583 GKYRYKVYV 592

Search completed: July 18, 2003, 15:10:44

Job time : 15.3 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2003, 15:01:44 ; Search time 37.18 Seconds  
(without alignments)  
39.423 Million cell updates/sec

Title: US-10-007-790-7

Perfect score: 61

Sequence: 1 SGAYRYGVVY 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_101002.\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	21	Murine PIP3 recogn
2	61	100.0	124	21	Murine PIP3 recogn
3	43	70.5	122	22	Human autoantibody
4	40	65.6	19	20	Carbohydrate antig
5	40	65.6	398	20	Porphorymonas ging
6	40	65.6	400	20	Porphorymonas ging
7	40	65.6	412	20	Porphorymonas ging
8	40	65.6	1805	22	Drosophila melanog
9	39	63.9	20	20	Carbohydrate antig
10	38	62.3	740	21	Plasmodium falcipa

11	38	62.3	981	19	AAW46499	Amino acid sequenc
12	38	62.3	1411	20	AAV31948	Plasmodium falcipa
13	38	62.3	1417	20	AAV31947	Plasmodium falcipa
14	38	62.3	1430	20	AAV31949	Plasmodium falcipa
15	38	62.3	4134	20	AAV31946	Plasmodium falcipa
16	37	60.7	104	22	AAU20895	Human novel foetal
17	37	60.7	158	21	AAB32986	Pinus radiata tran
18	37	60.7	384	21	AAG54380	Arabidopsis thalia
19	37	60.7	499	21	AAG41345	Arabidopsis thalia
20	37	60.7	560	21	AAB42484	Human ORFX ORF2248
21	37	60.7	560	23	AAO17144	Human blood coagul
22	37	60.7	560	23	AAO17145	Human blood coagul
23	36	59.0	19	23	ABP47134	Human Blys binding
24	36	59.0	128	22	AAE07014	Human heavy chain
25	36	59.0	139	23	ABP10506	Human ORFX protein
26	36	59.0	142	21	AAV53622	A bone marrow secr
27	36	59.0	144	20	AAV28813	pk65 4 secreted pr
28	36	59.0	144	20	AAV41306	Human cornichon pr
29	36	59.0	144	20	AAV41732	Human PRO181 prote
30	36	59.0	144	20	AAV32925	Transmembrane doma
31	36	59.0	144	21	AAAB44288	Human PRO181 (UNQ1
32	36	59.0	144	21	AAAB19524	Antitumour PRO181
33	36	59.0	144	22	ABB61865	Drosophila melanog
34	36	59.0	144	22	ABB61866	Drosophila melanog
35	36	59.0	144	22	AAW93330	Human polypeptide,
36	36	59.0	144	22	AAW76851	Human lung tumour
37	36	59.0	144	23	ABB95423	Human angiogenesis
38	36	59.0	144	23	AAE20143	Human cornichon pr
39	36	59.0	144	23	AAU85506	Clone #19110 of lu
40	36	59.0	144	23	ABB84817	Human PRO181 prote
41	36	59.0	144	23	AAU83651	Human PRO protein,
42	36	59.0	145	20	AAV04316	Human secreted pro
43	36	59.0	148	22	AAU30619	Novel human secret
44	36	59.0	241	22	AAV85635	Antigen recognised
45	36	59.0	241	23	AAU77177	Murine G-CSF-induc

ALIGNMENTS

RESULT 1

AAV87659  
ID AAV87659 standard; Protein; 11 AA.

XX AAV87659;

DT 11-AUG-2000 (first entry)

DE Murine PIP3 recognizing Mab variable region heavy chain CDR3 region.

KW PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region; CDR3;

KW immunogen; antibody; heavy chain; complementarity determining region.

OS Mus sp.

PN JP2000083664-A.

PD 28-MAR-2000.

XX 07-SEP-1998; 98JP-0252921.

XX 07-SEP-1998; 98JP-0252921.

PA (FUKU/) FUKUI Y.

PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.

PT A monoclonal antibody recognizing

phosphatidylinositol-3,4,5-triphosphate

PS Claim 9; Page 13; 15pp; Japanese.

XX

CC This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain complementarity determining region, CDR3 described in the method of  
 CC the invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00037;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 11  
 |||||  
 DB 1 SGAYRYGVVY 11

# RESULT 2

AY87655  
 ID AAY87655 standard; Protein; 124 AA.

AC AAY87655;

XX 11-AUG-2000 (first entry)

DE Murine PIP3 recognizing Mab variable region heavy chain protein.

XX PIP3; phosphatidylinositol-3,4,5-triphosphate; variable region;  
 KW immunogen; antibody; heavy chain.

XX Mus sp.

XX JP2000083664-A.

XX 28-MAR-2000.

XX 07-SEP-1998; 98JP-0252921.

XX 07-SEP-1998; 98JP-0252921.

XX (FUKU)/ FUKUI Y.

XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2000-353334/31.

XX N-PSDB; AAA12202.

XX A monoclonal antibody recognizing

PT phosphatidylinositol-3,4,5-triphosphate -

PS Claim 5; Page 11; 15pp; Japanese.

XX This invention describes a novel antibody specifically recognizing  
 CC phosphatidylinositol-3,4,5-triphosphate (PIP3). The antibody of the  
 CC invention is used in immunogenic compositions in which a dead  
 CC Salmonella genus microbe is used as an adjuvant and mixed with PIP3. The  
 CC antibody can be used in an immunoassay containing a step in which the  
 CC above antibody or its variable region is reacted with PIP3 present in a  
 CC sample and the bond based on their immunological reaction. The method  
 CC can determine PIP3 easily in a high sensitivity. This sequence represents  
 CC the murine PIP3 recognizing monoclonal antibody variable region heavy  
 CC chain described in the method of the invention.

XX SQ Sequence 124 AA;

Query Match 100.0%; Score 61; DB 21; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 0.0051;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 11  
 |||||  
 DB 99 SGAYRYGVVY 109

# RESULT 3

AAG80211  
 ID AAG80211 standard; Protein; 122 AA.

XX AAG80211;

XX 22-JAN-2002 (first entry)

DE Human autoantibody MICA-3 variable region light chain.

XX Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;  
 KW glutamate decarboxylase; diabetes mellitus type 1; stiff-man syndrome;  
 KW polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;  
 KW variable region; light chain; MICA-3.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /label= OTHER  
 FT /note= "Xaa encoded by NAG"

XX EPI149914-A2.

XX 31-OCT-2001.

XX 29-MAR-2001; 2001EP-0107702.

XX 10-APR-2000; 2000DE-1017782.

XX 25-MAY-2000; 2000DE-1025840.

XX (LABO-) LABOR KOCH MERK GMBH.

XX Richter W, Rickert M, Rapp I, Dangel W;

XX WPI; 2001-640702/74.

XX N-PSDB; AAI68760.

XX New fusion protein, useful for diagnosis of diabetes type I and other  
 PT metabolic diseases, is reactive with autoantibodies against both  
 PT glutamate decarboxylase and islet cell antigen -

XX Disclosure; Page 28-29; 68pp; German.

XX This invention describes a novel fusion protein (I) that has, at its  
 CC N-terminus, one or more epitopes that bind specifically to autoantibodies  
 CC (AAB) against the islet cell antigen IA2 and, at its C-terminus, one or  
 CC more epitopes that bind specifically to antibodies (Ab) directed against  
 CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding  
 CC it, vectors containing (II) and transformed cells, are useful for  
 CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,  
 CC polyglandular autoimmune syndrome or other autoimmune conditions  
 CC associated with AAB against GAD65 or IA2. (I) provides a rapid and simple  
 CC diagnosis of high specificity and sensitivity, capable of recognizing  
 CC antibodies against both IA2 and GAD65, simultaneously. Unlike known  
 CC fusions, where the GAD65 component is at the N-terminus, (I) contains  
 CC correctly folded conformational epitopes that can react with most MICA  
 CC autoantibodies. This sequence represents the human autoantibody MICA-3  
 CC variable region light chain used in the method of the invention.

XX SQ Sequence 122 AA;

Query Match 70.5%; Score 43; DB 22; Length 122;  
 Best Local Similarity 77.8%; Pred. No. 6.1;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11

XX  
XX  
XX

```

XX DE Porphorymonas gingivalis protein PG84.
XX KW Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
XX KW vaccine; antigenic.
XX OS Porphorymonas gingivalis.
XX PN WO9929870-A1.
XX PD 17-JUN-1999.
XX PF 10-DEC-1998; 98WO-AU01023.
XX PR 04-AUG-1998; 98AU-0005028.
XX PR 10-DEC-1997; 97AU-0000839.
XX PR 31-DEC-1997; 97AU-0001182.
XX PR 30-JAN-1998; 98AU-0001546.
XX PR 10-MAR-1998; 98AU-0002264.
XX PR 09-APR-1998; 98AU-0002911.
XX PR 23-APR-1998; 98AU-0003128.
XX PR 05-MAY-1998; 98AU-0003338.
XX PR 22-MAY-1998; 98AU-0003654.
XX PR 29-JUL-1998; 98AU-0004917.
XX PA (CSLC-) CSL LTD.
XX PI Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
XX PI Ross BC, Rothel LJ, Webb EA;
XX PS WPI; 1999-385613/32.
XX DR N-PSDB; AAX91776.
XX CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
XX CC Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
XX CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
XX CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
XX CC activity with a vaccine mechanism of action. The PG polypeptides can be
XX CC used as vaccines especially against Porphorymonas gingivalis. Probes can
XX CC be used to detect Porphorymonas gingivalis in standard hybridisation
XX CC assays. Porphorymonas gingivalis is involved in periodontal disease
XX CC especially gingivitis.
XX SQ Sequence 400 AA;
    Query Match 65.6%; Score 40; DB 20; Length 400;
    Best Local Similarity 87.5%; Pred. No. 73;
    Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYRG 8
DB 254 SGAYSYG 261
    |||||
    |||||

RESULT 7
AAY34422
ID. AAY34422 standard; Protein; 412 AA.
XX AC AAY34422;
XX XX
XX 25-AUG-1999 (first entry)
XX DE Porphorymonas gingivalis protein PG84.
XX KW Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
XX KW vaccine; antigenic.
XX OS Porphorymonas gingivalis.

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XX PN WO9929870-A1.
XX PD 17-JUN-1999.
XX PF 10-DEC-1998; 98WO-AU01023.
XX PR 04-AUG-1998; 98AU-0005028.
XX PR 10-DEC-1997; 97AU-0000839.
XX PR 31-DEC-1997; 97AU-0001182.
XX PR 30-JAN-1998; 98AU-0001546.
XX PR 10-MAR-1998; 98AU-0002264.
XX PR 09-APR-1998; 98AU-0002911.
XX PR 23-APR-1998; 98AU-0003128.
XX PR 05-MAY-1998; 98AU-0003338.
XX PR 22-MAY-1998; 98AU-0003654.
XX PR 29-JUL-1998; 98AU-0004917.
XX PA (CSLC-) CSL LTD.
XX PI Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
XX PI Ross BC, Rothel LJ, Webb EA;
XX PS WPI; 1999-385613/32.
XX DR N-PSDB; AAX91640.
XX CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
XX CC Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
XX CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
XX CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
XX CC activity with a vaccine mechanism of action. The PG polypeptides can be
XX CC used as vaccines especially against Porphorymonas gingivalis. Probes can
XX CC be used to detect Porphorymonas gingivalis in standard hybridisation
XX CC assays. Porphorymonas gingivalis is involved in periodontal disease
XX CC especially gingivitis.
XX SQ Sequence 412 AA;
    Query Match 65.6%; Score 40; DB 20; Length 412;
    Best Local Similarity 87.5%; Pred. No. 76;
    Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYRG 8
DB 266 SGAYSYG 273
    |||||
    |||||

RESULT 8
ABB65262
ID ABB65262 standard; Protein; 1805 AA.
XX AC ABB65262;
XX XX
XX 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 22578.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX XX

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PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 PA (PEKE ) PE CORP NY.  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI; 2001-656860/75.  
 DR N-PSDB; ABL09365.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX Disclosure; SEQ ID NO 22578; 21pp + Sequence Listing; English.  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 1805 AA;  
 Query Match 65.6%; Score 40; DB 22; Length 1805;  
 Best Local Similarity 54.5%; Pred. No. 3.8e+02;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SGAYRYGVVY 11  
 Db 1754 SGVIFKYGQY 1764  
 RESULT 9  
 AAY33068  
 ID AAY33068 standard; peptide; 20 AA.  
 XX AC AAY33068;  
 XX 03-NOV-1999 (first entry)  
 DT Carbohydrate antigen peptide mimotope 41.  
 DE Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;  
 KW tumour immunity; cancer therapy; antibacterial; immune response;  
 KW immunogenicity; anti-idiotypic; T cell response manipulation.  
 XX Synthetic.  
 XX WO9940433-A1.  
 PN 12-AUG-1999.  
 PD 04-FEB-1999; 99WO-US02405.  
 XX 04-FEB-1998; 98US-0073690.  
 PR (UYPE-) UNIV PENNSYLVANIA.  
 XX Kieber-Emmons T;  
 PI WPI; 1999-527317/44.  
 DR Peptides and recombinant antibody mimics of carbohydrate antigens,  
 XX used for, e.g. treatment of cancer and infection  
 PT Claim 21; Page 80; 88pp; English.  
 PS

XX This invention describes a novel method for preparing a peptide or  
 CC recombinant antibody, which mimics an antigenic carbohydrate. The  
 CC peptides and recombinant antibodies prepared to mimic antigenic  
 CC carbohydrates can be used to enhance binding of anti-antigenic  
 CC carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine  
 CC adjuvants. The peptides can be used to inhibit binding of a ligand to a  
 CC receptor, which is an antigenic carbohydrate. The methods are used to  
 CC prepare the peptides and antigenic antibodies, which mimic the antigenic  
 CC carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour  
 CC immunity and cancer therapy. The peptides and antibodies can also be  
 CC used as antibacterials. Peptides that mimic carbohydrate antigens can be  
 CC formulated to develop a longer lasting immune response. Other advantages  
 CC of the peptide mimics are: (1) the chemical composition and purity of  
 CC synthesized peptides can be precisely defined; (2) the immunogenicity  
 CC of the peptides can be significantly enhanced by polymerization or  
 CC addition of antigen required for immunization; (3) peptide synthesis may  
 CC be more practical than synthesis of carbohydrate-protein conjugates or  
 CC the production of anti-idiotypes; (4) peptide mimicking sequences can  
 CC be engineered into DNA plasmids for DNA vaccination to further  
 CC manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate  
 CC antigen peptide mimotopes described in the invention.  
 XX SQ Sequence 20 AA;  
 Query Match 63.9%; Score 39; DB 20; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 4.2;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GAYRYGVVY 11  
 Db 2 GIVRYDIVY 11  
 RESULT 10  
 AAB18330  
 ID AAB18330 standard; Protein; 740 AA.  
 XX AC AAB18330;  
 XX 07-NOV-2000 (first entry)  
 DT Plasmodium falciparum chromosome 2 related protein SEQ ID NO:188.  
 DE Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;  
 KW antimalarial; malaria; protozoicide; infection; insecticide.  
 XX Plasmodium falciparum.  
 OS WO200025728-A2.  
 XX 11-MAY-2000.  
 PD 05-NOV-1999; 99WO-US26796.  
 XX 05-NOV-1998; 98US-0107131.  
 PR (HOPE/) HOFFMAN S.  
 PA (CARU/) CARUCCI D.  
 PA (GARD/) GARDNER M.  
 PA (VENT/) VENTER J C.  
 XX Hoffman S, Carucci D, Gardner M, Venter JC;  
 XX WPI; 2000-365347/31.  
 DR Proteins encoded by chromosome 2 of the human malarial parasite,  
 XX Plasmodium falciparum, useful as antimalarial vaccines and in the  
 PT diagnosis of P.falciparum infection -  
 XX Disclosure; Page 422-424; 577pp; English.  
 PS

CC The present invention describes proteins and their fragments (I) encoded  
 CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum.  
 CC Also described are: (i) nucleotide sequences (ii) encoding (ii); and (2)  
 CC vaccines against P. falciparum infection comprising (i) or (ii).  
 CC (i) and (ii) are useful for the development of vaccines against  
 CC P. falciparum infection. (i) and polyclonal antisera or a monoclonal  
 CC antibody raised to immunogens comprising the sequences of (i), are  
 CC useful in the detection of infection with P. falciparum. Furthermore,  
 CC (i) especially when they are rifins or secreted or membrane proteins)  
 CC can aid the identification of drugs to treat or prevent P. falciparum  
 CC infection, or they can be used to identify drug resistance in  
 CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the  
 CC subsequent identification of proteins encoded by it will help to expand  
 CC our understanding of parasite biology, a process hampered by the  
 CC complexity of the parasitic lifecycle, and provide new targets for  
 CC vaccine and drug development. Parasite resistance to drugs and mosquito  
 CC resistance to insecticides have led to a resurgence of malaria in many  
 CC parts of the world, and there is a pressing need for vaccines and new  
 CC drugs. AA70078 to AA70287 and AAB18144 to AAB18352 represent nucleotide  
 CC and protein sequences given in the present invention, but which are not  
 CC specifically mentioned within the specification.  
 CC  
 SQ Sequence 740 AA;

Query Match 62.3%; Score 38; DB 21; Length 740;  
 Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YRYGVVY 11  
 Db 188 FYKGIIV 195

RESULT 11  
 AA46499

ID AA46499 standard; Protein; 981 AA.

XX AA46499;

DT 19-MAY-1998 (first entry)

DE Amino acid sequence of the spindly (SPY) protein of Arabidopsis.

KW Gibberellin signal transduction; spindly phenotype; SPY gene; rescue;  
 KW spy mutant gene; Gibberellin overdose syndrome; paclobutrazol; spy-4 DNA;  
 KW modulation; plant development; plant height; fruit growth;  
 KW flower development; leaf size.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT Region 1..76

FT /note= "N-terminus"

FT Domain 77..430

FT /note= "Tetratricopeptide repeat region which is  
 FT important for SPY protein function"

FT Region 77..110

FT /note= "Tetratricopeptide repeat 1"

FT Region 111..151

FT /note= "Tetratricopeptide repeat 2"

FT Region 152..185

FT /note= "Tetratricopeptide repeat 3"

FT Region 186..219

FT /note= "Tetratricopeptide repeat 4"

FT Region 220..260

FT /note= "Tetratricopeptide repeat 5"

FT Region 261..294

FT /note= "Tetratricopeptide repeat 6"

FT Region 295..328

FT /note= "Tetratricopeptide repeat 7"

FT Region 329..362

FT /note= "Tetratricopeptide repeat 8"

FT Region 363..396

FT Region /note= "Tetratricopeptide repeat 9"  
 FT 397..430  
 FT /note= "Tetratricopeptide repeat 10"  
 FT 431..914  
 FT /note= "C-terminus"  
 XX  
 XX WO9743419-A2.  
 XX  
 XX 20-NOV-1997.  
 XX  
 XX 16-MAY-1997; 97WO-US08765.  
 XX  
 XX 16-MAY-1996; 96US-0649046.  
 XX  
 XX (MINU ) UNIV MINNESOTA.  
 XX  
 XX Jacobsen SE, Olszewski NE;  
 XX  
 XX WPI; 1998-008888/01.  
 XX  
 XX N-PSDB; AAV05171.  
 XX  
 XX New isolated spindly gene from plants - is involved in gibberellin  
 FT signal transduction, used to develop products for altering plant  
 FT development  
 XX  
 XX Disclosure; Fig 2; 54pp; English.

XX The present sequence represents a protein that is involved in gibberellin  
 CC signal transduction. Inactivation of the gene produces a spindly  
 CC phenotype (hence the SPY gene). The spindly mutation is characterised by  
 CC elongated petioles, yellow-green leaves, early flowering, long spindly  
 CC bolts, partial male sterility and parthenocarpic fruit development. These  
 CC phenotypes are also observed in wild type plants exhibiting a gibberellin  
 CC overdose syndrome due to external application of gibberellin. A spy  
 CC phenotypic mutant was isolated from a library of Agrobacterium-mediated  
 CC seed transformation lines of Arabidopsis having T-DNA insertions  
 CC positioned throughout the genome. Seeds from the library were selected  
 CC for their ability to germinate in the presence of paclobutrazol.  
 CC Restriction mapping was used to identify spy mutant (spy-4) DNA from  
 CC resistant seeds. This DNA was used as a probe to obtain the SPY cDNA.  
 CC Introduction of the SPY gene into plants rescues the spindly phenotype.  
 CC The SPY DNA, vectors and proteins can be used to modulate plant  
 CC development including plant height, fruit growth, flower development and  
 CC leaf size.

SQ Sequence 981 AA;

Query Match 62.3%; Score 38; DB 19; Length 981;  
 Best Local Similarity 77.8%; Pred. No. 4.3e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AYRYGVVY 11  
 Db 255 AYNLGVVY 263

RESULT 12

AA31948

ID AA31948 standard; Protein; 1411 AA.

XX AA31948;

XX 21-DEC-1999 (first entry)

XX Plasmodium falciparum cytoadherence gene protein CLAG3.2.

DE CLAG3.2; cytoadherence linked asexual gene; CLAG; erythrocyte;

XX red blood cell; malaria; infection; therapy; vaccine.

XX Plasmodium falciparum.

XX WO9949048-A1.

PD 30-SEP-1999.  
 XX  
 XX 25-MAR-1999; 99WO-AU00213.  
 XX  
 XX 25-MAR-1998; 98AU-0002580.  
 XX  
 XX (MENZ-) MENZIES SCHOOL HEALTH RES.  
 XX  
 XX Kemp DJ, Trenholme KR, Gardiner DL, Holt DC, Cowman AF;  
 XX WPI; 1999-591099/50.  
 XX  
 XX New proteins useful for treatment of Plasmodium infections in humans,  
 PT especially malaria -  
 XX  
 XX Claim 17; Page 126-135; 150pp; English.  
 XX  
 XX This sequence represents the Plasmodium falciparum cytoadherence  
 CC linked asexual gene 3.2 (CLAG3.2) protein that facilitates  
 CC cytoadherence of erythrocytes parasitised with Plasmodium spp. to  
 CC other cells. It is encoded by a gene located on chromosome 3 of  
 CC P. falciparum. It is a member of a family of CLAG proteins (see  
 CC also AAY31945-49). The identification of clag genetic species, and  
 CC the products encoded by them, enables a range of therapeutic agents  
 CC to be rationally designed and/or identified that are useful for the  
 CC prophylaxis and treatment of disease conditions caused or  
 CC exacerbated by infection with Plasmodium spp., e.g. malaria,  
 CC especially in humans.  
 XX  
 XX Sequence 1411 AA;  
 SQ  
 Query Match 62.3%; Score 38; DB 20; Length 1411;  
 Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 Db 858 FVKYGIY 865  
 :|:|:|:  
 RESULT 13  
 AAY31947  
 ID AAY31947 standard; Protein; 1417 AA.  
 XX  
 XX AC AAY31947;  
 XX  
 XX 21-DEC-1999 (first entry)  
 XX  
 XX Plasmodium falciparum cytoadherence gene protein CLAG3.1.  
 DE  
 XX CLAG3.1; cytoadherence linked asexual gene; CLAG; erythrocyte;  
 KW red blood cell; malaria; infection; therapy; vaccine.  
 KW  
 XX Plasmodium falciparum.  
 OS  
 XX WO9949048-A1.  
 PN  
 XX 30-SEP-1999.  
 PD  
 XX 25-MAR-1999; 99WO-AU00213.  
 PF  
 XX 25-MAR-1998; 98AU-0002580.  
 XX  
 XX (MENZ-) MENZIES SCHOOL HEALTH RES.  
 XX  
 XX Kemp DJ, Trenholme KR, Gardiner DL, Holt DC, Cowman AF;  
 XX WPI; 1999-591099/50.  
 XX  
 XX New proteins useful for treatment of Plasmodium infections in humans,  
 PT especially malaria -  
 XX  
 XX Claim 16; Page 117-126; 150pp; English.

XX  
 CC This sequence represents the Plasmodium falciparum cytoadherence  
 CC linked asexual gene 3.1 (CLAG3.1) protein that facilitates  
 CC cytoadherence of erythrocytes parasitised with Plasmodium spp. to  
 CC other cells. It is encoded by a gene located on chromosome 3 of  
 CC P. falciparum. It is a member of a family of CLAG proteins (see  
 CC also AAY31945-49). The identification of clag genetic species, and  
 CC the products encoded by them, enables a range of therapeutic agents  
 CC to be rationally designed and/or identified that are useful for the  
 CC prophylaxis and treatment of disease conditions caused or  
 CC exacerbated by infection with Plasmodium spp., e.g. malaria,  
 CC especially in humans.  
 XX  
 XX Sequence 1417 AA;  
 SQ  
 Query Match 62.3%; Score 38; DB 20; Length 1417;  
 Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 Db 861 FVKYGIY 868  
 :|:|:|:  
 RESULT 14  
 AAY31949  
 ID AAY31949 standard; Protein; 1430 AA.  
 XX  
 XX AC AAY31949;  
 XX  
 XX 21-DEC-1999 (first entry)  
 XX  
 XX Plasmodium falciparum cytoadherence gene protein CLAG2.  
 DE  
 XX CLAG2; cytoadherence linked asexual gene; CLAG; erythrocyte;  
 KW red blood cell; malaria; infection; therapy; vaccine.  
 KW  
 XX Plasmodium falciparum.  
 OS  
 XX WO9949048-A1.  
 PN  
 XX 30-SEP-1999.  
 PD  
 XX 25-MAR-1999; 99WO-AU00213.  
 PF  
 XX 25-MAR-1998; 98AU-0002580.  
 PR  
 XX (MENZ-) MENZIES SCHOOL HEALTH RES.  
 XX  
 XX Kemp DJ, Trenholme KR, Gardiner DL, Holt DC, Cowman AF;  
 XX WPI; 1999-591099/50.  
 XX  
 XX New proteins useful for treatment of Plasmodium infections in humans,  
 PT especially malaria -  
 XX  
 XX Claim 18; Page 136-145; 150pp; English.  
 PS  
 XX This sequence represents the Plasmodium falciparum cytoadherence  
 CC linked asexual gene 2 (CLAG2) protein that facilitates  
 CC cytoadherence of erythrocytes parasitised with Plasmodium spp. to  
 CC other cells. It is encoded by a gene located on chromosome 2 of  
 CC P. falciparum. It is a member of a family of CLAG proteins (see  
 CC also AAY31945-48). The identification of clag genetic species, and  
 CC the products encoded by them, enables a range of therapeutic agents  
 CC to be rationally designed and/or identified that are useful for the  
 CC prophylaxis and treatment of disease conditions caused or  
 CC exacerbated by infection with Plasmodium spp., e.g. malaria,  
 CC especially in humans.  
 XX  
 XX Sequence 1430 AA;  
 SQ  
 Query Match 62.3%; Score 38; DB 20; Length 1430;

Best Local Similarity 50.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
Db 879 FYKYGIIY 886  
::|::|::|

## RESULT 15

AAU20895  
ID AAU20895 standard; Protein; 4134 AA.

XX AC AAU20895;  
XX

DT 21-DEC-1999 (first entry)

XX Plasmodium falciparum cytoadherence gene protein GLAG9 paralogue.

XX CLAG9; paralogue; cytoadherence linked asexual gene; CLAG;  
KW erythrocyte; red blood cell; malaria; infection; therapy; vaccine.

XX Plasmodium falciparum.

XX WO9949048-A1.

XX 30-SEP-1999.

XX 25-MAR-1999; 99WO-AU00213.

XX 25-MAR-1998; 98AU-0002580.

XX (MENZ-) MENZIES SCHOOL HEALTH RES.

XX Kemp DJ, Trenholme KR, Gardiner DL, Holt DC, Cowman AF;  
PI WPI; 1999-591099/50.

XX New proteins useful for treatment of Plasmodium infections in humans,  
PT especially malaria

XX Disclosure; Page 90-115; 150pp; English.

XX This sequence represents the protein product of a clag9 paralogue  
CC gene (see also AA220056) on chromosome 3 of Plasmodium falciparum.  
CC It is a paralogue of the newly identified cytoadherence linked  
CC asexual gene 9 (CLAG9) protein (see AAU20895) encoded by the clag9  
CC gene on chromosome 9 of P. falciparum. CLAG9 facilitates  
CC cytoadherence of erythrocytes parasitised with Plasmodium to other  
CC cells. The identification of clag genetic species, and the  
CC products encoded by them, enables a range of therapeutic agents to  
CC be rationally designed and/or identified that are useful for the  
CC prophylaxis and treatment of disease conditions caused or  
CC exacerbated by infection with Plasmodium spp., e.g. malaria,  
CC especially in humans.

XX Sequence 4134 AA;

Query Match 62.3%; Score 38; DB 20; Length 4134;

Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
Db 2193 FYKYGIIY 2200  
::|::|::|

## RESULT 16

AAU20895  
ID AAU20895 standard; Protein; 104 AA.

XX AC AAU20895;  
XX

DT 18-DEC-2001 (first entry)

XX DE  
XX

Human novel foetal antigen, SEQ ID NO 1139.

XX Human; foetal tissue antigen; antiinflammatory; neuroprotective;  
KW immunomodulator; cardiovascular; cytostatic; nephrothropic;  
KW cardiovacular; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; breast neoplasm; cancer;  
KW cardiovacular disorder; cardiac arrest; cerebrovascular disorder;  
KW cerebral ischaemia; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; epithelial cell proliferation; food additive.

OS Homo sapiens.

XX WO20015312-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01321.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

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XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

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XX 07-JUL-2000; 2000US-0216647.

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XX 08-SEP-2000; 2000US-0231242.

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XX 14-SEP-2000; 2000US-0232397.

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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-488782/53.
XX N-PSDB; AAS33715.
XX
XX New polynucleotides and polypeptides for diagnosing, treating,
PT preventing or prognosing e.g. diseases or disorders of the nervous,
PT musculoskeletal, excretory, gastrointestinal, reproductive, and
PT respiratory systems
XX
XX Claim 11; SEQ ID No 1139; 642pp; English.
XX
XX The invention relates to novel nucleic acids encoding novel human foetal
CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g.
CC by gene therapy) or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. The antibodies to the antigens can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. Numerous
CC examples of diseases and disorders treated by the nucleic acids and
CC proteins are given in the specification. The present sequence
Query Match 60.7%; Score 37; DB 22; Length 104;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SCAYRYRG 8
Db 29 SNSYRYRG 36
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AAB32986
ID AAB32986 standard; Protein; 158 AA.
XX
XX AAB32986;
AC
XX
XX 25-JAN-2001 (first entry)
DE Pinus radiata transcription factor protein sequence #113.
XX
XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bz1p; g-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
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KW type 2 Cys2His2; CCAAT box element; MYB.  
XX Pinus radiata.  
OS  
XX WO200053724-A2.  
PN  
XX 14-SEP-2000.  
XX  
XX  
XX 09-MAR-2000; 2000WO-US06112.  
PF  
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XX 11-MAR-1999; 99US-0266513.  
PR  
XX 18-AUG-1999; 99US-0149485.  
PR  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
PA  
XX Wood M, McGrath A, Shenk MA, Glenn M;  
XX WPI; 2000-579369/54.  
XX  
XX New isolated polynucleotide encoding a plant transcription factor for  
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
PT having modified gene expression or modified activity of a polypeptide  
PT  
XX  
XX Claim 8; Page 380; 747pp; English.  
PS  
XX The present invention relates to novel plant transcription factors from  
CC Eucalyptus grandis or Pinus radiata. The present sequence is one such  
CC transcription factor. The transcription factor may be used to produce a  
CC plant having modified gene expression such as a woody plant e.g. a  
CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or  
CC to modify the activity of a polypeptide in a plant. The transcription  
CC factors of the present invention are members from the following families  
CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic  
CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/WADS, homeodomain  
CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2  
CC Cys2His2, CCAAT box elements and MYB.  
XX  
XX  
SQ Sequence 158 AA;  
  
Query Match 60.7%; Score 37; DB 21; Length 158;  
Best Local Similarity 70.0%; Pred. No. 87;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
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Db 143 GAYYGGQGY 152  
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AC AAG54380;  
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DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69332.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX EP1033405-A2.  
PN  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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PR 04-JUN-1999; 99US-0137502.  
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PR 26-OCT-1999; 99US-0161361.
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Query Match 60.7%; Score 37; DB 21; Length 384;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
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QY 3 AYYRYGV 9
Db 124 AYYRYGL 130
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AC AAG41345;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 51429.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 24-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140931.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 09-AUG-1999; 99US-0148171.  
PR 10-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149502.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 13-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.

PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	18-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	28-OCT-1999;	99US-0162142.
QY	Query Match	60.7%; Score 37; DB 21; Length 499;
Dd	Best Local Similarity	85.7%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;
Xx	MATCHES 6; Conservative	1;
XX	Sequence	560 AA;
AAAB42484	ID AAB42484 standard; Protein; 560 AA.	
AC	AAB42484;	
XX	08-FEB-2001 (first entry)	
DT	Human ORFX ORF2248 polypeptide sequence SEQ ID NO:4496.	
XX	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective; anticoagulant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.	
OS	Homo sapiens.	
XX	WO200058473-A2.	
PX	05-OCT-2000.	
PD	31-MAR-2000; 2000WO-US08621.	
PF	31-MAR-1999; 99US-0127607.	
XX	02-APR-1999; 99US-0127636.	
XX	05-APR-1999; 99US-0127728.	
XX	30-MAR-2000; 2000US-0540763.	

PA	(CURA-) CURAGEN CORP.	
XX	Shinkets RA, Leach M;	
PI	WPI; 2000-602362/57.	
XX	N-PSDB; AAC76693.	
DR	Novel nucleic acids and peptides derived from open reading frame X,	
PT	useful for treating e.g. cancers, proliferative disorders,	
PT	neurodegenerative disorders and cardiovascular disease -	
XX	Claim 11; Page 3681-3683; 5507pp; English.	
XX	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,	
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX	
CC	sequences have activities such as: cytostatic; hepatotropic; vulnerary;	
CC	antisporadic; antiparkinsonian; neurotropic; neuroprotective;	
CC	osteopathic; anticoagulant; antiarthritic; immunosuppressant;	
CC	immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;	
CC	antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;	
CC	antithyroid; and antianaemic. The sequences can be used for determining	
CC	the presence of or predisposition to, or preventing or treating	
CC	pathological conditions associated with an ORFX-associated disorder. The	
CC	nucleic acids can be used to express ORFX proteins in gene therapy	
CC	vectors. The proteins and nucleic acids may be used to treat cancers,	
CC	proliferative disorders, neurodegenerative disorders, osteoarthritis,	
CC	graft vs host disease, cardiovascular disease, diabetes mellitus, lupus	
CC	hypertension, hypothyroidism, cholesterol ester storage, systemic lupus	
CC	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,	
CC	bacterial or fungal infection, malaria, autoimmune disorders, asthma,	
CC	allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,	
CC	nocturnal haemoglobinuria, antiinflammatory disease; to enhance	
CC	coagulation; to inhibit thrombosis; and as a contraceptive.	
XX	Seq	
SX	Sequence	560 AA;
QY	Query Match	60.7%; Score 37; DB 21; Length 560;
Dd	Best Local Similarity	66.7%; Pred. No. 3.5e+02;
XX	MATCHES 6; Conservative	1; Mismatches 2; Indels 0; Gaps 0;
XX	Sequence	560 AA;
AAAO17144	ID AAO17144 standard; protein; 560 AA.	
AC	AAO17144;	
XX	13-JUN-2002 (first entry)	
DT	Human blood coagulation factor VII activating protease.	
DE	Human; blood coagulation factor VII activating protease; FSAP;	
XX	single-chain plasminogen activator; bleeding disorder; haematological;	
KW	haemostatic.	
OS	Homo sapiens.	
XX	EP1182258-A1.	
PX	27-FEB-2002.	
PD	05-JUL-2001; 2001EP-0115691.	
PF	26-JUL-2000; 2000DE-1036641.	
XX	10-OCT-2000; 2000DE-1050040.	
XX	21-OCT-2000; 2000DE-1052319.	
XX	12-APR-2001; 2001DE-1018706.	

[illegible]

XX (AVET ) AVENTIS BEHRING GMBH.  
 XX Roemisch J, Stoehr H, Feussner A, Lang W, Weimer T, Becker M;  
 PI Nerlich C, Muth-Naumann G;  
 XX WPI; 2002-270939/32.  
 DR N-PSDB; AAL45696.  
 XX New nucleic acid encoding mutant factor 7 activating protease, useful  
 PT for diagnosis, treatment and prevention of coagulation disorders, also  
 PT related protein and antibodies -  
 XX Claim 4; Page 17-19; 27pp; German.  
 XX The present invention relates to a mutant of the DNA sequence encoding  
 CC the protease (FSAP) that activates blood coagulation factor VII (FVII)  
 CC and single-chain plasminogen activator, where at least one of the base  
 CC changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is  
 CC present. The mutant sequences can be used in the treatment and prevention  
 CC of bleeding disorders associated with inherited or acquired defects of  
 CC blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's  
 CC factor and/or with antibodies against any of these proteins. The present  
 CC sequence is the human FSAP protein.  
 XX Sequence 560 AA;  
 SQ Query Match 60.7%; Score 37; DB 23; Length 560;  
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAYRYGVW 10  
 Db 519 GTYVYGVIV 527  
 RESULT 22  
 AAO17145  
 ID AAO17145 standard; protein; 560 AA.  
 XX AAO17145;  
 AC AAO17145;  
 XX 13-JUN-2002 (first entry)  
 DT Human blood coagulation factor VII activating protease mutant.  
 DE Human, blood coagulation factor VII activating protease; FSAP;  
 KW single-chain plasminogen activator; bleeding disorder; haematological;  
 KW haemostatic; mutant; mutein.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX EP1182258-A1.  
 PN 27-FEB-2002.  
 PD 05-JUL-2001; 2001EP-0115691.  
 XX 26-JUL-2000; 2000DE-1036641.  
 PR 10-OCT-2000; 2000DE-1050040.  
 PR 21-OCT-2000; 2000DE-1052319.  
 PR 12-APR-2001; 2001DE-1018706.  
 XX (AVET ) AVENTIS BEHRING GMBH.  
 PA Roemisch J, Stoehr H, Feussner A, Lang W, Weimer T, Becker M;  
 XX Nerlich C, Muth-Naumann G;  
 PI WPI; 2002-270939/32.  
 DR N-PSDB; AAL45697.  
 XX New nucleic acid encoding mutant factor 7 activating protease, useful  
 PT for diagnosis, treatment and prevention of coagulation disorders, also  
 PT related protein and antibodies -  
 XX Disclosure; Page 20-22; 27pp; German.  
 XX The present invention relates to a mutant of the DNA sequence encoding  
 CC the protease (FSAP) that activates blood coagulation factor VII (FVII)  
 CC and single-chain plasminogen activator, where at least one of the base  
 CC changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is  
 CC present. The mutant sequences can be used in the treatment and prevention  
 CC of bleeding disorders associated with inherited or acquired defects of  
 CC blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's  
 CC factor and/or with antibodies against any of these proteins. The present  
 CC sequence is the mutant human FSAP protein.  
 XX Sequence 560 AA;  
 SQ Query Match 60.7%; Score 37; DB 23; Length 560;  
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAYRYGVV 10  
 Db 519 GTYVYGVIV 527  
 RESULT 23  
 ABP47134  
 ID ABP47134 standard; peptide; 19 AA.  
 XX ABP47134;  
 AC ABP47134;  
 XX 19-AUG-2002 (first entry)  
 DT Human Blys binding scFv VH CDR3 SEQ ID 3145.  
 DE Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX Homo sapiens.  
 OS WO200202641-A1.  
 PN 10-JAN-2002.  
 PD 15-JUN-2001; 2001WO-US19110.  
 PF 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI; 2002-114799/15.  
 DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX Claim 2; Page 3123; 3148pp; English.  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antineoplastic and anti-AIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
CC and so may be used to detect and quantitate the presence of BlyS in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of BlyS. They may also be  
CC administered to treat diseases associated with aberrant BlyS expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.

XX SQ Sequence 19 AA;  
Query Match 59.0%; Score 36; DB 23; Length 19;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9  
||| |||  
Db 9 SGGYVYGM 17

RESULT 24  
AAE07014  
ID AAE07014 standard; Protein; 128 AA.  
XX AC AAE07014;  
XX DT 16-OCT-2001 (first entry)  
XX DE Human heavy chain variable (VH) region, 038062.  
KW Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;  
KW AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody;  
KW neointimal hyperplasia; VH; heavy chain variable region.

XX OS Homo sapiens.  
XX PH Key Location/Qualifiers  
FT Region 31..35 /label= CDR1  
FT /note= "Complementarity determining region 1"  
FT Region 50..66 /label= CDR2  
FT /note= "Complementarity determining region 2"  
FT Region 99..117 /label= CDR3  
FT /note= "Complementarity determining region 3"  
FT Misc-difference 109  
FT /label= Unknown  
XX WO200157226-A1.  
XX PD 09-AUG-2001.  
XX PF 02-FEB-2001; 2001WO-US03537.  
XX PR 03-FEB-2000; 2000US-0497625.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;  
XX WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor  
PT 2-mediated disorder in a patient, comprises a binding specificity for  
PT CCR2, and a non-human antigen binding region and human immunoglobulin  
PT -  
XX Disclosure; Page 168; 183pp; English.  
XX The patent discloses a humanised antibody or its antigen-binding  
CC fragment, having binding specificity for CC-chemokine receptor 2  
CC (CCR2), comprising an antigen binding region of non-human origin  
CC and at least a portion of an immunoglobulin of human origin. The  
CC humanised antibodies are useful for inhibiting the interaction of  
CC a cell expressing CCR2. They are useful for inhibiting or treating  
CC HIV infection. The proteins of the invention are useful for inhibiting  
CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
CC inflammatory disorder, autoimmune disorders such as rheumatoid  
CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
CC and in the manufacture of a medicament for treating CCR-2 mediated  
CC disease. They are also useful for treating allergy, anaphylaxis,  
CC malignancy, chronic and acute inflammation, histamine and IgE-  
CC mediated allergic reaction, shock, stenosis, allograft rejection,  
CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
CC intervention, including angioplasty and/or stent placement in a mammal.  
CC Humanised antibodies are also useful for inhibiting narrowing of the  
CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
CC a vessel in a mammal, preferably associated with vascular intervention.  
CC The present sequence is human heavy chain variable (VH) region, 038062.

XX SQ Sequence 128 AA;  
Query Match 59.0%; Score 36; DB 22; Length 128;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9  
||| |||  
Db 107 SGXYVYGM 115

RESULT 25  
ABP10506  
ID ABP10506 standard; Protein; 139 AA.  
XX AC ABP10506;  
XX DT 24-JUN-2002 (first entry)  
XX DE Human ORFX protein sequence SEQ ID NO:20994.  
XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
KW hypertension; hypothyroidism; cholesterol ester storage disease;  
KW immune deficiency; immune disorder; infectious disease; thyroiditis;  
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
KW myasthenia gravis.  
XX OS Homo sapiens.  
XX PN WO200192523-A2.  
XX PD 06-DEC-2001.  
XX PF 29-MAY-2001; 2001WO-US10836.  
XX PR 30-MAY-2000; 2000US-206132P.  
XX PR 29-AUG-2000; 2000US-228716P.  
XX PA (CURA-) CURAGEN CORP.



KW secreted protein; transmembrane domain; cytokine; tissue growth;  
 KW TopPred II computer program; COS cell expression system;  
 KW membrane fraction; SDS polyacrylamide gel electrophoresis;  
 KW nutritional activity; cell proliferation; immune stimulation;  
 KW immune suppression; hematopoiesis regulation; tumour inhibition.  
 XX  
 OS Homo sapiens.

XX WO9950405-A1.  
 XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06946.

XX 31-MAR-1998; 98US-0080110.  
 XX 29-MAR-1999; 99US-0280591.

XX (GEMY ) GENETICS INST INC.  
 XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;  
 XX N-PSDB; AAX90853.

XX WPI: 1999-610849/52.  
 XX N-PSDB; AAX90853.

XX Polynucleotides encoding secreted human proteins, derived from human  
 PT adult brain, human fetal brain, human fetal kidney, and human adult  
 PT blood cDNA libraries  
 XX  
 PS Claim 20; Page 105; 122pp; English.

XX The present sequence is the pk65.4 secreted protein encoded by the cDNA  
 CC clone pk65.4. pk65.4 was isolated from a human foetal kidney CDNA  
 CC library using methods specific for secreted protein cDNAs. The TopPred II  
 CC computer program predicts three potential transmembrane domains within  
 CC the protein sequence, centered around amino acids 16, 67, and 133.  
 CC pk65.4 protein was expressed in a COS cell expression system, and an  
 CC expressed band of approximately 15kDa was detected in membrane fractions  
 CC using SDS polyacrylamide gel electrophoresis. The polynucleotide and  
 CC protein may effect nutritional activity, cytokine and cell proliferation,  
 CC immune stimulation or suppression, hematopoiesis regulation, tissue  
 CC growth, tumour inhibition etc.

XX Sequence 144 AA;  
 SQ

Query Match 59.0%; Score 36; DB 20; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 ||| |||:  
 Db 132 YLYGMIY 139

RESULT 28  
 AAY41306  
 ID AAY41306 standard; Protein; 144 AA.

XX AAY41306;  
 XX 18-JAN-2000 (first entry).

XX Human cornichon protein.  
 DE  
 XX Human; cornichon; differentiation; body plan; metazoan; oogenesis;  
 KW embryogenesis; dorsalization; oocyte; dorsal-ventral axis; bicoid;  
 KW anterior-posterior axis; microtubule; cytoskeleton; oskar; diagnosis;  
 KW developmental disorder; hereditary neuropathy; seizure disorder;  
 KW reproductive disorder; immunological disorder; neoplastic disorder;  
 KW cancer; infection; spina bifida; cataract.

XX Homo sapiens.  
 OS

PN US968744-A.

XX 19-OCT-1999.

XX 14-OCT-1997; 97US-0950168.

XX 14-OCT-1997; 97US-0950168.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Shah P, Corley NC;  
 XX WPI: 1999-590398/50.  
 XX N-PSDB; AAZ30544.

XX Isolated nucleic acids encoding human cornichon molecules, useful in  
 PT the recombinant production of cornichon proteins and in the prevention,  
 PT diagnosis and treatment of developmental, reproductive, immunological  
 PT and neoplastic disorders -  
 XX Claim 1; Fig 1; 28pp; English.

XX This sequence represents the human cornichon (CORN) protein (I). CORN  
 CC is involved in the differentiation and determination of body plan in  
 CC metazoans during oogenesis and embryogenesis. It is involved in  
 CC controlling the correct dorsalization of the oocyte (i.e. determining  
 CC the dorsal-ventral axis) and is essential in the correct induction of  
 CC the anterior-posterior axis. In this case, CORN is implicated in the  
 CC formation of correctly polarized microtubule cytoskeletons, which are  
 CC required for proper localization of the anterior and posterior  
 CC determinant genes (bicoid and oskar) and for the asymmetric positioning  
 CC of the oocyte nucleus (see Roth et al., Cell (1995)).  
 CC (I) may be used for the diagnosis, prevention and treatment of  
 CC disorders associated with inappropriate expression and/or activity of  
 CC CORN proteins. These disorders include developmental disorders (e.g.  
 CC anenia, Cushing's syndrome, epilepsy and achondroplastic dwarfism),  
 CC hereditary neuropathies (e.g. Charcot-Marie-Tooth disease), seizure  
 CC disorders (e.g. Sydenham's chorea and cerebral palsy), reproductive  
 CC disorders (e.g. infertility, disorders of prolactin production, tumors  
 CC and disruptions of the menstrual cycle), immunological disorders (e.g.  
 CC acquired immune deficiency syndrome (AIDS), Addison's disease and  
 CC asthma), neoplastic disorders (e.g. adenocarcinoma, leukemia, cancers  
 CC of the breast, lung, testis, ovaries and prostate and melanomas),  
 CC complications of cancers, bacterial, viral, parasitic, protozoal,  
 CC helminthic and fungal infections and other disorders such as spina  
 CC bifida and cataracts.

XX Sequence 144 AA;  
 SQ

Query Match 59.0%; Score 36; DB 20; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 ||| |||:  
 Db 132 YLYGMIY 139

RESULT 29  
 AAY41732  
 ID AAY41732 standard; Protein; 144 AA.

XX AAY41732;  
 XX 07-DEC-1999 (first entry)

XX Human PRO181 protein sequence.  
 DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.

XX Homo sapiens.  
 OS



KW activin; inhibin activity; chemotaxis; chemokinesis; haemostasis;  
 KW thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor;  
 KW tumour inhibitor.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO9943802-A2.  
 XX PD  
 XX PF 02-SEP-1999.  
 XX PR 25-FEB-1999; 99WO-JF00875.  
 XX PR 27-FEB-1998; 98JP-0046607.  
 XX PA (PROT-) PROTEGENE INC.  
 XX PA (SAGA ) SAGAMI CHEM RES CENT.  
 XX PI Kato S, Kimura T, Nakamura N, Sekine S;  
 XX WPI; 1999-527617/44.  
 DR N-PSDB; AAZ11179, AAZ11186.  
 XX New proteins and DNA useful for preventing tumours  
 PT Claim 1; Page 72-73; 96pp; English.  
 XX This sequence is a human transmembrane protein of the invention. The  
 CC DNAs are useful for expressing recombinant protein for analysis.  
 CC characterisation or therapeutic use, and are useful as markers for  
 CC tissues in which the corresponding protein is preferentially expressed.  
 CC They are also useful as molecular weight markers on Southern gels, as  
 CC chromosome markers or tags (when labelled) to identify potential genetic  
 CC disorders, as probes to hybridise and thus discover novel, related DNA  
 CC sequences, as a source of PCR primers for genetic fingerprinting, as  
 CC probes to subtract-out known sequences in the process of discovering  
 CC other novel DNAs, for selecting and making oligomers for attachment to a  
 CC gene chip or other support, including for examination of expression  
 CC patterns, to raise anti-protein antibodies using DNA immunisation  
 CC techniques, and as an antigen to raise anti-DNA antibodies or elicit  
 CC another immune response. Where the DNA encodes a protein which binds to  
 CC be used in interaction trap assays to identify DNAs encoding the other  
 CC protein with which binding occurs or to identify inhibitors of the  
 CC binding interaction. The DNAs and proteins can have e.g. nutritional  
 CC activity, cytokine and cell proliferation/differentiation activity,  
 CC immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity.  
 XX  
 SQ Sequence 144 AA;  
 Query Match 59.0%; Score 36; DB 20; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 DB 132 YYLYGMVY 139  
 RESULT 31  
 AAB44288  
 ID AAB44288 standard; Protein; 144 AA.  
 XX AAB44288;  
 AC  
 XX 08-FEB-2001 (first entry)  
 DT  
 XX Human PRO181 (UNQ155) protein sequence SEQ ID NO:322.  
 DE  
 XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO200053756-A2.  
 XX PD  
 XX PF 14-SEP-2000.  
 XX PR 18-FEB-2000; 2000WO-US04341.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 XX PR 12-MAR-1999; 99US-0123957.  
 XX PR 29-MAR-1999; 99US-0126773.  
 XX PR 21-APR-1999; 99US-0130232.  
 XX PR 28-APR-1999; 99US-0131445.  
 XX PR 14-MAY-1999; 99US-0134287.  
 XX PR 23-JUN-1999; 99US-0141037.  
 XX PR 26-JUL-1999; 99US-0145698.  
 XX PR 29-OCT-1999; 99US-0162506.  
 XX PR 30-NOV-1999; 99WO-US28313.  
 XX PR 02-DEC-1999; 99WO-US28551.  
 XX PR 02-DEC-1999; 99WO-US28565.  
 XX PR 16-DEC-1999; 99WO-US30095.  
 XX PR 30-DEC-1999; 99WO-US31243.  
 XX PR 05-JAN-2000; 99WO-US31274.  
 XX PR 06-JAN-2000; 2000WO-US00219.  
 XX PR 06-JAN-2000; 2000WO-US00277.  
 XX PR 06-JAN-2000; 2000WO-US00376.  
 XX (GETH ) GENENTECH INC.  
 XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 XX Ferrera N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 XX Kijavoin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI; 2000-611443/58.  
 DR N-PSDB; AAC78538.  
 XX Novel PRO polypeptides and polynucleotides used in detection methods,  
 PT to target bioactive molecules to specific cells, and to modulate  
 PT cellular activities -  
 XX Claim 12; Fig 129; 636pp; English.  
 XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.  
 XX  
 SQ Sequence 144 AA;  
 Query Match 59.0%; Score 36; DB 21; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 DB 132 YYLYGMVY 139  
 RESULT 32  
 AAB19524  
 ID AAB19524 standard; Protein; 144 AA.



XX Drosophila melanogaster polypeptide SEQ ID NO 12390.  
DE  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
PN  
XX  
XX  
XX 27-SEP-2001.  
PD  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
PF  
XX  
XX 23-MAR-2000; 2000US-191637P.  
PR  
XX 11-JUL-2000; 2000US-0614150.  
PR  
XX (PEKE ) PE CORP NY.  
PA  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI; 2001-656860/75.  
DR  
XX N-PSDB; ABL05969.  
DR  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
PT  
XX  
XX Disclosure; SEQ ID NO 12390; 21pp + Sequence Listing; English.  
PS  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX  
SQ Sequence 144 AA;  
Query Match 59.0%; Score 36; DB 22; Length 144;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 YRYRGVYV 11  
DB 132 YYTGMVY 139  
||| |||:  
||| |||:  
RESULT 35  
AAW93330  
ID AAW93330 standard; Protein; 144 AA.  
XX  
XX  
XX AAW93330;  
AC  
XX  
XX  
XX 06-NOV-2001 (first entry)  
DT  
XX  
XX Human polypeptide, SEQ ID NO: 2859.  
DE  
XX  
XX Human; full length cDNA; cDNA synthesis; oligo-capping.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP1130094-A2.  
PN  
XX  
XX 05-SEP-2001.  
PD  
XX  
XX 07-JUL-2000; 2000EP-0114089.  
PF  
XX

PR 08-JUL-1999; 99JP-0194486.  
PR 11-JAN-2000; 2000JP-0118774.  
PR 02-MAY-2000; 2000JP-0183765.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
XX WPI; 2001-524255/58.  
DR  
XX N-PSDB; AAK94250.  
DR  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their  
PT use in genetic manipulation -  
PT  
XX  
XX Claim 8; SEQ ID NO 2859; 1380pp + sequence listing; English.  
PS  
XX  
XX The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA  
CC molecules have been determined. Primers for synthesising the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesised by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily  
CC without any special methods. The present sequence is a polypeptide  
CC encoded by a full length human cDNA of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.  
XX  
XX  
SQ Sequence 144 AA;  
Query Match 59.0%; Score 36; DB 22; Length 144;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 YRYRGVYV 11  
DB 132 YYTGMVY 139  
||| |||:  
||| |||:  
RESULT 36  
AAB76851  
ID AAB76851 standard; Protein; 144 AA.  
XX  
XX  
XX AAB76851;  
AC  
XX  
XX 12-APR-2001 (first entry)  
DT  
XX  
XX Human lung tumour protein related protein sequence SEQ ID NO:327.  
DE  
XX  
XX Human; lung cancer; lung tumour; lung tumour protein; gene therapy;  
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;  
KW cytostatic; antisense inhibition.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200100828-A2.  
PN  
XX  
XX 04-JAN-2001.  
PD  
XX  
XX 30-JUN-2000; 2000WO-US18061.  
PF  
XX  
XX 30-JUN-1999; 99US-0346492.  
PR 15-OCT-1999; 99US-0419356.  
PR 17-DEC-1999; 99US-0466867.  
PR 30-DEC-1999; 99US-0476300.  
PR 06-MAR-2000; 2000US-0519642.  
PR 22-MAR-2000; 2000US-0533077.  
PR 10-APR-2000; 2000US-0546259.  
PR 27-APR-2000; 2000US-0560406.  
PR 05-JUN-2000; 2000US-0589184.  
XX

PA (CORI-) CORIXA CORP.  
 XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;  
 PI Retter MW, Mannion J;  
 XX WPI; 2001-071488/08.  
 XX Lung tumor-associated proteins and the nucleic acids that encode them,  
 PT useful for preventing, diagnosing and treating lung cancer -  
 XX  
 PS Example 1; Page 254; 436pp; English.  
 XX The present invention describes immunogenic portions of lung tumour-  
 CC associated proteins (I) and the nucleic acids (NAs) that encode them.  
 CC (I) have cytosolic activity and can be used in gene therapy, antisense  
 CC inhibition and in vaccines. The NAs and the lung tumour-associated  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with their inappropriate expression,  
 CC especially lung cancers. For example, the NAs may be administered to  
 CC treat diseases by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of the protein by expressing inactive proteins  
 CC or to supplement the patients own production of (I). Additionally, the  
 CC NAs may be used to produce the lung-tumour associated protein, according  
 CC to standard recombinant DNA methodology. Conversely, antisense NA  
 CC molecules may be administered to down regulate protein expression by  
 CC binding with the cells own genes and preventing their expression. The NA  
 CC and complementary sequences may also be used as DNA probes in diagnostic  
 CC assays to detect and quantitate the presence of similar NA sequences in  
 CC samples, and hence which patients may be in need of treatment for lung  
 CC cancer. The (I) may be used as antigens in the production of antibodies  
 CC and in assays to identify modulators (agonists and antagonists) of the  
 CC expression and activity of the protein. AAF68083 to AAF68878 and  
 CC AAF6848 to AAF6878 represent human lung tumour protein related  
 CC nucleotide and protein sequences which are used in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 144 AA;  
 Query Match 59.08; Score 36; DB 22; Length 144;  
 Best Local Similarity 62.54; Pred. NO. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 YRYGVVY 11  
 DB 132 YLYGMVY 139  
 RESULT 37  
 ABB95423  
 ID ABB95423 standard; Protein; 144 AA.  
 XX  
 AC ABB95423;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related protein PRO181 SEQ ID NO: 2.  
 XX  
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulneryary;  
 KW antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208284-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 09-JUL-2001; 2001WO-US21735.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.

PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0806889.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 DR WPI; 2002-171999/22.  
 DR N-PSDB; ABL95561.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 XX infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11; Fig 2; 567pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX SQ Sequence 144 AA;  
Query Match 59.0%; Score 36; DB 23; Length 144;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 YYRYGVVY 11  
DB 132 YYLYGMIV 139  
RESULT 38  
AAE20143  
ID AAE20143 standard; Protein; 144 AA.  
XX AC AAE20143;  
DT 18-JUN-2002 (first entry)  
XX Human cornichon protein (CORN).  
XX Human; cornichon protein; CORN; Cushing's syndrome; muscular dystrophy;  
KW developmental disorder; neoplastic; seizure; reproductive; immunological;  
KW tubular acidosis; anaemia; polycystic ovary; autoimmune disorder; tumour;  
KW breast cancer; prostate; testis; epilepsy; neuropathy; Addison's disease;  
KW ulcerative colitis; spermatogenesis; hypothyroidism; cataract; arthritis;  
KW infertility; galactorrhoea; gynaecomastia; diabetes mellitus; fungicide;  
KW dermatitis; acquired immunodeficiency syndrome; AIDS; glomerulonephritis;  
KW atherosclerosis; allergy; asthma; bronchitis; Crohn's disease; auditory;  
KW gout; Graves' disease; multiple sclerosis; haemodialysis; anticonvulsant;  
KW trauma; drug screening; ophthalmological; cytostatic; immunosuppressive;  
KW gynaecological; antitumor; nephrotropic; neuroprotective; antihelminthic;  
KW antibacterial; tranquilizer; osteoporosis; antiparasitic; protozoacide;  
KW vulnerary; virucide; gene therapy.  
XX OS Homo sapiens.  
XX US6348576-B1.  
PN 19-FEB-2002.  
XX 02-AUG-1999; 99US-0365705.  
XX 14-OCT-1997; 97US-0950168.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Hillman JL, Corley NC, Shah P;  
PI WPI; 2002-266544/31.  
XX N-PSDB; AAD31079.  
XX New human cornichon protein, useful for diagnosis, prevention and  
PT treatment of developmental, reproductive, immunological and neoplastic  
PT disorders and to screen for molecules that bind the protein  
XX Claim 1; Fig 2; 29pp; English.  
XX The invention relates to a purified human cornichon protein (CORN). CORN  
CC is useful for diagnosis, prevention and treatment of developmental,  
CC reproductive, immunological and neoplastic disorders. Developmental,  
CC disorders include renal tubular acidosis, anaemia, Cushing's syndrome,  
CC achondroplastic dwarfism, Duchenne and Becker muscular dystrophy,  
CC epilepsy, hereditary neuropathies such as Charcot-Marie-Tooth disease,  
CC neurofibromatosis, hypothyroidism, seizure disorders such as cerebral  
CC palsy, cataract and sensorineural hearing loss and reproductive disorders  
CC include disorders of prolactin production, infertility, ovulatory  
CC defects, endometriosis, disruptions of the oestrous cycle, disruptions of  
CC the menstrual cycle, polycystic ovary syndrome, endometrial and ovarian  
CC tumours, autoimmune disorders, ectopic pregnancy, cancer of the breast,  
CC galactorrhoea, disruptions of spermatogenesis, cancer of the testis,  
CC cancer of the prostate, prostatitis and carcinoma of the male breast and

CC gynaecomastia. Immunological disorders include acquired immunodeficiency  
CC syndrome (AIDS), diabetes mellitus, arthritis, including rheumatoid  
CC arthritis, osteoarthritis, Addison's disease, allergies, asthma,  
CC atherosclerosis, bronchitis, Crohn's disease, ulcerative colitis, atopic  
CC dermatitis, glomerulonephritis, gout, Graves' disease, multiple  
CC sclerosis, osteoporosis, autoimmune thyroiditis, complications of cancer,  
CC haemodialysis and extracorporeal circulation, viral, bacterial, fungal,  
CC parasitic, protozoal and helminthic infections, and trauma. CORN, is  
CC catalytic or immunogenic fragments is useful for screening libraries of  
CC compounds in a variety of drug screening techniques. The present  
CC sequence is human CORN. CORN gene is useful in gene therapy.  
XX SQ Sequence 144 AA;  
Query Match 59.0%; Score 36; DB 23; Length 144;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 YYRYGVVY 11  
DB 132 YYLYGMIV 139  
RESULT 39  
AAU85506  
ID AAU85506 standard; Protein; 144 AA.  
XX AC AAU85506;  
XX 21-MAY-2002 (first entry)  
XX Clone #19110 of lung tumour protein.  
DE Lung tumour; cancer; T cell; immune response stimulator;  
KW cytostatic.  
XX OS Homo sapiens.  
XX WO200204514-A2.  
PN 17-JAN-2002.  
XX 10-JUL-2001; 2001WO-US22058.  
XX 11-JUL-2000; 2000US-0614124.  
PR 29-AUG-2000; 2000US-0651563.  
PR 08-SEP-2000; 2000US-0658824.  
PR 26-SEP-2000; 2000US-0671325.  
PR 06-OCT-2000; 2000US-0677419.  
PR 30-OCT-2000; 2000US-0702705.  
PR 13-DEC-2000; 2000US-0736457.  
PR 03-MAY-2001; 2001US-0849626.  
XX (CORI-) CORIXA CORP.  
PA Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;  
PI Marxerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;  
PI McNabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;  
XX WPI; 2002-164634/21.  
DR N-PSDB; ABK38061.  
XX Novel polynucleotide encoding a lung tumour polypeptide useful for  
PT stimulating and/or expanding T cells specific for a tumour protein  
XX Example 1; SEQ ID No 327; 223pp; English.  
XX The invention describes an isolated polynucleotide and polypeptide  
CC useful for stimulating and/or expanding T cells specific for a tumour  
CC protein for determining the presence of a cancer in a patient. A  
CC composition containing the polynucleotide and/or polypeptide is useful  
CC for treating a lung cancer in a patient. The polypeptide is useful for  
CC removing tumour cells from a biological sample. The polynucleotide is

CC also useful as probe or primer to detect the level of mRNA encoding a  
 CC tumour protein. This is the amino acid sequence of a lung tumour  
 CC associated protein, described in the method of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 144 AA;

Query Match 59.0%; Score 36; DB 23; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
 ||| ||:|  
 Db 132 YLYGMIV 139

RESULT 40  
 ABB84817  
 ID ABB84817 standard; Protein; 144 AA.

XX AC ABB84817;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Human PRO181 protein sequence SEQ ID NO:2.  
 XX  
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 28-JUL-2000; 2000US-220664P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-0643657.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 18-SEP-2000; 2000US-0864610.  
 XX 18-SEP-2000; 2000US-0865350.  
 XX 24-OCT-2000; 2000US-242922P.  
 XX 08-NOV-2000; 2000US-0709238.  
 XX 08-NOV-2000; 2000WO-US30952.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 22-JAN-2001; 2001US-0767609.  
 XX 28-FEB-2001; 2001US-0796498.  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX 01-MAR-2001; 2001WO-US06666.  
 XX 09-MAR-2001; 2001US-0802706.  
 XX 14-MAR-2001; 2001US-0808689.  
 XX 22-MAR-2001; 2001US-0816744.  
 XX 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Baker KP, Ferrata N, Gerbert H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 DR WPI; 2002-090516/12.  
 DR N-PSDB; ABL88072.  
 XX  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11; Fig 2; 565pp; English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 XX  
 SQ Sequence 144 AA;

Query Match 59.0%; Score 36; DB 23; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
 ||| ||:|  
 Db 132 YLYGMIV 139

Search completed: July 18, 2003, 15:06:42  
 Job time : 38.18 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2003, 15:03:46 ; Search time 12.76 Seconds  
(without alignments)  
25.365 Million cell updates/sec

Title: US-10-007-790-7  
Perfect score: 61  
Sequence: 1 SGAYRYGVVY 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	4	US-09-257-069-7
2	61	100.0	124	4	US-09-257-069-2
3	38	62.3	981	2	US-08-849-046-2
4	36	59.0	144	2	US-08-950-168-1
5	36	59.0	144	2	US-08-950-168-3
6	36	59.0	144	4	US-09-365-705-1
7	36	59.0	144	4	US-09-365-705-3
8	36	59.0	145	4	US-09-257-179-63
9	34	55.7	106	4	US-09-376-330-25
10	34	55.7	119	2	US-08-652-816A-10
11	34	55.7	522	4	US-08-894-818B-3
12	34	55.7	522	4	US-09-445-472-4
13	34	55.7	654	4	US-08-894-818B-35
14	34	55.7	654	4	US-09-445-472-16
15	33.5	54.9	1090	4	US-09-346-237-5
16	33.5	54.9	1096	4	US-09-346-237-6
17	33	54.1	33	1	US-08-053-131-78
18	33	54.1	33	1	US-08-645-641-78
19	33	54.1	33	1	US-07-853-408B-78
20	33	54.1	33	2	US-08-096-762-78
21	33	54.1	33	4	US-08-308-865-78
22	33	54.1	33	4	US-09-042-353-275
23	33	54.1	33	4	US-08-758-417A-123
24	33	54.1	33	5	PCT-US92-10983-78
25	33	54.1	267	1	US-08-015-973-3
26	33	54.1	267	1	US-08-448-164-3
27	33	54.1	267	4	US-08-081-929-3

28	33	54.1	315	1	US-07-757-390-8	Sequence 8, Appli
29	33	54.1	315	1	US-08-442-282-8	Sequence 8, Appli
30	33	54.1	315	1	US-08-442-281-8	Sequence 8, Appli
31	33	54.1	315	2	US-08-939-727-8	Sequence 8, Appli
32	33	54.1	332	1	US-07-757-390-7	Sequence 7, Appli
33	33	54.1	332	1	US-08-442-282-7	Sequence 7, Appli
34	33	54.1	332	1	US-08-442-281-7	Sequence 7, Appli
35	33	54.1	332	2	US-08-939-727-7	Sequence 7, Appli
36	33	54.1	332	2	US-08-958-642-2	Sequence 4, Appli
37	33	54.1	332	3	US-08-778-394-4	Sequence 2, Appli
38	33	54.1	332	3	US-08-778-423A-2	Sequence 3, Appli
39	33	54.1	335	1	US-07-947-130-3	Sequence 3, Appli
40	33	54.1	335	1	US-08-421-822-3	Sequence 3, Appli
41	33	54.1	335	1	US-08-421-823-3	Sequence 3, Appli
42	33	54.1	380	3	US-08-486-099-115	Sequence 115, App
43	33	54.1	380	3	US-08-360-107A-125	Sequence 125, App
44	33	54.1	380	3	US-08-484-223B-115	Sequence 115, App
45	33	54.1	380	3	US-08-919-597-115	Sequence 115, App

ALIGNMENTS

RESULT 1  
US-09-257-069-7  
; Sequence 7, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; TITLE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; CURRENT FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-7

Query Match 100.0%; Score 61; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGAYRYGVVY 11  
||| ||||| |||||  
Db 1 SGAYRYGVVY 11

RESULT 2  
US-09-257-069-2  
; Sequence 2, Application US/09257069  
; Patent No. 6348580  
; GENERAL INFORMATION:  
; APPLICANT: Medical & Biological Laboratories Co., Ltd.  
; TITLE OF INVENTION: Monoclonal Antibody Specific for  
; FILE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate  
; TITLE REFERENCE: M3-008-US  
; CURRENT APPLICATION NUMBER: US/09/257,069  
; CURRENT FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: JP 1998-252921  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-257-069-2

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Query Match      100.0%; Score 61; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGAYRYGVVY 11
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Db      99 SGAYRYGVVY 109

RESULT 3
US-08-649-046-2
; Sequence 2, Application US/08649046
; Patent No. 5912415
; GENERAL INFORMATION:
; APPLICANT: OLSZEWSKI, NEIL E.
; APPLICANT: JACOBSEN, STEVEN E.
; TITLE OF INVENTION: THE SPINDLY GENE, METHODS OF
; TITLE OF INVENTION: IDENTIFICATION AND USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; * COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/649,046
; APPLICATION NUMBER: US/08/649,046
; FILING DATE: 16-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCORMACK, MYRA H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00340101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1225
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-649-046-2

Query Match      62.3%; Score 38; DB 2; Length 981;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AYRYGVVY 11
      |||||
Db      255 AYNLGVVY 263

RESULT 4
US-08-950-168-1
; Sequence 1, Application US/08950168
; Patent No. 5968744
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; * COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; * COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0401 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1318847
US-08-950-168-1

Query Match      59.0%; Score 36; DB 2; Length 144;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 YRYGVVY 11
      |||||
Db      132 YLYGMVY 139

RESULT 5
US-08-950-168-3
; Sequence 3, Application US/08950168
; Patent No. 5968744
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; * COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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/
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0401 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 144 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 886769
/ US-08-950-168-3
/
/ Query Match 59.0%; Score 36; DB 2; Length 144;
/ Best Local Similarity 75.0%; Pred. No. 34;
/ Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 4 YYRYGVVY 11
/ Db 132 YYIYGMVY 139
/
/ RESULT 6
/ US-09-365-705-1
/ Sequence 1, Application US/09365705
/ Patent No. 6348576
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ Corley, Neil C.
/ Shah, Purvi
/ TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/365,705
/ FILING DATE: 02-Aug-1999
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/950,168
/ FILING DATE: 14-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0401 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 144 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 886769
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 144 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BLADNOT04
/
/ Query Match 59.0%; Score 36; DB 4; Length 144;
/ Best Local Similarity 75.0%; Pred. No. 34;
/ Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 4 YYRYGVVY 11
/ Db 132 YYIYGMVY 139
/
/ RESULT 7
/ US-09-365-705-3
/ Sequence 3, Application US/09365705
/ Patent No. 6348576
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ Corley, Neil C.
/ Shah, Purvi
/ TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/365,705
/ FILING DATE: 02-Aug-1999
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/950,168
/ FILING DATE: 14-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0401 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 144 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 886769
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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/ US-09-365-705-3
/
/ Query Match 59.0%; Score 36; DB 4; Length 144;
/ Best Local Similarity 75.0%; Pred. No. 34;
/ Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 4 YYRYGVVY 11
/ Db 132 YYIYGMVY 139
/
/ RESULT 8
/ US-09-257-179-63
/ Sequence 63, Application US/09257179
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; Patent No. 6410709.  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 29 Human Secreted Proteins  
; FILE REFERENCE: P2015P1  
; CURRENT APPLICATION NUMBER: US/09/257,179  
; CURRENT FILING DATE: 1999-02-25  
; EARLIER APPLICATION NUMBER: PCT/US98/17709  
; EARLIER FILING DATE: 1998-08-27  
; EARLIER APPLICATION NUMBER: 60/056,270  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER APPLICATION NUMBER: 60/056,271  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER APPLICATION NUMBER: 60/056,247  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER APPLICATION NUMBER: 60/056,073  
; EARLIER FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (145)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-257-179-63  
  
Query Match 59.0%; Score 36; DB 4; Length 145;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 4 YRYGVVY 11  
Db 132 YLYGMIV 139  
  
RESULT 9  
US-09-376-330-25  
; Sequence 25, Application US/09376330  
; Patent No. 6399321  
; GENERAL INFORMATION:  
; APPLICANT: Tessier, Daniel C.  
; APPLICANT: Dignard, Daniel  
; APPLICANT: Bergeron, John J.M.  
; APPLICANT: Thomas, David Y.  
; TITLE OF INVENTION: Method for screening for  
; TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity  
; TITLE OF INVENTION: and nucleic acid encoding for UGGT  
; FILE REFERENCE: 2139-9"US"  
; CURRENT APPLICATION NUMBER: US/09/376,330  
; CURRENT FILING DATE: 1999-08-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: GLUT-E. col  
US-09-376-330-25  
  
Query Match 55.7%; Score 34; DB 4; Length 106;  
Best Local Similarity 60.0%; Pred. No. 54;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 GAYRYGVVY 11  
Db 57 GQYFNSGVVY 66

RESULT 10

US-08-652-816A-10  
; Sequence 10, Application US/08652816A  
; Patent No. 5872215  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, JK  
; APPLICANT: Allen, DJ  
; APPLICANT: McCafferty, JG  
; TITLE OF INVENTION: Specific binding members, materials and  
; TITLE OF INVENTION: methods.  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,816A  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.4  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.8  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 23-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9525004.9  
; FILING DATE: 07-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9610824.6  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/02240  
; FILING DATE: 02-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/244,597  
; FILING DATE: 01-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/33308  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-652-816A-10  
  
Query Match 55.7%; Score 34; DB 2; Length 119;  
Best Local Similarity 66.7%; Pred. No. 61;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 SGAYRYGVY 9  
Db 98 SGAYDNYGI 106  
  
RESULT 11  
US-08-894-818B-3  
; Sequence 3, Application US/08894818B

; Patent No. 6261822  
; GENERAL INFORMATION:  
; APPLICANT: TAKAKURA, Hikaru  
; APPLICANT: MORISHITA, Mio  
; APPLICANT: YAMAMOTO, Katsuhiko  
; APPLICANT: MITTA, Masanori  
; APPLICANT: ASADA, Kiyozo  
; APPLICANT: TSUNASAWA, Susumu  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States of America  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,818B  
; FILING DATE: 20-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP96/03253  
; FILING DATE: 07-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 323285/1995  
; FILING DATE: 12-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TAKAKURA=1  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 522 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: /note= Xaa at position 428 is Gly or Val.  
; US-08-894-818B-3

Query Match 55.7%; Score 34; DB 4; Length 522;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11  
Db 504 AYYTYGWAY 512

RESULT 12  
US-09-445-472-4  
; Sequence 4, Application US/09445472  
; Patent No. 6359726  
; GENERAL INFORMATION:  
; APPLICANT: TAKAKURA, Hikaru  
; APPLICANT: MORISHITA, Mio  
; APPLICANT: SHIMOJO, Tonoko  
; APPLICANT: ASADA, Kiyozo  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE  
; FILE REFERENCE: TAKAKURA=6  
; CURRENT APPLICATION NUMBER: US/09/445,472

; CURRENT FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 151969/1997  
; PRIOR FILING DATE: 1997-06-10  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Pyrococcus furiosus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (428)..(428)  
; OTHER INFORMATION: Xaa at position 428 is Gly or Val.  
; US-09-445-472-4

Query Match 55.7%; Score 34; DB 4; Length 522;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AYYRYGVVY 11  
Db 504 AYYTYGWAY 512

RESULT 13  
US-08-894-818B-35  
; Sequence 35, Application US/08894818B  
; Patent No. 6261822  
; GENERAL INFORMATION:  
; APPLICANT: TAKAKURA, Hikaru  
; APPLICANT: MORISHITA, Mio  
; APPLICANT: YAMAMOTO, Katsuhiko  
; APPLICANT: MITTA, Masanori  
; APPLICANT: ASADA, Kiyozo  
; APPLICANT: TSUNASAWA, Susumu  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States of America  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,818B  
; FILING DATE: 20-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP96/03253  
; FILING DATE: 07-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 323285/1995  
; FILING DATE: 12-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TAKAKURA=1  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 654 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-894-818B-35

Query Match      55.7%; Score 34; DB 4; Length 654;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 AYRYGVVY 11
      ||| |||
Db      636 AYTGYWAY 644

RESULT 14
US-09-445-472-16
; Sequence 16, Application US/09445472
; Patent No. 6358726
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA=6
; CURRENT APPLICATION NUMBER: US/09/445,472
; CURRENT FILING DATE: 1999-12-06
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-09-445-472-16

Query Match      55.7%; Score 34; DB 4; Length 654;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 AYRYGVVY 11
      ||| |||
Db      636 AYTGYWAY 644

RESULT 15
US-09-346-237-5
; Sequence 5, Application US/09346237A
; Patent No. 6265197
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 5629.200-US
; CURRENT APPLICATION NUMBER: US/09/346,237A
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: PA 1998 00868
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: 60/094,353
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1090
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(1090)
; OTHER INFORMATION: pullulanase
US-09-346-237-5

Query Match      54.9%; Score 33.5; DB 4; Length 1090;
Best Local Similarity 63.6%; Pred. No. 7.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY      2 GAYRYGV-VY 11
      ||| |||
Db      371 GAFYRYAMTVY 381

RESULT 16
US-09-346-237-6
; Sequence 6, Application US/09346237A
; Patent No. 6265197
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 5629.200-US
; CURRENT APPLICATION NUMBER: US/09/346,237A
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: PA 1998 00868
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: 60/094,353
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1096
; TYPE: PRT
; ORGANISM: Klebsiella aerogenes
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(1096)
; OTHER INFORMATION: Pullulanase
US-09-346-237-6

Query Match      54.9%; Score 33.5; DB 4; Length 1096;
Best Local Similarity 63.6%; Pred. No. 7.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY      2 GAYRYGV-VY 11
      ||| |||
Db      371 GAFYRYAMTVY 381

RESULT 17
US-08-053-131-78
; Sequence 78, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
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/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: US 07/810,279
/ ; FILING DATE: 17-DEC-1991
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: US 07/853,408
/ ; FILING DATE: 18-MAR-1992
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: Smith, William M.
/ ; REGISTRATION NUMBER: 30,223
/ ; REFERENCE/DOCKET NUMBER: 14643-9-3
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 415-326-2400
/ ; TELEFAX: 415-326-2422
/ ; INFORMATION FOR SEQ ID NO: 78:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 33 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
/ ; US-08-053-131-78

Query Match 54.1%; Score 33; DB 1; Length 33;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAYRYGV 9
Db 9 GSYYYGM 16

RESULT 18
US-08-645-641-78
; Sequence 78, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

/ ; MOLECULE TYPE: peptide
/ ; US-08-645-641-78

Query Match 54.1%; Score 33; DB 1; Length 33;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAYRYGV 9
Db 9 GSYYYGM 16

RESULT 19
US-07-853-408B-78
; Sequence 78, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
/ ; US-07-853-408B-78

Query Match 54.1%; Score 33; DB 1; Length 33;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAYRYGV 9
Db 9 GSYYYGM 16

RESULT 20
US-08-096-762-78
; Sequence 78, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend Kourie and Crew  
;; STREET: One Market Plaza, Steuart Tower, Suite 200  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/096,762  
;; FILING DATE: 22-JUL-1993

;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/053,131  
;; FILING DATE: 26-APR-1993

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/990,860  
;; FILING DATE: 16-DEC-1992

;; APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/904,068  
;; FILING DATE: 23-JUN-1992

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/853,408  
;; FILING DATE: 18-MAR-1992

;; APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/810,279  
;; FILING DATE: 17-DEC-1991

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223

;; REFERENCE/DOCKET NUMBER: 14643-9-4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400

;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 78:  
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 33 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide

;; US-08-096-762-78

Query Match 54.1%; Score 33; DB 2; Length 33;  
Best Local Similarity 62.5%; Pred. No. 24;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAYRYGV 9

Db 9 GSYYYGM 16

RESULT 21

;; US-08-865-78  
;; Sequence 78, Application US/08308865  
;; Patent No. 5877397

;; GENERAL INFORMATION:

;; APPLICANT: Lonberg, Nils

;; APPLICANT: Kay, Robert M.

;; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for

;; PRODUCING HETEROLOGOUS ANTIBODIES

;; NUMBER OF SEQUENCES: 150

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: William M. Smith

;; STREET: One Market Plaza, Steuart Tower, Suite 2000

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94105

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/308,865  
;; FILING DATE:

;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/145,707

;; FILING DATE:

;; APPLICATION NUMBER: US 07/904,068

;; FILING DATE: 23-JUN-1992

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Smith, William M.

;; REGISTRATION NUMBER: 30,223

;; REFERENCE/DOCKET NUMBER: 14643-9-1-1

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415-326-2400

;; TELEFAX: 415-326-2422

;; INFORMATION FOR SEQ ID NO: 78:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 33 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; US-08-308-865-78

Query Match 54.1%; Score 33; DB 2; Length 33;  
Best Local Similarity 62.5%; Pred. No. 24;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAYRYGV 9

Db 9 GSYYYGM 16

RESULT 22

;; US-09-042-353-275

;; Sequence 275, Application US/09042353

;; Patent No. 6255458

;; GENERAL INFORMATION:

;; APPLICANT: Lonberg, Nils

;; APPLICANT: Kay, Robert M.

;; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for

;; PRODUCING HETEROLOGOUS ANTIBODIES

;; NUMBER OF SEQUENCES: 421

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP

;; STREET: Two Embarcadero Center, Eighth Floor

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94111-3834

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/042,353

;; FILING DATE: 13-MAR-1998

;; CLASSIFICATION: 800

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/810,279

;; FILING DATE: 17-DEC-1991

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/853,408

;; FILING DATE: 18-MAR-1992

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/904,068

TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for

NUMBER OF SEQUENCES: 152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10983  
FILING DATE: 19921217  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-2  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US92-10983-78

Query Match 54.1%; Score 33; DB 5; Length 33;  
Best Local Similarity 62.5%; Pred. No. 24;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAYRYGV 9  
|:|||||  
Db 9 GSYIYGM 16

RESULT 25  
US-08-015-973-3  
Sequence 3, Application US/08015973  
Patent No. 5604094  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-BETA  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/015,973  
FILING DATE: 10-FEB-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090

TELEFAX: (212)869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-015-973-3

Query Match 54.1%; Score 33; DB 1; Length 267;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAYRY 7  
|:|||||  
Db 192 GSYRY 197

RESULT 26  
US-08-448-164-3  
Sequence 3, Application US/08448164  
Patent No. 5925536  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-BETA  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,164  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/015,973  
FILING DATE: 10-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)790-9090  
TELEFAX: (212)869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-448-164-3

Query Match 54.1%; Score 33; DB 2; Length 267;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAYRY 7  
|:|||||  
Db 192 GSYRY 197

RESULT 27  
US-08-081-929-3  
; Sequence 3, Application US/08081929  
; Patent No. 6160090  
; GENERAL INFORMATION:  
; APPLICANT: Schlesinger, Joseph  
; APPLICANT: Barnea, Gilad  
; APPLICANT: Grumet, Martin H.  
; APPLICANT: Margolis, Richard U.  
; TITLE OF INVENTION: A NEW CLASS OF RPTases: THEIR  
; STRUCTURAL DOMAINS AND LIGANDS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/081,929  
; FILING DATE: 23-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30742  
; REFERENCE/DOCKET NUMBER: 7683-041-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-081-929-3

Query Match 54.1%; Score 33; DB 4; Length 267;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAYRY 7  
Db 192 GSYRY 197

RESULT 28  
US-07-757-390-8  
; Sequence 8, Application US/07757390  
; Patent No. 5453491  
; GENERAL INFORMATION:  
; APPLICANT: Takatsu, Kiyoshi  
; APPLICANT: Tomimaga, Akira  
; APPLICANT: Takagi, Satoshi  
; APPLICANT: Murata, Yoshiyuki  
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/757,390  
FILING DATE: 19910910  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7005-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 8698864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-757-390-8

Query Match 54.1%; Score 33; DB 1; Length 315;  
Best Local Similarity 71.4%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYRYGV 10  
Db 152 YVRFGVL 158

RESULT 29  
US-08-442-282-8  
; Sequence 8, Application US/08442282  
; Patent No. 5760204  
; GENERAL INFORMATION:  
; APPLICANT: Takatsu, Kiyoshi  
; APPLICANT: Tomimaga, Akira  
; APPLICANT: Takagi, Satoshi  
; APPLICANT: Murata, Yoshiyuki  
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,282  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/757,390  
; FILING DATE: 10-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7005-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 8698864/9741  
; TELEX: 66141 PENNIE

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-282-8

Query Match          54.1%; Score 33; DB 1; Length 315;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 YRYGVV 10
Db      152 YYRFGVL 158

RESULT 30
US-08-442-281-8
; Sequence 8, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: U.S.A.
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-8

Query Match          54.1%; Score 33; DB 1; Length 315;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 YRYGVV 10
Db      152 YYRFGVL 158

RESULT 31
US-08-939-727-8
; Sequence 8, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: U.S.A.
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-8

Query Match          54.1%; Score 33; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 YRYGVV 10
Db      152 YYRFGVL 158

RESULT 32
US-07-757-390-7
; Sequence 7, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
```

;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patentin Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/07/757,390  
;/ FILING DATE: 19910910  
;/ CLASSIFICATION: 530  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Misrock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 7005-030  
;/ TELEPHONE: 212 790-9090  
;/ TELEFAX: 212 8698864/9741  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 7:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 332 amino acids  
;/ TYPE: AMINO ACID  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-07-757-390-7

Query Match 54.1%; Score 33; DB 1; Length 332;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVV 10  
DB 169 YYRFGVL 175

RESULT 33  
US-08-442-282-7  
;/ Sequence 7, Application US/08442282  
;/ Patent No. 5760204  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Takatsu, Kiyoshi  
;/ APPLICANT: Tomimaga, Akira  
;/ APPLICANT: Takagi, Satoshi  
;/ APPLICANT: Murata, Yoshiyuki  
;/ TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor  
;/ NUMBER OF SEQUENCES: 18  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patentin Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/442,282  
;/ FILING DATE:  
;/ CLASSIFICATION: 536  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/757,390  
;/ FILING DATE: 10-SEP-1991  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Misrock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 7005-030  
;/ TELEPHONE: 212 790-9090

;/ TELEFAX: 212 8698864/9741  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 7:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 332 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-442-282-7

Query Match 54.1%; Score 33; DB 1; Length 332;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVV 10  
DB 169 YYRFGVL 175

RESULT 34  
US-08-442-281-7  
;/ Sequence 7, Application US/08442281  
;/ Patent No. 5807991  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Takatsu, Kiyoshi  
;/ APPLICANT: Tomimaga, Akira  
;/ APPLICANT: Takagi, Satoshi  
;/ APPLICANT: Murata, Yoshiyuki  
;/ TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor  
;/ NUMBER OF SEQUENCES: 18  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/442,281  
;/ FILING DATE:  
;/ CLASSIFICATION:

;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/757,390  
;/ FILING DATE: 10-SEP-1991  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Misrock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 7005-030  
;/ TELEPHONE: 212 790-9090  
;/ TELEFAX: 212 8698864/9741  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 7:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 332 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-442-281-7

Query Match 54.1%; Score 33; DB 1; Length 332;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVV 10  
DB 169 YYRFGVL 175

Db 169 YYRFGVL 175

## RESULT 35

US-08-939-727-7  
; Sequence 7, Application US/08939727  
; Patent No. 5916767  
; GENERAL INFORMATION:  
; APPLICANT: Takatsu, Kiyoshi  
; APPLICANT: Tominaga, Akira  
; APPLICANT: Takagi, Satoshi  
; APPLICANT: Murata, Yoshiyuki  
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/939,727  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/757,390  
; FILING DATE: 10-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7005-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 8698864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-939-727-7

Query Match 54.1%; Score 33; DB 2; Length 332;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YYRYGVV 10

Db 169 YYRFGVL 175

## RESULT 36

US-08-958-642-2  
; Sequence 2, Application US/08958642  
; Patent No. 5948623  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE  
; DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/958,642  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/778,423  
; FILING DATE: December 31, 1996  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-958-642-2

Query Match 54.1%; Score 33; DB 2; Length 332;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAYRYGVV 10

Db 59 GRYRTGVL 67

## RESULT 37

US-08-778-394-4  
; Sequence 4, Application US/08778394  
; Patent No. 6028184  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE  
; DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL  
; NUMBER OF SEQUENCES: 4  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA: US/08/778,394  
; FILING DATE:  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-778-394-4

Query Match 54.1%; Score 33; DB 3; Length 332;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAYRYGVV 10

Db 59 GRYRTGVL 67

## RESULT 38

US-08-778-423A-2  
; Sequence 2, Application US/08778423A  
; Patent No. 6071697  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE  
; DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/778,423A  
FILING DATE: December 31, 1996  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-778-423A-2

Query Match 54.1%; Score 33; DB 3; Length 332;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVV 10  
DB 59 GRYRTGVL 67

RESULT 39  
US-07-947-130-3  
Sequence 3, Application US/07947130  
Patent No. 5455337  
GENERAL INFORMATION:  
APPLICANT: Devos, Rene  
APPLICANT: Fiers, Walter  
APPLICANT: Tavernier, Jan  
TITLE OF INVENTION: Chimeric Interleukin-5  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mr. George M. Gould, Esq.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/947,130  
FILING DATE: 19920916  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 91810738.4  
FILING DATE: 18-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 4105/144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-235-6326  
TELEFAX: 201-235-3500

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: mouse  
CELL TYPE: B-cell precursor  
CELL LINE: B13  
US-07-947-130-3

Query Match 54.1%; Score 33; DB 1; Length 335;

Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVV 10  
DB 172 YRFGVL 178

RESULT 40  
US-08-421-822-3  
Sequence 3, Application US/08421822  
Patent No. 568256  
GENERAL INFORMATION:  
APPLICANT: Devos, Rene  
APPLICANT: Fiers, Walter  
APPLICANT: Tavernier, Jan  
TITLE OF INVENTION: Chimeric Interleukin-5  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mr. George M. Gould, Esq.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,822  
FILING DATE: 13-APR-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/947,130  
FILING DATE: 16-SEP-1992  
APPLICATION NUMBER: EP 91810738.4  
FILING DATE: 18-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 4105/144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-235-6326  
TELEFAX: 201-235-3500

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: mouse  
CELL TYPE: B-cell precursor  
CELL LINE: B13  
US-08-421-822-3

Query Match 54.1%; Score 33; DB 1; Length 335;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRYGVV 10  
DB 172 YRFGVL 178

Search completed: July 18, 2003, 15:11:49  
Job time : 13.76 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2003, 15:09:56 ; Search time 28.38 Seconds  
(without alignments)  
46.031 Million cell updates/sec

Title: US-10-007-790-7  
Perfect score: 61  
Sequence: 1 SGAYRYGVV 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pdb.\*  
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5: /cgn2\_6/ptodata/1/pubpaa/PCTU5\_PUBCOMB.pdb.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pdb.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pdb.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pdb.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	65.6	14	11	US-09-828-708-33
2	40	65.6	116	11	US-09-828-708-12
3	37	60.7	420	15	US-10-156-761-14372
4	37	60.7	560	11	US-09-912-559-3
5	37	60.7	560	11	US-09-912-559-4
6	37	60.7	560	15	US-10-172-712-32
7	36	59.0	19	12	US-09-880-748-3145
8	36	59.0	128	11	US-09-840-459-77
9	36	59.0	128	11	US-09-840-459-79
10	36	59.0	142	10	US-09-765-205-2
11	36	59.0	144	9	US-09-978-375A-322
12	36	59.0	144	11	US-09-978-295A-322
13	36	59.0	144	11	US-09-736-457-327
14	36	59.0	144	11	US-09-978-697-322
15	36	59.0	144	11	US-09-902-941-327
16	36	59.0	144	11	US-09-978-192A-322

17	36	59.0	144	11	US-09-999-832A-322.	Sequence 322, App
18	36	59.0	144	11	US-09-849-626-327	Sequence 327, App
19	36	59.0	144	12	US-09-978-189-327	Sequence 322, App
20	36	59.0	144	12	US-09-978-608A-322	Sequence 322, App
21	36	59.0	144	12	US-09-978-585A-322	Sequence 322, App
22	36	59.0	144	12	US-09-978-131A-322	Sequence 322, App
23	36	59.0	144	12	US-09-978-403A-322	Sequence 322, App
24	36	59.0	144	12	US-09-978-564A-322	Sequence 322, App
25	36	59.0	144	12	US-09-999-833A-322	Sequence 322, App
26	36	59.0	144	12	US-09-981-915A-322	Sequence 322, App
27	36	59.0	144	12	US-09-978-824-322	Sequence 322, App
28	36	59.0	144	12	US-09-918-585A-322	Sequence 322, App
29	36	59.0	144	12	US-09-978-423A-322	Sequence 322, App
30	36	59.0	144	12	US-09-978-193A-322	Sequence 322, App
31	36	59.0	144	12	US-09-999-830A-322	Sequence 322, App
32	36	59.0	144	12	US-09-978-757A-322	Sequence 322, App
33	36	59.0	144	12	US-09-978-187B-322	Sequence 322, App
34	36	59.0	144	12	US-09-978-643A-322	Sequence 322, App
35	36	59.0	144	12	US-09-476-300-327	Sequence 327, App
36	36	59.0	144	15	US-10-044-477-1	Sequence 1, Appli
37	36	59.0	144	15	US-10-044-477-3	Sequence 3, Appli
38	36	59.0	144	15	US-10-227-884-120	Sequence 120, App
39	36	59.0	144	15	US-10-230-163-120	Sequence 120, App
40	36	59.0	144	15	US-10-230-338-120	Sequence 120, App
41	36	59.0	144	15	US-10-218-631-120	Sequence 120, App
42	36	59.0	144	15	US-10-017-081A-322	Sequence 322, App
43	36	59.0	144	15	US-10-230-414-120	Sequence 120, App
44	36	59.0	144	15	US-10-017-754-327	Sequence 327, App
45	36	59.0	144	15	US-10-167-749-322	Sequence 322, App

#### ALIGNMENTS

#### RESULT 1

US-09-828-708-33  
; Sequence 33, Application US/09828708  
; Patent No. US20020146753A1  
; GENERAL INFORMATION:  
; APPLICANT: Ditzel, H.  
; APPLICANT: Burton, D.  
; APPLICANT: Schaller, M.  
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl  
; FILE REFERENCE: 1361.005US1  
; CURRENT APPLICATION NUMBER: US/09/828,708  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-828-708-33

Query Match 65.6%; Score 40; DB 11; Length 14;

Best Local Similarity 77.8%; Pred. No. 0.95;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGAYRYGVV 9

Db 4 SGAYYYGM 12

#### RESULT 2

US-09-828-708-12  
; Sequence 12, Application US/09828708  
; Patent No. US20020146753A1  
; GENERAL INFORMATION:  
; APPLICANT: Ditzel, H.  
; APPLICANT: Burton, D.  
; APPLICANT: Schaller, M.  
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl

```
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005U1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-828-708-12

Query Match      65.6%; Score 40; DB 11; Length 116;
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 SGAYRYGV 9
Db 95 SGAYRYGYM 103

RESULT 3
US-10-156-761-14372
; Sequence 14372, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14372
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; US-10-156-761-14372

Query Match      60.7%; Score 37; DB 15; Length 420;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGAYRY 7
Db 109 SGSYRY 115

RESULT 4
US-09-912-559-3
; Sequence 3, Application US/09912559
; Patent No. US20020142316A1
; GENERAL INFORMATION:
; APPLICANT: ROEMISCH, JUERGEN
; APPLICANT: STOEHR, HANS-ARNOLD
; APPLICANT: FEUSSNER, ANNETTE
; APPLICANT: LANG, WIEGAND
; APPLICANT: WEIMER, THOMAS
; APPLICANT: BECKER, MARGRET
; APPLICANT: NERLICH, CLAUDIA
; APPLICANT: MUTH-NAUMANN, GUDRUN
; TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
; TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES
; FILE REFERENCE: 06478.1457

Query Match      60.7%; Score 37; DB 11; Length 560;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGV 10
Db 519 GYYVGV 527

RESULT 5
US-09-912-559-4
; Sequence 4, Application US/09912559
; Patent No. US20020142316A1
; GENERAL INFORMATION:
; APPLICANT: ROEMISCH, JUERGEN
; APPLICANT: STOEHR, HANS-ARNOLD
; APPLICANT: FEUSSNER, ANNETTE
; APPLICANT: LANG, WIEGAND
; APPLICANT: WEIMER, THOMAS
; APPLICANT: BECKER, MARGRET
; APPLICANT: NERLICH, CLAUDIA
; APPLICANT: MUTH-NAUMANN, GUDRUN
; TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
; TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES
; FILE REFERENCE: 06478.1457
; CURRENT APPLICATION NUMBER: US/09/912,559
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: DE 100 36 641.4
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: DE 100 50 040.4
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: DE 100 52 319.6
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: DE 101 18 706.8
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-912-559-4

Query Match      60.7%; Score 37; DB 11; Length 560;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGV 10
Db 519 GYYVGV 527

RESULT 6
US-10-172-712-32
; Sequence 32, Application US/10172712
```

Publication No. US20030125232A1  
GENERAL INFORMATION:  
APPLICANT: GRIFFIN, JOHN H.  
APPLICANT: GALE, ANDREW J.  
APPLICANT: GETZOFF, ELIZABETH D.  
APPLICANT: PELLERUE, JEAN-LUC  
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS  
FILE REFERENCE: 4198-4001US1  
CURRENT APPLICATION NUMBER: US/10/172,712  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: 60/298,578  
PRIOR FILING DATE: 2001-06-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 560  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-172-712-32

Query Match 60.7%; Score 37; DB 15; Length 560;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAYRYGVV 10  
DB 519 GTYYVYGV 527

RESULT 7  
US-09-880-748-3145  
Sequence 3145, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3145  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-3145

Query Match 59.0%; Score 36; DB 12; Length 19;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9  
DB 9 SGGVYYGM 17

RESULT 8  
US-09-840-459-77  
Sequence 77, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 77  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(128)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-840-459-77

Query Match 59.0%; Score 36; DB 11; Length 128;  
Best Local Similarity 66.7%; Pred. No. 47;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9  
DB 107 SGYYVYGM 115

RESULT 9  
US-09-840-459-79  
Sequence 79, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 79  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(128)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-840-459-79

Query Match 59.0%; Score 36; DB 11; Length 128;  
Best Local Similarity 66.7%; Pred. No. 47;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGAYRYGV 9  
|||  
DB 107 SGXYYYGM 115

## RESULT 10

US-09-765-205-2  
; Sequence 2, Application US/09765205  
; Patent No. US2002034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: human  
US-09-765-205-2

Query Match 59.0%; Score 36; DB 10; Length 142;  
Best Local Similarity 62.5%; Pred. No. 52;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
|||  
DB 130 YYLYGMY 137

## RESULT 11

US-09-978-375A-322  
; Sequence 322, Application US/09978375A  
; Publication No. US20030130181A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PIC24  
; CURRENT APPLICATION NUMBER: US/09/978,375A  
; CURRENT FILING DATE: 2002-04-19  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 624  
; SEQ ID NO 322  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-375A-322

Query Match 59.0%; Score 36; DB 9; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
|||  
DB 132 YYLYGMY 139

## RESULT 12

US-09-978-295A-322  
; Sequence 322, Application US/09978295A  
; Patent No. US2002015606A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; TITLE OF INVENTION: Acids Encoding the Same



; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 11; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YYRYGVVY 11  
||| |||::|  
Db 132 YYLYGMIV 139

## RESULT 13

US-09-736-457-327

; Sequence 327, Application US/09736457

; Patent No. US20020168637A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; APPLICANT: Wang, Aijun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736.457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 327

; LENGTH: 144

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-736-457-327

Query Match 59.0%; Score 36; DB 11; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YYRYGVVY 11  
||| |||::|  
Db 132 YYLYGMIV 139

## RESULT 14

US-09-978-697-322

; Sequence 322, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.

;  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
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; PRIOR FILING DATE: 1998-04-08  
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; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
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; PRIOR APPLICATION NUMBER: 60/082804  
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; PRIOR FILING DATE: 1998-05-06  
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; PRIOR FILING DATE: 1998-05-07

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; PRIOR APPLICATION NUMBER: 60/084639  
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; PRIOR FILING DATE: 1998-05-07  
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; PRIOR APPLICATION NUMBER: 60/084643  
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; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 11; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVYGVVY 11  
||| ||:|  
Db 132 YLYGMVY 139

RESULT 15  
US-09-902-941-327  
; Sequence 327, Application US/09902941  
; Patent No. US20020172952A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Carter, Darrick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.478C17  
; CURRENT APPLICATION NUMBER: US/09/902,941  
; NUMBER OF SEQ ID NOS: 2002  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 327  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-902-941-327  
Query Match 59.0%; Score 36; DB 11; Length 144;

Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 4 YRYGVVY 11  
||| |::|  
Db 132 YLYGMIY 139

## RESULT 16

US-09-978-192A-322

; Sequence 322, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13

; PRIOR APPLICATION NUMBER: 60/078886

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083336

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
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; PRIOR APPLICATION NUMBER: 60/079920  
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; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
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; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
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; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
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; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
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101 PRIOR FILING DATE: 1998-04-27  
102 PRIOR APPLICATION NUMBER: 60/083322  
103 PRIOR FILING DATE: 1998-04-28  
104 PRIOR APPLICATION NUMBER: 60/083392  
105 PRIOR FILING DATE: 1998-04-29  
106 PRIOR APPLICATION NUMBER: 60/083495  
107 PRIOR FILING DATE: 1998-04-29  
108 PRIOR APPLICATION NUMBER: 60/083496  
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111 PRIOR FILING DATE: 1998-04-29  
112 PRIOR APPLICATION NUMBER: 60/083545  
113 PRIOR FILING DATE: 1998-04-29  
114 PRIOR APPLICATION NUMBER: 60/083554  
115 PRIOR FILING DATE: 1998-04-29  
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117 PRIOR FILING DATE: 1998-04-29  
118 PRIOR APPLICATION NUMBER: 60/083559  
119 PRIOR FILING DATE: 1998-04-29  
120 PRIOR APPLICATION NUMBER: 60/083500  
121 PRIOR FILING DATE: 1998-04-29  
122 PRIOR APPLICATION NUMBER: 60/083742  
123 PRIOR FILING DATE: 1998-04-30  
124 PRIOR APPLICATION NUMBER: 60/084366  
125 PRIOR FILING DATE: 1998-05-05  
126 PRIOR APPLICATION NUMBER: 60/084414  
127 PRIOR FILING DATE: 1998-05-06  
128 PRIOR APPLICATION NUMBER: 60/084441  
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132 PRIOR APPLICATION NUMBER: 60/084639  
133 PRIOR FILING DATE: 1998-05-07  
134 PRIOR APPLICATION NUMBER: 60/084640  
135 PRIOR FILING DATE: 1998-05-07  
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137 PRIOR FILING DATE: 1998-05-07  
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139 PRIOR FILING DATE: 1998-05-07  
140 PRIOR APPLICATION NUMBER: 60/084627  
141 PRIOR FILING DATE: 1998-05-07  
142 PRIOR APPLICATION NUMBER: 60/084643  
143 PRIOR FILING DATE: 1998-05-07  
144 PRIOR APPLICATION NUMBER: 60/085339  
145 PRIOR FILING DATE: 1998-05-13  
146 PRIOR APPLICATION NUMBER: 60/085338  
147 PRIOR FILING DATE: 1998-05-13  
148 PRIOR APPLICATION NUMBER: 60/085323  
149 PRIOR FILING DATE: 1998-05-13  
150 PRIOR APPLICATION NUMBER: 60/085582  
151 PRIOR FILING DATE: 1998-05-15  
152 PRIOR APPLICATION NUMBER: 60/085700  
153 PRIOR FILING DATE: 1998-05-15  
154 PRIOR APPLICATION NUMBER: 60/085689  
155 PRIOR FILING DATE: 1998-05-15  
156 PRIOR APPLICATION NUMBER: 60/085579  
157 PRIOR FILING DATE: 1998-05-15  
158 PRIOR APPLICATION NUMBER: 60/085580  
159 PRIOR FILING DATE: 1998-05-15  
160 PRIOR APPLICATION NUMBER: 60/085573  
161 PRIOR FILING DATE: 1998-05-15  
162 PRIOR APPLICATION NUMBER: 60/085704  
163 PRIOR FILING DATE: 1998-05-15  
164 PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 11; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YRYGVVY 11

Db 132 YLYGYMY 139

RESULT 17

US-09-999-832A-322  
; Sequence 322, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR FILING DATE: 1998-03-25  
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; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664

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; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 11; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVRYGVVY 11  
Db 132 YDYGMIY 139

RESULT 18  
US-09-849-626-327  
; Sequence 327, Application US/09849626  
; Publication No. US20020197669A1  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya

APPLICANT: Fanger, Gary  
 APPLICANT: Wang, Aijun  
 APPLICANT: Wang, Tongcong  
 APPLICANT: Switzer, Anne  
 APPLICANT: McNeill, Patricia  
 APPLICANT: Clapper, Jonathan  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 FILE REFERENCE: 210121.478C16  
 CURRENT APPLICATION NUMBER: US/09/849,626  
 CURRENT FILING DATE: 2001-05-03  
 NUMBER OF SEQ ID NOS: 1926  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 327  
 LENGTH: 144  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-849-626-327

Query Match 59.0%; Score 36; DB 11; Length 144;  
 Best Local Similarity 62.5%; Pred. No. 53;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
 Db 132 YYLYGMIV 139

# RESULT 19

US-09-978-189-322  
 : Sequence 322, Application US/09/978189  
 : Publication No. US20030004102A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Ashkenazi, Avi  
 : APPLICANT: Baker Kevin P.  
 : APPLICANT: Botstein, David  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Eaton, Dan  
 : APPLICANT: Ferrara, Napoleon  
 : APPLICANT: Filvaroff, Ellen  
 : APPLICANT: Fong, Sherman  
 : APPLICANT: Gao, Wei-Qiang  
 : APPLICANT: Gerber, Hanspeter  
 : APPLICANT: Gerritsen, Mary E.  
 : APPLICANT: Goddard, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Grimaldi, J. Christopher  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Hillan, Kenneth J.  
 : APPLICANT: Kijavini, Ivar J.  
 : APPLICANT: Kuo, Sophia S.  
 : APPLICANT: Napier, Mary A.  
 : APPLICANT: Pan, James  
 : APPLICANT: Paoni, Nicholas F.  
 : APPLICANT: Roy, Margaret Ann  
 : APPLICANT: Shelton, David L.  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tumas, Daniel  
 : APPLICANT: Williams, P. Mickey  
 : APPLICANT: Wood, William I.  
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 : FILE REFERENCE: P2630P1C7  
 : CURRENT APPLICATION NUMBER: US/09/978,189  
 : CURRENT FILING DATE: 2001-10-15  
 : PRIOR APPLICATION NUMBER: 09/918598  
 : PRIOR FILING DATE: 2001-07-30  
 : PRIOR APPLICATION NUMBER: 60/062250  
 : PRIOR FILING DATE: 1997-10-17  
 : PRIOR APPLICATION NUMBER: 60/064249  
 : PRIOR FILING DATE: 1997-11-03  
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PRIOR FILING DATE: 1998-04-15  
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
DB 132 YYLYGMIY 139

RESULT 20  
US-09-978-608A-322  
Sequence 322, Application US/09978608A  
Publication No. US20030045462A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C22  
CURRENT FILING DATE: 2001-10-16  
CURRENT APPLICATION NUMBER: US/09/978,608A  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 322  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-608A-322

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
DB 132 YYLYGMIY 139

## RESULT 21

US-09-978-585A-322  
; Sequence 322, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, James  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C15

; CURRENT APPLICATION NUMBER: US/09/978,585A

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 322

; LENGTH: 144

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-585A-322

Query Match 59.0%; Score 36; DB 12; Length 144;

Best Local Similarity 62.5%; Pred. No. 53;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY

4 YYRYGVVY 11

||| |||::|

132 YYLYGMVY 139

Db

## RESULT 22

US-09-978-191A-322  
; Sequence 322, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey

;  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
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; PRIOR FILING DATE: 1998-04-01  
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; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
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; PRIOR FILING DATE: 1998-05-13  
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; PRIOR FILING DATE: 1998-05-13  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVRYGVVY 11  
DB 132 XYLYGMIY 139

RESULT 23  
US-09-978-403A-322  
; Sequence 322, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
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PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
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;; PRIOR FILING DATE: 1998-05-15  
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Query Match 59.0%; Score 36; DB 12; Length 144;

Best Local Similarity 62.5%; Pred. No. 53;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11

Db 132 YYLYGMIV 139

RESULT 24

US-09-978-564A-322

; Sequence 322, Application US/09978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630PIC25  
;; CURRENT APPLICATION NUMBER: US/09/978,564A  
;; CURRENT FILING DATE: 2001-10-16  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-05-07  
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; PRIOR APPLICATION NUMBER: 60/085339  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YYRYGVVY 11  
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Db 132 YYLYGMIY 139

RESULT 25

US-09-999-833A-322  
; Sequence 322, Application US/0999833A  
; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC65  
; CURRENT APPLICATION NUMBER: US/09/999,833A  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 09/918585

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; PRIOR FILING DATE: 1998-05-13  
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; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YRYGVVY 11

Db 132 YDYGMIY 139

RESULT 26

US-09-981-915A-322  
; Sequence 322, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C12  
; CURRENT APPLICATION NUMBER: US/09/981,915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
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; PRIOR FILING DATE: 1997-11-13

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; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
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; PRIOR FILING DATE: 1998-03-10  
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; PRIOR APPLICATION NUMBER: 60/081817  
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7; PRIOR APPLICATION NUMBER: 60/085573  
8; PRIOR FILING DATE: 1998-05-15  
9; PRIOR APPLICATION NUMBER: 60/085704  
10; PRIOR FILING DATE: 1998-05-15  
11; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Caps 0;

QY 4 YYRYGVVY 11  
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Db 132 YYLYGMIY 139

RESULT 27

US-09-978-824-322  
; Sequence 322, Application US/09978824  
; Publication No. US2003005216A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C14  
; CURRENT APPLICATION NUMBER: US/09/978,824  
; CURRENT FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641



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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          59.0%; Score 36; DB 12; Length 144;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Caps 0;

QY      4 YRYGVVY 11
      ||| |||:|
Db      132 YLYGMIY 139

RESULT 28
US-09-918-585A-322
; Sequence 322, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR FILING DATE: 1998-03-30
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 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnuyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
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 ; APPLICANT: Kljavin, Ivar J.  
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 ; APPLICANT: Pan, James;  
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 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Daniel  
 ; APPLICANT: Tumas, Timothy A.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2630PIC21  
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 ; CURRENT FILING DATE: 2002-05-16  
 ; PRIOR APPLICATION NUMBER: 09/918585  
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Query Match 59.0%; Score 36; DB 12; Length 144;  
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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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 ; APPLICANT: Ferrara, Napoleon  
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 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
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Db 132 YLYGMVY 139

RESULT 32  
US-09-978-757A-322  
; Sequence 322, Application US/09978757A  
; Publication No. US20030083248A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C26  
CURRENT APPLICATION NUMBER: US/09/978,757A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11

Db 132 YLYGMIY 139

## RESULT 33

US-09-978-187B-322  
; Sequence 322, Application US/09978187B  
; Publication No. US2003009674A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
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; APPLICANT: Filvaroff, Ellen  
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; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC5  
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.0%; Score 36; DB 12; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YRYGVVY 11  
Db 132 YLYGMIV 139

RESULT 34  
US-09-978-643A-322  
; Sequence 322, Application US/09978643A  
; Publication No. US20030104998A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.

```
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C16
; CURRENT APPLICATION NUMBER: US/09/978,643A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-643A-322

Query Match          59.0%; Score 36; DB 12; Length 144;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 YYRYGVVY 11
      ||| |||::|
Db      132 YYLYGMIY 139

RESULT 35
US-09-476-300-327
; Sequence 327, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-327

Query Match          59.0%; Score 36; DB 12; Length 144;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 YYRYGVVY 11
      ||| |||::|
Db      132 YYLYGMIY 139

RESULT 36
US-10-044-477-1
; Sequence 1, Application US/10044477
; Publication No. US20020103342A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHOX PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,477
; FILING DATE: 10-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/365,705
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: 14-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

```
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,477
; FILING DATE: 10-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/365,705
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: 14-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0401 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1318847
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-477-1

Query Match          59.0%; Score 36; DB 15; Length 144;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 YYRYGVVY 11
      ||| |||::|
Db      132 YYLYGMIY 139

RESULT 37
US-10-044-477-3
; Sequence 3, Application US/10044477
; Publication No. US20020103342A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHOX PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,477
; FILING DATE: 10-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/365,705
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: 14-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

```
;
;
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0401 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 144 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 886769
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
US-10-044-477-3
;
Query Match          59.0%   Score 36;   DB 15;   Length 144;
Best Local Similarity 75.0%   Pred.No. 53;
Matches 6;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      4  YRYGVVY 11
      || |||
Db     132 YRYGVVY 139

RESULT 38
US-10-227-884-120
;   Sequence 120, Application US/10227884
;   Publication No. US20030027988A1
;   GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Gerritsen, Mary
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, J. Christopher
;   APPLICANT: Garney, Austin L.
;   APPLICANT: Smith, Victoria
;   APPLICANT: Stephan, Jean-Philippe F.
;   APPLICANT: Watanabe, Colin L.
;   APPLICANT: Wood, William I.
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: F3530PIC79
;   CURRENT APPLICATION NUMBER: US/10/227,884
;   CURRENT FILING DATE: 2002-08-26
;   PRIOR APPLICATION NUMBER: 10/119,480
;   PRIOR FILING DATE: 2002-04-09
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR FILING DATE: 1997-10-31
;   PRIOR FILING DATE: 1997-10-31
;   PRIOR FILING DATE: 1997-12-17
;   PRIOR FILING DATE: 1997-12-17
;   PRIOR FILING DATE: 1998-03-20
;   PRIOR FILING DATE: 1998-03-20
;   PRIOR FILING DATE: 1998-03-25
;   PRIOR FILING DATE: 1998-03-26
;   PRIOR FILING DATE: 1998-03-26
;   PRIOR FILING DATE: 1998-03-27
;   PRIOR FILING DATE: 1998-03-27
;   PRIOR FILING DATE: 1998-04-15
;   PRIOR FILING DATE: 1998-04-15
;   PRIOR APPLICATION NUMBER: 60/081955
;   PRIOR APPLICATION NUMBER: 60/082804
;
;   PRIOR FILING DATE: 1998-04-22
;   PRIOR APPLICATION NUMBER: 60/084441
;   PRIOR FILING DATE: 1998-05-06
;   PRIOR APPLICATION NUMBER: 60/085323
;   PRIOR FILING DATE: 1998-05-13
;   PRIOR APPLICATION NUMBER: 60/085579
;   PRIOR FILING DATE: 1998-05-15
;   PRIOR APPLICATION NUMBER: 60/086392
;   PRIOR FILING DATE: 1998-05-22
;   PRIOR APPLICATION NUMBER: 60/089532
;   PRIOR FILING DATE: 1998-06-17
;   PRIOR APPLICATION NUMBER: 60/089538
;   PRIOR FILING DATE: 1998-06-17
;   PRIOR APPLICATION NUMBER: 60/089905
;   PRIOR FILING DATE: 1998-06-18
;   PRIOR APPLICATION NUMBER: 60/090472
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090557
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090691
;   PRIOR FILING DATE: 1998-06-25
;   PRIOR APPLICATION NUMBER: 60/090695
;   PRIOR FILING DATE: 1998-06-25
;   PRIOR APPLICATION NUMBER: 60/091982
;   PRIOR FILING DATE: 1998-07-07
;   PRIOR APPLICATION NUMBER: 60/095302
;   PRIOR FILING DATE: 1998-08-04
;   PRIOR APPLICATION NUMBER: 60/095318
;   PRIOR FILING DATE: 1998-08-04
;   PRIOR APPLICATION NUMBER: 60/095916
;   PRIOR FILING DATE: 1998-08-10
;   PRIOR APPLICATION NUMBER: 60/096146
;   PRIOR FILING DATE: 1998-08-11
;   PRIOR APPLICATION NUMBER: 60/096791
;   PRIOR FILING DATE: 1998-08-17
;   PRIOR APPLICATION NUMBER: 60/097986
;   PRIOR FILING DATE: 1998-08-26
;   PRIOR APPLICATION NUMBER: 60/098544
;   PRIOR FILING DATE: 1998-08-31
;   PRIOR APPLICATION NUMBER: 60/099596
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099598
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099803
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099811
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099812
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099816
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/100038
;   PRIOR FILING DATE: 1998-09-11
;   PRIOR APPLICATION NUMBER: 60/100385
;   PRIOR FILING DATE: 1998-09-15
;   PRIOR APPLICATION NUMBER: 60/100390
;   PRIOR FILING DATE: 1998-09-15
;   PRIOR APPLICATION NUMBER: 60/100627
;   PRIOR FILING DATE: 1998-09-16
;   PRIOR APPLICATION NUMBER: 60/100848
;   PRIOR FILING DATE: 1998-09-18
;   PRIOR APPLICATION NUMBER: 60/100919
;   PRIOR FILING DATE: 1998-09-17
;   PRIOR APPLICATION NUMBER: 60/101477
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101738
;   PRIOR FILING DATE: 1998-09-24
;   PRIOR APPLICATION NUMBER: 60/101741
;   PRIOR FILING DATE: 1998-09-24
;   PRIOR APPLICATION NUMBER: 60/101786
;   PRIOR FILING DATE: 1998-09-25
;   PRIOR APPLICATION NUMBER: 60/101916
;   PRIOR FILING DATE: 1998-09-24
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PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/126773  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: 60/127887  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/131270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131445  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/140650  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/140723  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146963  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/149320  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149638  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/151733

PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/164418  
PRIOR FILING DATE: 1999-11-09  
PRIOR APPLICATION NUMBER: 60/166361  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/169445  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835

Query Match 59.0%; Score 36; DB 15; Length 144;  
Best Local Similarity 62.5%; Pred. No. 53;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YRYGVVY 11  
|||::|

Db 132 YLYGMIY 139

## RESULT 39

US-10-230-163-120  
; Sequence 120, Application US/10230163  
; Publication No. US200303635A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC96  
; CURRENT APPLICATION NUMBER: US/10/230,163  
; CURRENT FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER:	60/086392
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/089532
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089538
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089905
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090691
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090695
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/095302
PRIOR FILING DATE:	1998-08-04
PRIOR APPLICATION NUMBER:	60/095318
PRIOR FILING DATE:	1998-08-04
PRIOR APPLICATION NUMBER:	60/095916
PRIOR FILING DATE:	1998-08-10
PRIOR APPLICATION NUMBER:	60/096146
PRIOR FILING DATE:	1998-08-11
PRIOR APPLICATION NUMBER:	60/096791
PRIOR FILING DATE:	1998-08-17
PRIOR APPLICATION NUMBER:	60/097986
PRIOR FILING DATE:	1998-08-26
PRIOR APPLICATION NUMBER:	60/098544
PRIOR FILING DATE:	1998-08-31
PRIOR APPLICATION NUMBER:	60/099596
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099598
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PRIOR APPLICATION NUMBER:	60/099811
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/100038
PRIOR FILING DATE:	1998-09-11
PRIOR APPLICATION NUMBER:	60/100385
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100390
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100627
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100848
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/101477
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101738
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101786
PRIOR FILING DATE:	1998-09-25
PRIOR APPLICATION NUMBER:	60/101916
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101922
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/106178
PRIOR FILING DATE:	1998-10-28
PRIOR APPLICATION NUMBER:	60/106248
PRIOR FILING DATE:	1998-10-29
PRIOR APPLICATION NUMBER:	60/106464

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; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      59.0% Score 36; DB 15; Length 144;
Best Local Similarity 62.5% Pred.No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 YRYGVVY 11
      ||| |::|
Db     132 YLYGMIY 139

RESULT 40
US-10-230-338-120
; Sequence 120, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 120
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-120

Query Match      59.0% Score 36; DB 15; Length 144;
Best Local Similarity 62.5% Pred.No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 YRYGVVY 11
      ||| |::|
Db     132 YLYGMIY 139
```

